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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:36:08 ; Search time 23 Seconds
(without alignments)
17.957 Million cell updates/sec

Title: US-09-610-118-66
Perfect score: 39
Sequence: 1 SYDSNVV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	22	56.4	7	1	US-08-044-547-10	Sequence 10, Appl
2	22	56.4	7	4	US-09-708-606-21	Sequence 21, Appl
3	22	56.4	8	2	US-08-466-860-21	Sequence 21, Appl
4	22	56.4	8	2	US-08-466-860-24	Sequence 24, Appl
5	22	56.4	8	3	US-08-472-040A-21	Sequence 21, Appl
6	22	56.4	8	3	US-08-472-040A-24	Sequence 24, Appl
7	22	56.4	8	3	US-08-756-849-116	Sequence 116, Appl
8	22	56.4	8	3	US-08-276-776-21	Sequence 21, Appl
9	22	56.4	8	3	US-08-276-776-24	Sequence 24, Appl
10	22	56.4	8	3	US-08-471-209-21	Sequence 21, Appl
11	22	56.4	8	3	US-08-471-209-24	Sequence 24, Appl
12	22	56.4	8	4	US-08-055-006-3	Sequence 3, Appl
13	22	56.4	8	4	US-09-708-606-18	Sequence 18, Appl
14	22	56.4	8	4	US-09-708-606-27	Sequence 27, Appl
15	21	53.8	7	1	US-08-201-046A-11	Sequence 11, Appl
16	21	53.8	7	2	US-08-540-412-107	Sequence 107, Appl
17	21	53.8	7	2	US-08-540-412-144	Sequence 144, Appl
18	21	53.8	7	2	US-08-926-412-57	Sequence 57, Appl
19	21	53.8	7	3	US-08-756-849-120	Sequence 120, Appl
20	21	53.8	7	3	US-09-051-342-107	Sequence 107, Appl
21	21	53.8	7	3	US-09-051-342-144	Sequence 144, Appl
22	21	53.8	7	3	US-08-468-161-107	Sequence 107, Appl
23	21	53.8	7	3	US-08-468-161-144	Sequence 144, Appl
24	21	53.8	7	3	US-09-051-759-107	Sequence 107, Appl
25	21	53.8	7	3	US-09-051-759-144	Sequence 144, Appl
26	21	53.8	7	4	US-09-254-892-57	Sequence 57, Appl
27	21	53.8	7	4	US-09-691-523A-47	Sequence 47, Appl

28	21	53.8	7	4	US-09-989-789-169	Sequence 169, App
29	21	53.8	7	4	US-09-989-789-170	Sequence 170, App
30	21	53.8	7	4	US-09-989-789-196	Sequence 196, App
31	21	53.8	7	4	US-09-989-789-197	Sequence 197, App
32	21	53.8	7	4	US-09-989-789-277	Sequence 277, App
33	21	53.8	7	4	US-09-989-789-333	Sequence 333, App
34	21	53.8	7	4	US-09-989-789-384	Sequence 384, App
35	21	53.8	7	4	US-09-989-789-385	Sequence 385, App
36	21	53.8	7	4	US-09-989-789-386	Sequence 386, App
37	21	53.8	7	4	US-09-989-789-742	Sequence 742, App
38	21	53.8	7	4	US-09-989-789-1888	Sequence 1888, Ap
39	21	53.8	7	4	US-09-989-789-1894	Sequence 1894, Ap
40	21	53.8	7	4	US-09-989-789-2514	Sequence 2514, Ap
41	21	53.8	7	4	US-09-989-789-3878	Sequence 3878, Ap
42	21	53.8	7	5	PCT-US95-08156-107	Sequence 107, App
43	21	53.8	7	5	PCT-US95-08156-144	Sequence 144, App
44	21	53.8	8	1	US-08-446-206B-18	Sequence 18, Appl
45	21	53.8	8	2	US-08-807-030-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-044-547-10
; Sequence 10, Application US/08044547
; Patent No. 5324715
; GENERAL INFORMATION:
; APPLICANT: Connolly, Thomas M.
; APPLICANT: Keller, Paul M.
; TITLE OF INVENTION: Protein for Inhibiting
; TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,547
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/594,917
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parr, Richard S.
; REGISTRATION NUMBER: 32,586
; REFERENCE/DOCKET NUMBER: 18053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4958
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-044-547-10

Query Match 56.4%; Score 22; DB 1; Length 7;
Best Local Similarity 66.7%; Pred No. 3e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 2; Gaps 0;

QY 2 YDGSNV 7
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Db 2 YDQNV 7

RESULT 2
US-09-708-606-21
; Sequence 21, Application US/09708606
; Patent No. 6682740
; GENERAL INFORMATION:
; APPLICANT: ERDEI, Anna
; APPLICANT: PECHT, Israel
; TITLE OF INVENTION: PEPTIDES DERIVED FROM COMPLEMENT PEPTIDE C3a SEQUENCE
; TITLE OF INVENTION: AND ANTIALLERGIC COMPOSITIONS
; FILE REFERENCE: ERDEI-1A
; CURRENT APPLICATION NUMBER: US/09/708,606
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/446,464
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/IL98/00292
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residue 7 may be amidated
US-09-708-606-21

Query Match 56.4%; Score 22; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DGSNV 8
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Db 1 DSSNYI 6

RESULT 3
US-08-466-860-21
; Sequence 21, Application US/08466860
; Patent No. 5985552
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 24-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-466-860-21

Query Match 56.4%; Score 22; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-466-860-21

Query Match 56.4%; Score 22; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSN 6
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Db 1 SSDSSN 6

RESULT 4
US-08-466-860-24
; Sequence 24, Application US/08466860
; Patent No. 5985552
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 24-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-466-860-24

Query Match 56.4%; Score 22; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 SYDSSN 6
    1
Db 1 SSDSSN 6

RESULT 5
US-08-472-040A-21
; Sequence 21, Application US/08472040A
; Patent No. 6090387
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,040A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 1641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal
; US-08-472-040A-21

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSN 6
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Db 1 SSDSSN 6

RESULT 6
US-08-472-040A-24
; Sequence 24, Application US/08472040A
; Patent No. 6090387
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
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; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,040A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 1641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal
; US-08-472-040A-24

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSN 6
    1
Db 1 SSDSSN 6

RESULT 7
US-08-756-849-116
; Sequence 116, Application US/08756849
; Patent No. 6093810
; GENERAL INFORMATION:
; APPLICANT: Bird, David Mck.
; APPLICANT: Wilson, Mark A.
; TITLE OF INVENTION: Nematode-Induced Genes in Tomato
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,849
; FILING DATE: 26-NOV-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,474
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-053510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
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; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-756-849-116

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSS 5
Db 4 SYDSS 8

RESULT 8
US-08-276-776-21
; Sequence 21, Application US/08276776
; Patent No. 6207645
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,867
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-776-21

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSS 6
Db 1 SYDSS 6

RESULT 10
US-08-471-209-21
; Sequence 21, Application US/08471209
; Patent No. 6221352
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,867
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-776-21

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSS 6
Db 1 SYDSS 6

RESULT 9
US-08-276-776-24
; Sequence 24, Application US/08276776
; Patent No. 6207645
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,867
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-776-24

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSS 6
Db 1 SYDSS 6

RESULT 10
US-08-471-209-21
; Sequence 21, Application US/08471209
; Patent No. 6221352
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,867
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-776-24

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSS 6
Db 1 SYDSS 6

RESULT 10
US-08-471-209-21
; Sequence 21, Application US/08471209
; Patent No. 6221352
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,867
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-276-776-24

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSS 6
Db 1 SYDSS 6

;/ CITY: SAN DIEGO
;/ STATE: CALIFORNIA
;/ COUNTRY: UNITED STATES
;/ ZIP: 92122
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/471,209
;/ FILING DATE:
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/813,867
;/ FILING DATE: 24-DEC-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: CAMPBELL, CATHRYN
;/ REGISTRATION NUMBER: 31,815
;/ REFERENCE/DOCKET NUMBER: P-IM 9107
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 619-535-9001
;/ TELEFAX: 619-535-8949
;/ INFORMATION FOR SEQ ID NO: 21:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FRAGMENT TYPE: N-terminal
;/ US-08-471-209-21

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYSDSN 6
Db 1 SSDSSN 6

RESULT 11
US-08-471-209-24
;/ Sequence 24, Application US/08471209
;/ Patent No. 6221352
;/ GENERAL INFORMATION:
;/ APPLICANT: HOWELL, MARK D.
;/ APPLICANT: BROSTOFF, STEVEN W.
;/ APPLICANT: CARLO, DENNIS J.
;/ TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
;/ TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
;/ TITLE OF INVENTION: POPULATIONS
;/ NUMBER OF SEQUENCES: 75
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: CAMPBELL AND FLORES
;/ STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;/ CITY: SAN DIEGO
;/ STATE: CALIFORNIA
;/ COUNTRY: UNITED STATES
;/ ZIP: 92122
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/471,209
;/ FILING DATE:
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/813,867
;/ FILING DATE: 24-DEC-1991
;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: CAMPBELL, CATHRYN
;/ REGISTRATION NUMBER: 31,815
;/ REFERENCE/DOCKET NUMBER: P-IM 9107
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 619-535-9001
;/ TELEFAX: 619-535-8949
;/ INFORMATION FOR SEQ ID NO: 24:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FRAGMENT TYPE: N-terminal
;/ US-08-471-209-24

Query Match 56.4%; Score 22; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYSDSN 6
Db 1 SSDSSN 6

RESULT 12
US-08-055-006-3
;/ Sequence 3, Application US/08055006
;/ Patent No. 6464978
;/ GENERAL INFORMATION:
;/ APPLICANT: BROSTOFF, STEVEN W.
;/ APPLICANT: WILSON, DARCY B.
;/ APPLICANT: SMITH, LAWRENCE R.
;/ APPLICANT: GOLD, DANIEL P.
;/ APPLICANT: CARLO, DENNIS J.

TITLE OF INVENTION: Vaccination and Methods Against Multiple
Sclerosis Resulting From Pathogenic Responses By Specific T
Cell Populations

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-055-006-3

Query Match 56.4%; Score 22; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSN 6
| | | | |
Db 1 SSDSSN 6

RESULT 13
US-09-708-606-18
; Sequence 18, Application US/09708606
; Patent No. 6682740
; GENERAL INFORMATION:
; APPLICANT: ERDEI, Anna
; APPLICANT: PECHT, Israel
; TITLE OF INVENTION: PEPTIDES DERIVED FROM COMPLEMENT PEPTIDE C3a SEQUENCE
; TITLE OF INVENTION: AND ANTIALLERGIC COMPOSITIONS
; FILE REFERENCE: ERDEI-1A
; CURRENT APPLICATION NUMBER: US/09/708,606
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/446,464
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/IL98/00292
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Xaa at pos. 1 is either present or absent. When
; OTHER INFORMATION: Xaa at pos. 1 is present it is Leu; when Xaa at
; OTHER INFORMATION: pos. 1 is absent, the Asp at pos. 2 may be modified
; OTHER INFORMATION: with a lower alkanoyl group.
; OTHER INFORMATION: Xaa at pos. 8 is either present or absent. When
; OTHER INFORMATION: Xaa at pos. 8 is present it is Arg, Arg-NH2,
; OTHER INFORMATION: or Arg (agmatine).
US-09-708-606-18

Query Match 56.4%; Score 22; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05; 1; Mismatches 0; Gaps 0;
Matches 4; Conservative 1; Indels 0; Gaps 0;

QY 3 DSSNVV 8
| | | | |
Db 2 DSSNYI 7

RESULT 14
US-09-708-606-27
; Sequence 27, Application US/09708606
; Patent No. 6682740
; GENERAL INFORMATION:
; APPLICANT: ERDEI, Anna
; APPLICANT: PECHT, Israel
; TITLE OF INVENTION: PEPTIDES DERIVED FROM COMPLEMENT PEPTIDE C3a SEQUENCE
; TITLE OF INVENTION: AND ANTIALLERGIC COMPOSITIONS
; FILE REFERENCE: ERDEI-1A
; CURRENT APPLICATION NUMBER: US/09/708,606
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/446,464
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/IL98/00292
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residue 6 may be amidated
US-09-708-606-27

Query Match 56.4%; Score 22; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05; 1; Mismatches 0; Gaps 0;
Matches 4; Conservative 1; Indels 0; Gaps 0;

QY 3 DSSNVV 8
| | | | |
Db 1 DSSNYI 6

RESULT 15
US-08-201-046A-11
; Sequence 11, Application US/08201046A
; Patent No. 5545719
; GENERAL INFORMATION:
; APPLICANT: Shashoua, Victor E.
; TITLE OF INVENTION: NERVE GROWTH PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Ave.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,046A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: N0260/7013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-201-046A-11

Query Match 53.8%; Score 21; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
| | | | |
Db 4 SYDS 7

Search completed: June 8, 2004, 19:39:31
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 19:37:34 ; Search time 41 Seconds
(without alignments)
54.895 Million cell updates/sec

Title: US-09-610-118-66
Perfect score: 39
Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 64135

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgm2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	9	US-09-832-312-66
2	39	100.0	8	11	US-09-829-495-66
3	28	71.8	8	9	US-09-809-517A-22
4	24	61.5	7	12	US-10-384-060-64
5	21	53.8	5	12	US-09-065-902-1
6	21	53.8	6	12	US-09-065-902-12
7	21	53.8	7	9	US-09-896-251-13
8	21	53.8	7	9	US-09-896-245-13
9	21	53.8	7	9	US-09-989-789-169
10	21	53.8	7	9	US-09-989-789-170
11	21	53.8	7	9	US-09-989-789-196
12	21	53.8	7	9	US-09-989-789-197
13	21	53.8	7	9	US-09-989-789-277
14	21	53.8	7	9	US-09-989-789-333
15	21	53.8	7	9	US-09-989-789-384

16	21	53.8	7	9	US-09-989-789-385	Sequence 385, App
17	21	53.8	7	9	US-09-989-789-386	Sequence 386, App
18	21	53.8	7	9	US-09-989-789-742	Sequence 742, App
19	21	53.8	7	9	US-09-989-789-1888	Sequence 1888, App
20	21	53.8	7	9	US-09-989-789-1894	Sequence 1894, App
21	21	53.8	7	9	US-09-989-789-2514	Sequence 2514, App
22	21	53.8	7	9	US-09-989-789-3878	Sequence 3878, App
23	21	53.8	7	9	US-09-989-244-13	Sequence 13, Appl
24	21	53.8	7	10	US-09-990-186-169	Sequence 169, App
25	21	53.8	7	10	US-09-990-186-170	Sequence 170, App
26	21	53.8	7	10	US-09-990-186-196	Sequence 196, App
27	21	53.8	7	10	US-09-990-186-197	Sequence 197, App
28	21	53.8	7	10	US-09-990-186-277	Sequence 277, App
29	21	53.8	7	10	US-09-990-186-333	Sequence 333, App
30	21	53.8	7	10	US-09-990-186-384	Sequence 384, App
31	21	53.8	7	10	US-09-990-186-385	Sequence 385, App
32	21	53.8	7	10	US-09-990-186-386	Sequence 386, App
33	21	53.8	7	10	US-09-990-186-742	Sequence 742, App
34	21	53.8	7	10	US-09-990-186-1888	Sequence 1888, App
35	21	53.8	7	10	US-09-990-186-1894	Sequence 1894, App
36	21	53.8	7	10	US-09-990-186-2514	Sequence 2514, App
37	21	53.8	7	10	US-09-990-186-3878	Sequence 3878, App
38	21	53.8	7	10	US-09-989-994-169	Sequence 169, App
39	21	53.8	7	10	US-09-989-994-170	Sequence 170, App
40	21	53.8	7	10	US-09-989-994-196	Sequence 196, App
41	21	53.8	7	10	US-09-989-994-197	Sequence 197, App
42	21	53.8	7	10	US-09-989-994-277	Sequence 277, App
43	21	53.8	7	10	US-09-989-994-333	Sequence 333, App
44	21	53.8	7	10	US-09-989-994-384	Sequence 384, App
45	21	53.8	7	10	US-09-989-994-385	Sequence 385, App

ALIGNMENTS

RESULT 1
US-09-832-312-66
; Sequence 66, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Rusfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-66

Query Match 100.0%; Score 39; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
Db 1 SYDSSNVV 8

RESULT 2
US-09-829-495-66
; Sequence 66, Application US/09829495

; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-66

Query Match 100.0%; Score 39; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
| | | | | | | |
Db 1 SYDSSNVV 8

RESULT 3
US-09-809-517A-22
; Sequence 22, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1e1 methods for displaying (poly)peptides/prote
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-22

Query Match 71.8%; Score 28; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 7
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Db 2 SYDSGNL 8

RESULT 4
US-10-384-060-64

; Sequence 64, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 33 CDR2 sequence
US-10-384-060-64

Query Match 61.5%; Score 24; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSN 6
| | | | |
Db 1 YDASN 5

RESULT 5
US-09-065-902-1
; Sequence 1, Application US/09065902
; Publication No. US20020086444A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; Kim, Tae-Wan
; TITLE OF INVENTION: A Purified 20 kDa Presenilin 2
; C-terminal Fragment and Methods of Screening for Compounds
; that Inhibit Proteolysis of Presenilin 2
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,902
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,262
; FILING DATE: 24-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.4270001/JAG/S-S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-065-902-1

Query Match 53.8%; Score 21; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. le+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
Db 2 SYDS 5

RESULT 6
US-09-065-902-12
Sequence 12, Application US/09065902
Publication No. US2002008444A1
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
Kim, Tae-Wan
TITLE OF INVENTION: A Purified 20 kDa Presenilin 2
C-terminal Fragment and Methods of Screening for Compounds
that Inhibit Proteolysis of Presenilin 2
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,902
FILING DATE: 24-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,262
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.4270001/JAG/S-S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-065-902-12

Query Match 53.8%; Score 21; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. le+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
Db 2 SYDS 5

US-09-896-251-13
Sequence 13, Application US/09896251
Patent No. US20020041880A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
DeFeo-Jones, Deborah
APPLICANT: Heimbrook, David C.
APPLICANT: Jones, Raymond E.
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: 20662
CURRENT APPLICATION NUMBER: US/09/896,251
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,934
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
NAME/KEY: ACETYLATION
LOCATION: (1)...(1)
OTHER INFORMATION: acetylated N-terminus amino acid
US-09-896-251-13

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. le+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
Db 1 SYQSSSL 7

US-09-896-245-13
Sequence 13, Application US/09896245
Patent No. US20020042375A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Heimbrook, David C.
APPLICANT: Yao, Siu-Long
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: 20664Y
CURRENT APPLICATION NUMBER: US/09/896,245
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/216,217
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
NAME/KEY: ACETYLATION
LOCATION: (1)...(1)
OTHER INFORMATION: acetylated N-terminus amino acid
US-09-896-245-13

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. le+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
Db 1 SYQSSSL 7

```
Db 1 SYQSSSL 7

RESULT 9
US-09-989-789-169
; Sequence 169, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-169

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
Db 1 DSSNL 5

RESULT 10
US-09-989-789-170
; Sequence 170, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-170

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
Db 1 DSSNL 5

RESULT 11
US-09-989-789-196
; Sequence 196, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-196

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
Db 1 DSSNL 5

RESULT 12
US-09-989-789-197
; Sequence 197, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-197

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
Db 1 DSSNL 5

RESULT 13
US-09-989-789-277
; Sequence 277, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 277
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-277

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
Db 1 DSSNL 5
```


Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
| | | |
Db 1 DSSNL 5

RESULT 14

US-09-989-789-333
; Sequence 333, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 333
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-333

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
| | | |
Db 1 DSSNL 5

RESULT 15

US-09-989-789-384
; Sequence 384, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 384
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-384

Query Match 53.8%; Score 21; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSSNV 7
| | | |
Db 1 DSSNL 5

Search completed: June 8, 2004, 19:43:27
Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 19:30:13 ; Search time 23 Seconds
(without alignments)
15.712 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38
Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 57228

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6C-TUS-COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	73.7	7	1	US-08-264-093-19
2	23	60.5	6	4	US-08-757-425B-36
3	23	60.5	7	4	US-09-383-667-31
4	22	57.9	4	1	US-08-377-687-17
5	22	57.9	4	2	US-08-777-192-17
6	22	57.9	4	3	US-08-971-982-17
7	22	57.9	7	1	US-07-988-925-5
8	22	57.9	7	2	US-08-362-780-5
9	22	57.9	7	4	US-08-918-148-51
10	21	55.3	6	4	US-09-077-948A-135
11	20	52.6	7	4	US-09-383-667-25
12	19	50.0	5	4	US-09-187-859-3201
13	19	50.0	5	4	US-09-839-542B-3201
14	19	50.0	5	4	US-09-535-852-545
15	19	50.0	6	4	US-09-187-859-3202
16	19	50.0	6	4	US-08-757-425B-32
17	19	50.0	6	4	US-09-839-542B-3202
18	19	50.0	6	4	US-09-535-852-546
19	19	50.0	7	2	US-08-672-345C-32
20	19	50.0	7	2	US-08-672-345C-35
21	19	50.0	7	3	US-09-214-095D-32
22	19	50.0	7	3	US-09-214-095D-35
23	19	50.0	7	4	US-09-187-859-3203
24	19	50.0	7	4	US-09-761-962A-34
25	19	50.0	7	4	US-09-839-542B-3203
26	19	50.0	7	4	US-09-535-852-547
27	18	47.4	5	4	US-09-057-897-10

28 18 47.4 6 4 US-09-057-897-23 Sequence 23, Appl
29 18 47.4 7 1 US-07-956-848A-36 Sequence 36, Appl
30 18 47.4 7 1 US-08-259-550A-47 Sequence 47, Appl
31 18 47.4 7 1 US-08-471-956-36 Sequence 36, Appl
32 18 47.4 7 2 US-08-672-345C-38 Sequence 38, Appl
33 18 47.4 7 2 US-08-672-345C-74 Sequence 74, Appl
34 18 47.4 7 3 US-08-776-059-48 Sequence 48, Appl
35 18 47.4 7 3 US-09-214-095D-38 Sequence 38, Appl
36 18 47.4 7 3 US-09-214-095D-74 Sequence 74, Appl
37 18 47.4 7 4 US-09-057-897-9 Sequence 9, Appl
38 18 47.4 7 4 US-09-057-897-16 Sequence 16, Appl
39 18 47.4 7 4 US-09-057-897-26 Sequence 26, Appl
40 18 47.4 7 4 US-09-057-897-27 Sequence 27, Appl
41 18 47.4 7 4 US-09-057-897-28 Sequence 28, Appl
42 18 47.4 7 4 US-08-918-148-10 Sequence 10, Appl
43 18 47.4 7 4 US-09-383-667-14 Sequence 14, Appl
44 17 44.7 4 1 US-08-584-579-10 Sequence 10, Appl
45 17 44.7 5 1 US-07-901-717-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-264-093-19
; Sequence 19, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
; US-08-264-093-19

Query Match 73.7%; Score 28; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7

DB 2 NNORPS 7

```
RESULT 2
US-08-757-425B-36
; Sequence 36, Application US/08757425B
; Patent No. 6500660
; GENERAL INFORMATION:
; APPLICANT: Pastrez, Jacques
; TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity
; FILE REFERENCE: 100390-09640
; CURRENT APPLICATION NUMBER: US/08/757,425B
; CURRENT FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mimotope
US-08-757-425B-36

Query Match          60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNRP 6
Db 1 EENRP 6

RESULT 3
US-09-383-667-31
; Sequence 31, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P166182
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 31
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-31

Query Match          60.5%; Score 23; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DNORPS 7
Db 2 NDQPS 7

RESULT 4
US-08-377-687-17
; Sequence 17, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKART, WILLEM F.
```

```
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /08/377,687
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-377-687-17

Query Match          57.9%; Score 22; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQ 4
Db 1 EDNQ 4

RESULT 5
US-08-777-192-17
; Sequence 17, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKART, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-777-192-17

Query Match 57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 EDNQ 4
DB 1 EDNQ 4

RESULT 6
US-08-971-982-17
Sequence 17, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NOV-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-971-982-17

Query Match 57.9%; Score 22; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 EDNQ 4
DB 1 EDNQ 4

RESULT 7
US-07-988-925-5
Sequence 5, Application US/07988925
Patent No. 5585097
GENERAL INFORMATION:
APPLICANT: Bolt, Sarah L.
APPLICANT: Clark, Michael R.
APPLICANT: Gorman, Scott D.
APPLICANT: Routledge, Edward G.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
STREET: 11th Floor, 1100 No. 5585097th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,925
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-988-925-5

Query Match 57.9%; Score 22; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;

QY 1 EDNORP 6
:|:|
Db 1 DDDKRP 6

RESULT 8

US-08-362-780-5
; Sequence 5, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Walldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-5

Query Match 57.9%; Score 22; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORP 6
:|:|
Db 1 DDDKRP 6

RESULT 9

US-08-918-148-51
; Sequence 51, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.

; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 51
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: 12E10scfv VL CDR2
; LOCATION: 1-7
; OTHER INFORMATION:
US-08-918-148-51

Query Match 57.9%; Score 22; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNORPS 7
:|:|
Db 1 EGSKRPS 7

RESULT 10

US-09-077-948A-135
; Sequence 135, Application US/09077948A
; Patent No. 6605698
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Melloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 109846-257(SYN-035)
; CURRENT APPLICATION NUMBER: US/09/077,948A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-948A-135

Query Match 55.3%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QRPSS 7
:|:|
Db 3 QRPSS 6

RESULT 11

US-09-383-667-25
; Sequence 25, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.

; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggestt, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 25
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-25

Query Match 52.6%; Score 20; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
| :|||
Db 1 EVSKRPS 7

RESULT 12

US-09-187-859-3201
; Sequence 3201, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3201
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3201

Query Match 50.0%; Score 19; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQR 5
| :|||
Db 1 DNQR 4

RESULT 13

US-09-839-542B-3201
; Sequence 3201, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1

; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3201
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-839-542B-3201

Query Match 50.0%; Score 19; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQR 5
| :|||
Db 1 DNQR 4

RESULT 14

US-09-535-852-545
; Sequence 545, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOGOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising desomglein
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-535-852-545

Query Match 50.0%; Score 19; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQR 5
| :|||
Db 1 DNQR 4

RESULT 15

US-09-187-859-3202
; Sequence 3202, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3202
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3202

Query Match      50.0%; Score 19; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNQR 5
      |||:
Db      1 DNQK 4
```

Search completed: June 8, 2004, 19:35:11
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:35:18 ; Search time 20 Seconds
(without alignments)
38.477 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSNVV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*

- 1: Pirl:*
- 2: Pirl2:*
- 3: Pirl3:*
- 4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	53.8	8	S11078	glucose-6-phosphat
2	20	51.3	8	A38887	T-cell receptor ga
3	15	38.5	5	A37114	hypoxanthine phosph
4	14	35.9	4	A40135	branched-chain-am
5	14	35.9	8	PA0035	protein QA300039 -
6	14	35.9	8	PT0030	inulinase (EC 3.2.
7	13	33.3	7	PT0620	T-cell receptor be
8	13	33.3	8	XGHUEU	urine glycopeptide
9	13	33.3	8	E47393	neuropeptide calla
10	12	30.8	4	A37832	phenol 2-monooxyge
11	12	30.8	5	I40469	dnazx-like protein
12	12	30.8	5	PT0308	Ig heavy chain CRD
13	12	30.8	5	PT0600	T-cell receptor be
14	12	30.8	5	PT0580	T-cell receptor be
15	12	30.8	6	S02617	alcohol dehydrogen
16	12	30.8	6	A31263	dihydrofolate redu
17	12	30.8	7	A15398	choline oxidase (E
18	11	28.2	5	PT0695	T-cell receptor be
19	11	28.2	7	1 NYE7	hypothalamic hepta
20	11	28.2	7	A60139	fatty-acid synthas
21	11	28.2	7	I40504	hypothetical prote
22	11	28.2	7	I56695	hypothetical l2 pr
23	11	28.2	8	S21288	lectin - potato (f
24	11	28.2	8	D27867	homeotic protein U
25	10	25.6	5	A26830	mitosis inhibiting
26	10	25.6	5	D60274	major protein anti
27	10	25.6	5	S51077	alpha-amylase - ri
28	10	25.6	6	A61419	sarcosine dehydrog
29	10	25.6	6	A44916	mosquitocidal toxi

30	10	25.6	6	2	PT0532	T-cell receptor be
31	10	25.6	6	2	PT0616	T-cell receptor be
32	10	25.6	6	2	PT0641	T-cell receptor be
33	10	25.6	6	2	PT0650	T-cell receptor be
34	10	25.6	7	1	A61324	dermorphin - Rohde
35	10	25.6	7	2	PC1316	large granule L3 c
36	10	25.6	7	2	S68004	lucolin, 7SK chain
37	10	25.6	7	2	PT0520	T-cell receptor be
38	10	25.6	7	2	PT0521	T-cell receptor be
39	10	25.6	7	2	A38081	amine oxidase (cop
40	10	25.6	8	2	A32523	peptidyl-dipeptida
41	10	25.6	8	2	E60588	sperm-activating p
42	10	25.6	8	2	S78036	ribosomal protein
43	10	25.6	8	2	US0316	leucokinin VI - Ma
44	10	25.6	8	2	A14683	aspartate transami
45	10	25.6	8	2	PT0716	T-cell receptor be

ALIGNMENTS

RESULT 1

S11078
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)
C:Species: Pichia jadinii, Candida utilis
C:Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #text_change 05-Aug-1994
C:Accession: S11078
R:Egestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol
FBSS Lett. 269, 194-196, 1990
A>Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations
A:Reference number: S11074; MUID:90353571; PMID:2387402
A:Accession: S11078
A:Molecule type: protein
A:Residues: 1-8 <EGE>
A>Note: the source is designated as Pichia jadinii
C:Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway
F1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 53.8%; Score 21; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4

DB 1 SYDS 4

RESULT 2

A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:WhetSELL, M.; Mosley, R.L.; WhetSELL, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A>Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: A38887
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHE>
C:Keywords: T-cell receptor

Query Match 51.3%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSS 5

DB 2 SWDSS 6

RESULT 3

A37114
 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragment)
 C;Species: Schistosoma mansoni
 C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
 C;Accession: A37114
 R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
 J. Biol. Chem. 265, 13528-13532, 1990
 A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Further characterization and purification of the enzyme
 A;Reference number: A37114; MUID:90337955; PMID:2199439
 A;Accession: A37114
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <YUA>
 C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 38.5%; Score 15; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSNV 7
 Db 2 SSNM 5

RESULT 4
 A40135
 branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)
 N;Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
 C;Accession: A40135
 R;Hutson, S.M.; Wallin, R.; Hall, T.R.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: A40135
 A;Accession: A40135
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <HUT>
 C;Keywords: aminotransferase; mitochondrion

Query Match 35.9%; Score 14; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSN 6
 Db 2 SSN 4

RESULT 5
 PA0035
 protein QA300039 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0035
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to GIPDB, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0035
 A;Molecule type: protein
 A;Residues: 1-8 <KAM>
 A;Experimental source: stem

Query Match 35.9%; Score 14; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DSSNV 7
 Db 4 DNSXV 8

RESULT 6
 PT0030
 inulinase (EC 3.2.1.7) - Aspergillus ficum (fragment)
 N;Alternate names: inulase
 C;Species: Aspergillus ficum
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C;Accession: PT0030
 R;Etalibi, M.; Baratti, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990
 A;Title: Molecular and kinetic properties of Aspergillus ficum inulinases.
 A;Reference number: PT0030; MUID:90344234; PMID:11368526
 A;Accession: PT0030
 A;Molecule type: protein
 A;Residues: 1-8 <ETT>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 35.9%; Score 14; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYD 3
 Db 2 NYD 4

RESULT 7
 PT0620
 T-cell receptor beta chain V-D-J region (120-200) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0620
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0620
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-7 <PEE>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 33.3%; Score 13; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSNV 7
 Db 2 SSDV 5

RESULT 8
 XGHUEU
 urine glycopeptide - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: A03188
 R;Lote, C.J.; Weiss, J.B.
 Biochem. J. 123, 25P, 1971
 A;Title: Identification in urine of a low-molecular-weight polar glycopeptide containing a hexose
 A;Reference number: A03188; MUID:72062338; PMID:5126885
 A;Accession: A03188
 A;Molecule type: protein
 A;Residues: 1-8 <LOT>
 C;Comment: The identity of the glycoprotein from which this peptide is derived is unknown. It has also been found (see PIR:XGHUEU).
 C;Superfamily: unassigned animal peptides
 C;Keywords: glycoprotein
 F;1/Binding site: carbonylate (Cys) (covalent) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 SYDSS 5
      ||| :
Db      4 SHDGA 8

RESULT 9
E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen
A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Experimental source: whole flies
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

      Query Match      33.3%; Score 13; DB 2; Length 8;
      Best Local Similarity 100.0%; Pred. No. 2.8e+05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YD 3
      ||| :
Db      4 YD 5

RESULT 10
A37832
phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
C;Species: Pseudomonas sp.
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
C;Accession: A37832
R;Powlowski, J.; Shingler, V.
J. Bacteriol. 172, 6834-6840, 1990
A;Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxyl
A;Reference number: A37832; MUID:91072231; PMID:2254259
A;Accession: A37832
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <POW>
C;Keywords: oxidoreductase

      Query Match      30.8%; Score 12; DB 2; Length 4;
      Best Local Similarity 56.7%; Pred. No. 2.8e+05;
      Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYD 3
      ||| :
Db      1 SYN 3

RESULT 11
I40469
dnaZX-like protein - Bacillus subtilis (fragment)
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A;Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A;Reference number: I40469; MUID:89218958; PMID:2468993
A;Accession: I40469
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CRAA32902.1; PID:g4376204
C;Genetics:
```

A;Start codon: GTG

Query Match 30.8%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDS 4
||| :
Db 2 SYQA 5

RESULT 12

PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotrimer; immunoglobulin

Query Match 30.8%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSS 5
:||| :
Db 2 WESS 5

RESULT 13

PT0600
T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0600
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0600
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDS 4
||| :
Db 2 SSDS 5

RESULT 14

PT0580

T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYD 3
|:
Db 3 SWD 5

RESULT 15

S02617

alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)

C;Species: Equus caballus (domestic horse)

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997

C;Accession: S02617

R;Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall

FEBS Lett. 222, 99-103, 1987

A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differenc

A;Reference number: S02617; MUID:88005160; PMID:3653405

A;Accession: S02617

A;Molecule type: protein

A;Residues: 1-6 <FAI>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 30.8%; Score 12; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SSNVV 8
|:
Db 1 SAEVI 5

Search completed: June 8, 2004, 19:38:55

Job time : 20 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:34:18 ; Search time 11 Seconds
(without alignments)
37.869 Million cell updates/sec

Title: US-09-610-118-66
Perfect score: 39
Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	38.5	8	1 B44K_PORGI	P81886 porphyron
2	14	35.9	8	1 UPAL_HUMAN	P30087 homo sapien
3	13	33.3	7	1 ALL7_CTDPO	P82158 cydia pomon
4	13	33.3	8	1 ALL5_CALVO	P41841 calliphora
5	13	33.3	8	1 ALL5_CYDPO	P82156 cydia pomon
6	13	33.3	8	1 FUSS_FUSSO	P81010 fusarium so
7	13	33.3	8	1 GLUR_HUMAN	P02729 homo sapien
8	12	30.8	4	1 OCP3_OCTMI	P58649 octopus min
9	12	30.8	7	1 CHOX_ALCSP	P16101 alcaligenes
10	11	28.2	5	1 UXAA4_CHLTR	P38005 chlamydia t
11	11	28.2	7	1 HY7_FIG	P01153 sus scrofa
12	11	28.2	8	1 ALL6_CARMA	P81819 carcinus ma
13	11	28.2	8	1 LCK4_LEUMA	P21143 leucophaea
14	10	25.6	8	1 LCK6_LEUMA	P19988 leucophaea
15	10	25.6	8	1 ORNY_ORCLI	P82455 orconectes
16	9	23.1	6	1 TRPI_PSEPU	P36414 pseudomonas
17	9	23.1	7	1 EIO5_LITRU	P82101 litorea rub
18	9	23.1	7	1 MNPI_LEPDE	P42984 leptinotars
19	9	23.1	8	1 HTF1_PERAM	P04548 periplaneta
20	9	23.1	8	1 HTF_TENMO	P25419 tenebrio mo
21	9	23.1	8	1 LCK1_LEUMA	P21140 leucophaea
22	8	20.5	5	1 BIOB_CITER	P12997 citrobacter
23	8	20.5	6	1 ASP2_LACSN	P82655 lactobacill
24	8	20.5	6	1 LOK1_LOCFI	P41491 locusta mig
25	8	20.5	6	1 OVM_LBPDE	P42985 leptinotars
26	8	20.5	6	1 TMOF_SARBU	P41495 sarcophaga
27	8	20.5	7	1 ALL2_CARMA	P81805 carcinus ma
28	8	20.5	7	1 FAR3_HAECC	P81298 haemochus
29	8	20.5	7	1 FAR3_PANRE	P41874 panagrellus
30	8	20.5	7	1 FAR4_PANRE	P41875 panagrellus
31	8	20.5	8	1 AKH_MEML	P25423 melolontha
32	8	20.5	8	1 ALL1_CYDPO	P82152 cydia pomon
33	8	20.5	8	1 ALL6_CYDPO	P82157 cydia pomon

34	8	20.5	8	1 LCK2_LEUMA	P21141 leucophaea
35	8	20.5	8	1 LCK3_LEUMA	P21142 leucophaea
36	8	20.5	8	1 LCK5_LEUMA	P19987 leucophaea
37	8	20.5	8	1 LCK7_LEUMA	P19989 leucophaea
38	8	20.5	8	1 NS3_WICTU	P81152 mycobacteri
39	8	20.5	8	1 RSI_ERWCH	P37985 erwinia chr
40	8	20.5	8	1 UF06_MOUSE	P38644 mus musculu
41	8	20.5	8	1 VGLG_HSV2B	P42562 hiruso med
42	7	17.9	4	1 FAR3_HIRME	P42563 hiruso med
43	7	17.9	4	1 FAR4_HIRME	P58706 antiopeleura
44	7	17.9	4	1 FYRI_ANTEL	P81817 carcinus ma
45	7	17.9	5	1 ALL4_CARMA	

ALIGNMENTS

RESULT 1
B44K_PORGI
ID B44K_PORGI STANDARD; PRT; 8 AA.
AC P81886;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=VPB 3492;
RX MEDLINE=20198497; PubMed=10731616;
RA Norris J.M., Love D.N.;
RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline Porphyromonas gingivalis.";
RL Vet. Microbiol. 73:37-49 (2000).
CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON TER
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;
Query Match 38.5%; Score 15; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YDSSNV 7
DB 3 YQKRNI 8

RESULT 2
UPAL_HUMAN
ID UPAL_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714 (1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown

```

CC protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1
FT UNSURE 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 35.9%; Score 14; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SNV 7
   |||
Db 4 SNV 6

RESULT 3
ALL7 CYDPO STANDARD; PRT; 7 AA.
ID ALL7 CYDPO STANDARD; PRT; 7 AA.
AC P82158; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YD 3
   ||
Db 3 YD 4

RESULT 4
ALL5 CALVO STANDARD; PRT; 8 AA.
ID ALL5 CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]

CHARACTERIZATION, AND HYDROXYLATION.
RP TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
J. Biol. Chem. 269:21059-21066(1994).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -1- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -1- SIMILARITY: Belongs to the allatostatin family.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD RES 3 3
FT MOD RES 8 8
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YD 3
   ||
Db 4 YD 5

RESULT 5
ALL5 CYDPO STANDARD; PRT; 8 AA.
ID ALL5 CYDPO STANDARD; PRT; 8 AA.
AC P82156;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 5.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YD 3
   ||
Db 4 YD 5

RESULT 6
FUSS_FUSSO STANDARD; PRT; 8 AA.
ID FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s f3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).

```

```
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrymectidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN-IARI 3596; TISSUR=Mycelium;
RA Verma J.; Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER
FT MOD RES 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SSVN 7
Db 4 SHNV 7

RESULT 7
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J.; Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25P-25P(1971).
CC -!- FUNCTION: The identity of the glycoprotein from which this peptide
CC is derived is unknown. No physiological function has been
CC attributed. An erythrocyte membrane glycopeptide having a
CC similar structure has also been found.
DR PIR; A03188; XGHUEU.
DR GO; GO:0005576; C:extracellular; NAS.
KW Glycoprotein.
FT CARBOHYD 1
FT SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1E1E CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSS 5
Db 4 SHDGA 8

RESULT 8
OCP3_OCTMI
ID OCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58619;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
```

```
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E.; Hisada M.; Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.
KW Hormone; D-amino acid.
FT MOD RES 2
FT SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYD 3
Db 2 SWD 4

RESULT 9
CHOX_ALCSP
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M.; Miyake Y.; Emi S.; Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Oxidoreductase.
FT NON TER 7
FT SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSSN 6
Db 1 DNPEN 4

RESULT 10
UXA4_CHLTR
ID UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
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RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vreton E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Siena-2DFAGE; P38005; -.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match      28.2%; Score 11; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDS 4
Db 2 SGDS 5

RESULT 11
ID HY7 PTG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match      28.2%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SY 2
Db 5 SY 6

RESULT 12
AL16 CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";

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RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
FT AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match      28.2%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SY 2
Db 5 SY 6

RESULT 13
LCK4 LEUMA STANDARD; PRT; 8 AA.
ID LCK4 LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin IV (I-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT AMIDATION.
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match      28.2%; Score 11; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DSS 5
Db 1 DAS 3

RESULT 14
LCK6 LEUMA STANDARD; PRT; 8 AA.
ID LCK6 LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin VI (I-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";

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RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 25.6%; Score 10; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
Db |:|
3 SFHS 6

RESULT 15
ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomyotropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacodea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdick S., Sauter A., Keller R.;
RT "Two orckokins and the novel octapeptide orcomyotropin in the hindgut
RT of the crayfish Orconectes limosus: identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion."
RL J. Exp. Biol. 203:2807-2818(2000).
CC -!- FUNCTION: Myotropic peptide, enhances both the frequency and
CC amplitude of spontaneous hindgut contractions. It is synthesized
CC by abdominal ganglionic neurons.
CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 25.6%; Score 10; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDS 4
Db |:|
1 FDA 3

Search completed: June 8, 2004, 19:37:31
Job time : 12 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:34:43 ; Search time 39 Seconds
(without alignments)
64.722 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39
Sequence: 1 SYDSNNV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	53.8	8	10 Q9SB24	Q9sb24 nicotiana t
2	14	35.9	8	3 Q05403	Q05403 saccharomyc
3	14	35.9	8	12 Q9IU19	Q9iu19 influenza a
4	14	35.9	8	12 Q9IU21	Q9iu21 influenza a
5	13	33.3	7	2 O07354	C07354 synechococc
6	13	33.3	8	2 Q9R3X0	Q9r3x0 planktothri
7	13	33.3	8	2 P83158	P83158 anabaena sp
8	13	33.3	8	2 Q35792	Q35792 saccharomyc
9	12	30.8	8	2 Q9ZEZ9	Q9zez9 buchmera ap
10	12	30.8	8	2 Q7X4C1	Q7x4c1 potato witec
11	12	30.8	8	4 Q15898	Q15898 homo sapien
12	12	30.8	8	5 P82685	P82685 periplaneta
13	12	30.8	8	5 P82687	P82687 periplaneta
14	12	30.8	8	10 Q40659	Q40659 oryza sativ
15	11	28.2	4	11 Q08433	Q08433 rattus sp.
16	11	28.2	6	2 P83533	P83533 lactobacill

17	11	28.2	7	8 Q8MFY6	Q8mfy6 taraxacum (
18	11	28.2	8	2 P77556	P77556 escherichia
19	11	28.2	8	3 P87225	P87225 saccharomyc
20	11	28.2	8	4 Q7Z719	Q7z719 homo sapien
21	11	28.2	8	4 Q7Z6G0	Q7z6g0 homo sapien
22	11	28.2	8	5 P82686	P82686 periplaneta
23	11	28.2	8	8 Q9MSX1	Q9msx1 jurinea hum
24	11	28.2	8	8 Q34909	Q34909 locusta mig
25	11	28.2	8	13 Q9PS69	Q9ps69 gallus gall
26	11	28.2	8	13 P82082	P82082 limnodynast
27	11	28.2	8	13 P82083	P82083 limnodynast
28	10	25.6	7	3 P83432	P83432 bionectria
29	10	25.6	7	12 Q65578	Q65578 bovine herp
30	10	25.6	8	2 P83532	P83532 lactobacill
31	10	25.6	8	3 Q9HDS4	Q9hds4 aspergillus
32	10	25.6	8	4 Q15893	Q15893 homo sapien
33	10	25.6	8	4 Q9UJ50	Q9uj50 homo sapien
34	10	25.6	8	4 Q9UMC7	Q9umc7 homo sapien
35	10	25.6	8	4 Q9HCQ0	Q9hqc0 homo sapien
36	10	25.6	8	6 Q8WNS1	Q8wns1 bos taurus
37	10	25.6	8	8 Q9T2W0	Q9t2w0 saccharomyc
38	10	25.6	8	8 Q94VF3	Q94vf3 varanus kei
39	10	25.6	8	10 Q7XB03	Q7xb03 zea mays (m
40	10	25.6	8	11 Q9QVJ8	Q9qvj8 mus sp. mep
41	10	25.6	8	11 Q62527	Q62527 mus spretus
42	10	25.6	8	13 P87488	P87488 oncorhynch
43	9	23.1	7	2 P70804	P70804 azotobacter
44	9	23.1	7	2 Q47029	Q47029 enterobacte
45	9	23.1	7	2 Q8KMS9	Q8kms9 enterobacte

ALIGNMENTS

RESULT 1

Q9SB24 PRELIMINARY; PRT; 8 AA.
AC Q9SB24;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Parat protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Niwa Y., Muranaka T., Baba A., Machida Y.;
RT "Organ-specific and auxin-inducible expression of two tobacco para-
RT related genes in transgenic plants.";
EL DNA Res. 0:0-0(1994).
DR EMBL; D42119; BAA07700.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 905 NM; FE32D2C44455BB16 CRC64;

Query Match 53.8%; Score 21; DB 10; Length 8;

Best Local Similarity 66.7%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSSNVV 8

:|:|:|

Db 2 ESSNVV 7

RESULT 2

Q05403 PRELIMINARY; PRT; 8 AA.
ID Q05403

AC Q05403;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

```
DE DNA for ORF's from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
RN NCBI_TaxID=4932;
RX STRAIN=FV1679;
RC SEQUENCE FROM N.A.
MEDLINE=96021609; PubMed=8533473;
RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL: X83121; CAA58183.1; -.
FT NON_TER 1 8
SQ SEQUENCE 8 AA; 879 MW; 7B532D2D4C41E058 CRC64;

Query Match 35.9%; Score 14; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVV 8
DB 4 NVV 6

RESULT 3
Q91U19 PRELIMINARY; PRT; 8 AA.
AC Q91U19
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
GN NS.
OS Influenza A virus (A/Hong Kong/503/97(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=155224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/503/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RT "Avian influenza A H5N1 and H9N2 viruses bearing a specific
RT constellation of nonglycoprotein genes caused illness in humans.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF256192; AAK49326.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 35.9%; Score 14; DB 12; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SNVV 8
DB 1 SNTV 4

RESULT 4
Q91U21 PRELIMINARY; PRT; 8 AA.
AC Q91U21
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
GN NS.
OS Influenza A virus (A/Hong Kong/491/97(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=155223;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/491/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RT "Avian influenza A H5N1 and H9N2 viruses bearing a specific
RT constellation of nonglycoprotein genes caused illness in humans.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF256191; AAK49324.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 35.9%; Score 14; DB 12; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SNVV 8
DB 1 SNTV 4

RESULT 5
O07354 PRELIMINARY; PRT; 7 AA.
AC O07354
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NfK (Fragment).
GN NfK.
OS Synchococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synchococcus sp. strain
RT RF-1.";
RL Microbiology 145:743-753(1999).
DR EMBL: AF003700; AAC35193.1; -.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYD 3
DB 2 SFD 4

RESULT 6
Q9R3X0 PRELIMINARY; PRT; 8 AA.
AC Q9R3X0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1, 5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Planktotox rubescens.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktotox.
OX NCBI_TaxID=59512;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, and BC-PLA 9303;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
RT "the diversity of gas vesicle genes in planktothrix rubescens from
RL Lake Zurich.";
RL Microbiology 145:2757-2768(1999).
DR EMBL; AJ132249; CAB59537.1; -.
DR EMBL; AJ132248; CAB59534.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 957 MW; 33D1AAA695BBI9CB CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDSSNVV 8
Db 2 FESMDTV 8

RESULT 7
P83158 PRELIMINARY; PRT; 8 AA.
AC P83158;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa
DE polypeptide) (PSI-C) (Fragment).
OS Anabaena sp. (strain 131).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apté S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -!- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
CC PHOTOSYSTEM I COMPLEX.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
DR GO; GO:0009522; C:photosystem I; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; PARTIAL.
KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
FT NON TER
SQ SEQUENCE 8 AA; 962 MW; C5BB505322D1A1F5 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YD 3
Db 7 YD 8

RESULT 8
Q35792 PRELIMINARY; PRT; 8 AA.
AC Q35792;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inside intron 3 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24063.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 8 AA; 1025 MW; 084693345B5AA337 CRC64;

Query Match 33.3%; Score 13; DB 8; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDSSN 6
Db 4 YNKWN 8

RESULT 9
Q9ZEZ9 PRELIMINARY; PRT; 8 AA.
AC Q9ZEZ9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OG Plasmid pBRC1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006874; CAA07290.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 30.8%; Score 12; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SSNVV 8
Db 2 NSQVI 6

RESULT 10
Q7X4C1 PRELIMINARY; PRT; 8 AA.
AC Q7X4C1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosomal protein S19 (Fragment).
GN RPS19.
OS Potato witches'-broom phytoplasma.
```

OC Bacteria; Firmicutes; Mollicutes; Achaeplasmatales;
 OC Achaeplasmataceae; Phytoplasma.
 OX NCBI_TaxID=37701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PWB;
 RA Lee I.-M., Martini M., Marcone C., Zhu S.;
 RT "Classification of phytoplasma strains in the elm yellows group
 (16S rV) and proposition of 'Candidatus Phytoplasma ulmi' for the
 RT phytoplasma associated with elm yellows and 'Candidatus Phytoplasma
 RT chinense' for the phytoplasma associated with cherry lethal yellowing
 RT in China.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY197682; AAP42406.1; -;
 KW Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 945 MW; 783326D44333AA8 CRC64;
 Query Match 30.8%; Score 12; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DSSN 6
 Db 2 DRKN 5
 RESULT 11
 ID Q15898 PRELIMINARY; PRT; 8 AA.
 AC Q15898;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (Clone XPeAllB) (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: L32078; AAA73888.1; -;
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;
 Query Match 30.8%; Score 12; DB 4; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDSS 5
 Db 2 SYPIS 6
 RESULT 12
 ID P82685 PRELIMINARY; PRT; 8 AA.
 AC P82685;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Kinin-1 (PEA-K-1).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;
 Query Match 30.8%; Score 12; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDS 4
 Db 3 SFNS 6
 RESULT 13
 ID P82687 PRELIMINARY; PRT; 8 AA.
 AC P82687;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Kinin-3 (PEA-K-3).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 RT americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;
 Query Match 30.8%; Score 12; DB 5; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDS 4
 Db 3 SFNS 6
 RESULT 14
 ID Q40659 PRELIMINARY; PRT; 8 AA.
 AC Q40659;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

```
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomycers
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
DR Gramene; Q40659; -.
FT NON TER 8
FT SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 30.8%; Score 12; DB 10; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SNVV 8
Db :|:|
5 NNVV 8

RESULT 15
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON TER 1
FT SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 28.2%; Score 11; DB 11; Length 4;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVV 8
Db ||:
1 NVL 3

Search completed: June 8, 2004, 19:38:23
Job time : 40 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:33:43 ; Search time 52 Seconds
(without alignments)
43.469 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	4	AAB61298 Anti-TANG
2	39	100.0	8	6	ABU11264 Human TAN
3	23	59.0	8	2	Aaw97549 Antigenic
4	22	56.4	7	2	AAY00724 Complemen
5	22	56.4	8	2	AAR26117 Beta-Chai
6	22	56.4	8	2	Aaw76997 Rat TCR V
7	22	56.4	8	4	AAB68384 Immunogen
8	22	56.4	8	4	AAB68387
9	21	53.8	5	2	Aaw79774 Alternati
10	21	53.8	6	2	Aaw83787 Peptide s
11	21	53.8	6	2	Aaw79767 Presenili
12	21	53.8	7	2	AAR29293 Nerve gro
13	21	53.8	7	2	AAR8689 Prostate
14	21	53.8	7	2	AAR89726
15	21	53.8	7	2	Aaw05566 Ependymin
16	21	53.8	7	2	Aaw33560 Oligopept
17	21	53.8	7	2	Aaw33525 Oligopept
18	21	53.8	7	2	Aaw79765 Presenili
19	21	53.8	7	2	Aaw79768 Presenili
20	21	53.8	7	3	AAB04002 Prostate
21	21	53.8	7	4	Aau03480 Human oli
22	21	53.8	7	5	ABg97374 Prostate
23	21	53.8	7	5	ABp48810 Zinc fing
24	21	53.8	7	5	ABp50798 Zinc fing
25	21	53.8	7	5	ABp48359 Zinc fing

26	21	53.8	7	5	ABP48353	Abp48353 Zinc fing
27	21	53.8	7	5	ABP49651	Abp49651 Zinc fing
28	21	53.8	7	5	ABP48349	Abp48349 Zinc fing
29	21	53.8	7	5	ABP48345	Abp48345 Zinc fing
30	21	53.8	7	5	ABP48342	Abp48342 Zinc fing
31	21	53.8	7	5	ABP48509	Abp48509 Zinc fing
32	21	53.8	7	5	ABP48400	Abp48400 Zinc fing
33	21	53.8	7	5	ABP49704	Abp49704 Zinc fing
34	21	53.8	7	5	ABP48399	Abp48399 Zinc fing
35	21	53.8	7	5	ABP48356	Abp48356 Zinc fing
36	21	53.8	7	5	ABP49633	Abp49633 Zinc fing
37	21	53.8	7	6	ABU69184	Abu69184 Oligopept
38	21	53.8	7	6	AAO16139	Aao16139 Prostate
39	21	53.8	7	6	ADA08179	Ada08179 Human Ned
40	21	53.8	7	6	ADA08173	Ada08173 Human Ned
41	21	53.8	7	6	ADA08198	Ada08198 Human Ned
42	21	53.8	7	6	ABO19886	Abol19886 Prostate
43	21	53.8	7	7	ADA62415	Ada62415 Zinc fing
44	21	53.8	7	7	ADA63923	Ada63923 Zinc fing
45	21	53.8	7	7	ADA62413	Ada62413 Zinc fing

ALIGNMENTS

RESULT 1
AAB61298
ID AAB61298 standard; peptide; 8 AA.
XX
AC AAB61298;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 66.
XX

Human; antibody; scFv; CDR; complementarity determining region;
TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
platelet membrane glycoprotein receptor; bleeding disorder;
blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
ischaemia; cardiovascular disease; immunological disease; liver disorder;
cancer.

XX Homo sapiens.

OS
XX WO200100810-A1.
PN

XX 04-JAN-2001.

PD 30-JUN-2000; 2000WO-US018152.

XX 30-JUN-1999; 99US-00345468.

PR 06-DEC-1999; 99US-00454824.

PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

PA Busfield SJ, Vallelial J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian MD, Kingsbury G;

DR WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor,

PT glycoprotein VI, and its modulators, useful for preventing, treating and

PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological

PT disorders.

XX Claim 32; Page 102; 227pp; English.

PS The present sequence is given in a specification relating to an isolated

XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor

CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

CC and polypeptides and their modulators, e.g. antisense nucleic acids,

CC

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 SQ

Sequence 8 AA;

Query Match 100.0%; Score 39; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
 |||||
 Db 1 SYDSSNVV 8

RESULT 2

ID ABU11264 standard; peptide; 8 AA.

AC ABU11264;

DT 06-FEB-2003 (first entry)

XX Human TANGO 268 VLCDR1 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

OS WO200280968-A1.

PN 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 12; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 XX heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 XX or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 XX binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 XX The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g. diseases
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ

Sequence 8 AA;

Query Match 100.0%; Score 39; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
 |||||
 Db 1 SYDSSNVV 8

RESULT 3

AAW97549

ID AAW97549 standard; peptide; 8 AA.

XX AAW97549;

XX 19-MAY-1999 (first entry)

XX Antigenic site of HN protein loop beta-5L23.

XX Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
 XX virus epitope; attachment protein; vaccine; immunodominant epitope.

XX Measles virus.

XX WO9902695-A2.

XX 21-JAN-1999.

XX 08-JUL-1998; 98WO-NL000390.

XX 08-JUL-1997; 97EP-00202100.

XX (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX Langedijk JPM, Van Oirschot JT;

XX WPI; 1999-120896/10.

XX Isolated proteinaceous substance - comprising at least one virus epitope
 XX derived from an attachment protein of a paramyxovirus.

XX Disclosure; Page 50; 63pp; English.

XX AAW97452-571 represent antigenic sites derived from the haemagglutinin-
 XX neuraminidase (HN) protein of the paramyxoviridae. The specification
 XX describes 3-D models identifying a proteinaceous substance comprising at
 XX least one virus epitope derived from the attachment protein, which

CC corresponds to an antigenic site present on one of the loops of HN. The
 CC antigenic sites can be used to produce vaccines, to detect the viruses,
 CC and to select the immunodominant epitope

XX SQ Sequence 8 AA;

Query Match 59.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSNV 7
 :|||:
 Db 1 TYDTSRV 7

RESULT 4

AAAY00724
 ID AAY00724 standard; peptide; 7 AA.

XX AC AAY00724;

DT 13-MAY-1999 (first entry)

DE Complement derived peptide C3a fragment, C3a11.

KW Complement derived peptide; peptide C3a; IgE-mediated triggering;

KW Fc epsilon RI-induced secretory response; mucosal mast cell; inhibitor;
 allergic disorder; IgE mediated (type I) hypersensitivity; therapy.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "optionally amidated"

XX WO9858960-A1.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-IL000292.

XX 22-JUN-1997; 97IL-00121134.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Erdei A, Pecht I;

XX WPI; 1999-105613/09.

XX New peptides derived from complement peptide C3a - used for the treatment
 of allergic disorders caused by IgE mediated hypersensitivity, e.g. hay
 fever, asthma, urticaria or allergic conjunctivitis.

XX Claim 11, 12; Page 21; 27pp; English.

XX This sequence represents an example of a peptide of the invention. The
 peptides correspond partially or entirely to the 50-77 sequence of the
 complement-derived peptide C3a and analogues capable of inhibiting IgE-
 mediated triggering and/or the Fc epsilon RI-induced secretory response
 of mucosal mast cells, the peptides are selected from: (a) X1-Cys-Asn-R1-
 Ile-Thr-R2-Leu-R3-R4-Gln-His-R5-R6-R7-R8-R9-R10-G-X4-Leu-Ala-R11; (b) X1-
 -Cys-Asn-R1-X4; (c) X2-Lys-Val-Phe-Leu-Asp-X3; and (d) X5-Asp-Ser-Ser-Asn-
 -Tyr-Ile-R11; X1 = H, lower alkanoyl, Cys, Asp-Cys or Arg-Arg-Cys; X2 =
 H, lower alkanoyl or Lys; X3 = Arg or a sequence selected from: (i) Ala-
 Ala-Asn-R1-Ile-Thr-R2-Leu-R3-R4; (ii) Cys-Cys-Asn-R1-Ile-Thr-R2-Leu-R3;
 and (iii) Cys-Cys-Asn-R1-Ile-Thr-R2-Leu-R3-R4-Gln-His-R5-R6; X4 = Gly,
 Ile-Thr-R2-Leu-R3, or Ile-Thr-Arg-R11; X5 = H, lower alkanoyl or Leu; R1
 = an aromatic amino acid residue; R2 = Glu or Lys; R3 = a positively
 charged amino acid residue; R4 = Arg or Glu; R5 = Ala or Arg; R6 = Arg or
 Lys; R7 = Ala or Asp; R8 = Ser or His; R9 = His or Val; R10 = Leu, Ile,
 Ala or Gly; and R11 = OH, Arg, Arg-NH2, or Arginine, and chemical
 derivatives and salts. The peptides can be used for the prevention or
 treatment of allergic disorders caused by IgE mediated (type I)

CC hypersensitivity where mucosal-type mast cells are involved. They can be
 CC used for the prevention and/or treatment of hay fever, asthma, some cases
 CC of urticaria, or allergic conjunctivitis

XX SQ Sequence 7 AA;

Query Match 56.4%; Score 22; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DSSNVV 8
 :|||:
 Db 1 DSSNVI 6

RESULT 5

AAAR26117
 ID AAR26117 standard; peptide; 8 AA.

XX AC AAR26117;

DT 25-MAR-2003 (revised)

DT 01-FEB-1993 (first entry)

DE Beta-Chain VDJ sequence from rat with EAE.

XX TCR; beta chain; rheumatoid arthritis; multiple sclerosis;

KW autoimmune disease; diabetes; T-cell lymphoma; vaccination; immunisation;

KW experimental allergic encephalomyelitis.

XX Rattus rattus.

XX WO9212996-A2.

XX 06-AUG-1992.

XX 21-JAN-1992; 92WO-US000482.

XX 22-JAN-1991; 91US-00644611.

XX (IMVU-) IMMUNE RESPONSE CORP.

XX Howell MD, Brostoff SW, Carlo DJ;

XX WPI; 1992-284600/34.

XX Treatment of auto-immune diseases e.g. rheumatoid arthritis - using
 PT vaccine contg. T-cell receptors from surface of T-cells which mediate the
 PT diseases.

XX Disclosure; Page 28; 87pp; English.

XX This sequence represents the VDJ sequence of VBeta4 from the T cell
 receptor from myelin basic protein reactive T cells mediating
 pathogenesis in experimental allergic encephalomyelitis. It has some
 CC homology to human VBeta4 from patients with multiple sclerosis
 CC (AAR26081). (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Query Match 56.4%; Score 22; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSN 6
 :|||:
 Db 1 SSDSSN 6

RESULT 6

AAW76997
 ID AAW76997 standard; protein; 8 AA.

XX

```

AC AAW76997;
XX
XX
DT 25-JAN-1999 (first entry)
XX
DE Rat TCR VDJ junction region peptide.
XX
XX T cell receptor; rat; TCR; beta chain; detection; prevention; treatment;
KW rheumatoid arthritis; autoaggressive; immune response; V-beta 17;
KW variable region; vaccine.
XX
XX Rattus sp.
XX
XX US5837246-A.
XX
XX 17-NOV-1998.
XX
XX 20-JAN-1995; 95US-00376049.
XX
XX 21-MAR-1989; 89US-00326314.
PR 18-JUL-1989; 89US-00382085.
PR 18-JUL-1989; 89US-00382086.
PR 30-MAY-1990; 90US-00530229.
PR 28-JAN-1993; 93US-00010483.
XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX
XX Howell MD, Brostoff SW, Carlo DJ;
XX
XX WPI; 1999-023376/02.
XX
XX New immunogenic peptides for treating rheumatoid arthritis - has amino
PT acid sequence for T cell receptor present of surface of autoaggressive T
PT cells mediating rheumatoid arthritis.
XX
XX Example II; Col 11; 15pp; English.
XX
XX This sequence is the rat T cell receptor (TCR) VDJ region junction
CC peptide which is used in a vaccine in a method for the detection,
CC prevention and treatment of rheumatoid arthritis (RA). The method
CC involves an amino acid sequence for a TCR which is present on the surface
CC of autoaggressive T cells mediating rheumatoid arthritis where the
CC peptide induces an immune response against autoaggressive T cells that
CC reduces the severity of RA
XX
XX Sequence 8 AA;
SQ
Query Match 56.4%; Score 22; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSN 6
Db 1 SSDSSN 6

RESULT 7
AAB68384
ID AAB68384 standard; peptide; 8 AA.
XX
XX AAB68384;
XX
XX 23-JUL-2001 (first entry)
DT
DE Immunogenic peptide from beta-chain VDJ region of Vbeta-chains.
XX
XX Vbeta14; Vbeta17; T cell; rheumatoid arthritis; multiple sclerosis;
KW T cell-mediated pathology; autoimmune disease; Vbeta4; Vbeta12.
XX
XX Rattus sp.
OS
XX US6221352-B1.
XX
XX 24-APR-2001.
PD

XX
XX 06-JUN-1995; 95US-00471209.
XX
XX 21-MAR-1989; 89US-00326314.
PR 18-JUL-1989; 89US-00382085.
PR 18-JUL-1989; 89US-00382086.
PR 30-MAY-1990; 90US-00530229.
PR 22-JAN-1991; 91US-00644611.
PR 24-DEC-1991; 91US-00813867.
PR 18-JUL-1994; 94US-00276776.
XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX
XX Howell MD, Brostoff SW, Carlo DJ;
XX
XX WPI; 2001-315571/33.
XX
XX Preventing proliferation of Vbeta14 or 17-expressing T cells, for
PT preventing, treating T-cell mediated pathologies such as autoimmune
PT diseases, by administering antibody that binds to Vbeta region of T cell
PT receptor.
XX
XX Disclosure; Col 13; 40pp; English.
XX
XX The specification describes a method for preventing the proliferation of
CC Vbeta14 or Vbeta17-expressing T cells in a human individual having
CC rheumatoid arthritis. The method comprises administering a cytotoxic or
CC cytostatic agent which comprises an antibody selectively binding to
CC Vbeta14 or Vbeta17 expressed by the T cells. The method is useful for
CC preventing the proliferation of T cells, which in turn is useful for
CC preventing, ameliorating or treating T cell-mediated pathologies of
CC autoimmune diseases, such as rheumatoid arthritis and multiple sclerosis.
CC The present sequence represents an immunogenic peptide from the B-chain
CC VDJ region of Vbeta-chains
XX
XX Sequence 8 AA;
SQ
Query Match 56.4%; Score 22; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSN 6
Db 1 SSDSSN 6

RESULT 8
AAB68387
ID AAB68387 standard; peptide; 8 AA.
XX
XX AAB68387;
XX
XX 23-JUL-2001 (first entry)
DT
DE VDJ junction of T cell receptor beta-chain of a rat.
XX
XX Vbeta14; Vbeta17; T cell; rheumatoid arthritis; multiple sclerosis;
KW T cell-mediated pathology; autoimmune disease.
XX
XX Rattus sp.
OS
XX US6221352-B1.
XX
XX 24-APR-2001.
PD
XX
XX 06-JUN-1995; 95US-00471209.
XX
XX 21-MAR-1989; 89US-00326314.
PR 18-JUL-1989; 89US-00382085.
PR 18-JUL-1989; 89US-00382086.
PR 30-MAY-1990; 90US-00530229.
PR 22-JAN-1991; 91US-00644611.
PR 24-DEC-1991; 91US-00813867.
PR

```

PR 18-JUL-1994; 94US-00276776.
 XX (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Howell MD, Brostoff SW, Carlo DJ;
 XX WPI; 2001-315571/33.
 XX
 PT Preventing proliferation of Vbeta14 or 17-expressing T cells, for
 PT preventing, treating T-cell mediated pathologies such as autoimmune
 PT diseases, by administering antibody that binds to Vbeta region of T cell
 PT receptor.
 XX
 PS Example 1; Col 15; 40pp; English.
 XX
 CC The specification describes a method for preventing the proliferation of
 CC Vbeta14 or Vbeta17-expressing T cells in a human individual having
 CC rheumatoid arthritis. The method comprises administering a cytotoxic or
 CC cytostatic agent which comprises an antibody selectively binding to
 CC Vbeta14 or Vbeta17 expressed by the T cells. The method is useful for
 CC preventing the proliferation of T cells, which in turn is useful for
 CC preventing, ameliorating or treating T cell-mediated pathologies of
 CC autoimmune diseases, such as rheumatoid arthritis and multiple sclerosis.
 CC The present sequence represents the VDJ junction of the T cell receptor
 CC of rat beta chains
 XX
 SQ Sequence 8 AA;
 Query Match 56.4%; Score 22; DB 4; Length 8;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SYDSGN 6
 Db | |||||
 1 SSDSGN 6
 RESULT 9
 AAW79774
 ID AAW79774 standard; peptide; 5 AA.
 XX
 AC AAW79774;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1999 (first entry)
 XX
 DE Alternative CPP32-protease cleavage site in PS2.
 XX
 KW Proteolytic processing; human; presenilin 2; inhibitor; apoptosis;
 KW cell death; early onset familial Alzheimer's disease; FAD; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9847917-A2.
 XX
 PD 29-OCT-1998.
 XX
 PF 24-APR-1998; 98WO-US008260.
 XX
 PR 24-APR-1997; 97US-0044262P.
 XX
 PA (TANZ/) TANZI R E.
 PA (KIMT/) KIM T.
 XX
 PI Tanzi RE, Kim T;
 XX WPI; 1998-583602/49.
 XX
 PT 20 kDa presenilin 2 C-terminal fragment, PS2-CTF - useful to screen for
 PT compounds inhibiting proteolysis of presenilin 2 and to produce
 PT antibodies used in diagnosis of familial Alzheimer's.
 XX
 PS Disclosure; Page 14; 84pp; English.

XX The invention relates to a C-terminal fragment from the human 20 kD
 CC presenilin 2 protein (PS2-CTF), useful in screening for compounds that
 CC inhibit proteolytic processing of PS2 in cells. Such inhibitory compounds
 CC can be administered to prevent proteolytic cleavage of presenilin 2 at a
 CC cleavage site which generates PS2-CTF, and therefore to inhibit apoptotic
 CC cell death. Peptides AAW79757-W79769 represent proteolytic cleavage sites
 CC in the presenilin 2 protein, especially for cleavage by the protease
 CC CPP32 (an apoptosis-induce protease). This sequence represents an
 CC alternative CPP32 protease cleavage site in presenilin 2. Mutations in
 CC the presenilin genes presenilin 1 and presenilin 2 (PS1 and PS2) cause a
 CC major portion (at least 50%) of early onset familial Alzheimer's disease
 CC (FAD), and detection of abnormal PS2-CTF levels can be indicative of a
 CC specific disease, e.g. FAD. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 5 AA;
 Query Match 53.8%; Score 21; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDS 4
 Db |||||
 2 SYDS 5
 RESULT 10
 AAW83787
 ID AAW83787 standard; peptide; 6 AA.
 XX
 AC AAW83787;
 XX
 DT 14-JAN-1999 (first entry)
 XX
 DE Peptide specific antigen (PSA) cleaved substrate sequence.
 XX
 KW Human prostate specific antigen; PSA; substrate; prostate cancer;
 KW metastatic prostate cancer; PSA inhibitor.
 XX
 OS Synthetic.
 XX
 PN WO9840738-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 09-MAR-1998; 98WO-US004557.
 XX
 PR 11-MAR-1997; 97US-0040174P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Rothman J, Blobel C, Roghani M;
 XX WPI; 1998-520833/44.
 XX
 PT Improved human prostate specific antigen substrates - useful to, e.g.
 PT measure prostate specific antigen activity, identify therapeutically
 PT useful inhibitors or diagnose metastatic prostate cancer.
 XX
 PS Claim 16; Fig 18; 147pp; English.
 XX
 CC AAW83772-854 represent peptides cleaved by 250 microgram/ml human
 CC prostate specific antigen (PSA). They correspond to the consensus
 CC sequence AAW83771. The PSA substrates are useful in assays which measure
 CC PSA activity. Such assays may provide a clinical evaluation of patients
 CC suffering from, or at risk for, prostate cancer. Elevated levels of PSA
 CC in serum are widely used as a marker of prostate cancer, and the
 CC substrates can be used e.g. to measure the amount of active PSA in
 CC patient serum to diagnose, or determine the malignant potential of, a
 CC patient's prostate disease. They are especially useful to diagnose
 CC metastatic prostate cancer. The substrates can also be used in assays to
 CC identify PSA inhibitors, which can be administered to treat or prevent
 CC prostate cancer

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XX SQ Sequence 6 AA;
Query Match 53.8%; Score 21; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SYDSN 6
   |||
Db 1 SYSSGN 6

RESULT 11
AAW79767
ID RAAW79767 standard; peptide; 6 AA.
XX AC AAW79767;
XX AC AAW79767;
DT 25-MAR-2003 (revised)
DT 02-MAR-1999 (first entry)
XX XX
DE Presenilin 2 proteolytic processing site #11.
XX XX
KW Proteolytic processing; human; presenilin 2; inhibitor; apoptosis;
KW cell death; early onset familial Alzheimer's disease; FAD; diagnosis.
XX OS Homo sapiens.
XX XX
XX WO9847917-A2.
XX XX
PD 29-OCT-1998.
XX XX
PF 24-APR-1998; 98WO-US008260.
XX XX
PR 24-APR-1997; 97US-0044262P.
XX XX
XX (TANZ/) TANZI R E.
XX PA (KIMT/) KIM T.
XX PI Tanzi RE, Kim T;
XX XX
XX WPI; 1998-583602/49.
XX XX
XX 20 kDa presenilin 2 C-terminal fragment, PS2-CTF - useful to screen for
XX compounds inhibiting proteolysis of presenilin 2 and to produce
XX antibodies used in diagnosis of familial Alzheimer's.
XX XX
XX Claim 11; Page 65; 84pp; English.
XX XX
XX The sequences AAW79757-W79769 represent proteolytic processing site found
XX within the human presenilin 2 protein. The invention relates to a C-
XX terminal fragment from the human 20 kD presenilin 2 protein (PS2-CTF).
XX The PS2-CTF is useful in screening for compounds that inhibit proteolytic
XX processing of PS2 in cells. Such inhibitory compounds can be administered
XX to prevent proteolytic cleavage of presenilin 2 at a cleavage site which
XX generates PS2-CTF, and therefore to inhibit apoptotic cell death.
XX Mutations in the presenilin genes presenilin 1 and presenilin 2 (PS1 and
XX PS2) cause a major portion (at least 50%) of early onset familial
XX Alzheimer's disease (FAD), and detection of abnormal PS2-CTF levels can
XX be indicative of a specific disease, e.g. FAD. (Updated on 25-MAR-2003 to
XX correct PA field.)
XX SQ Sequence 6 AA;
Query Match 53.8%; Score 21; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
   |||
Db 3 SYDS 6

RESULT 12
AAR29293
ID AAR29293 standard; peptide; 7 AA.
XX XX
XX AAR29293;
XX AC AAR29293;
DT 25-MAR-2003 (revised)
DT 07-APR-1993 (first entry)
XX XX
DE Nerve growth stimulating protein fragment.
XX XX
KW Ependymin; neuroactive domain; treatment; Huntington's chorea;
KW Parkinson's disease; Alzheimer's disease.
XX XX
XX Synthetic.
XX XX
XX WO9220362-A1.
XX XX
XX 26-NOV-1992.
XX XX
XX 14-MAY-1991; 91WO-US003346.
XX PF
XX 14-MAY-1991; 91WO-US003346.
XX PR
XX (SHAS/) SHASHOUA V E.
XX PA
XX Shashoua VE;
XX PI
XX WPI; 1992-415465/50.
XX XX
XX Protein fragment comprising neuro-active domain of ependymin - enhances
XX nerve connectivity and growth and is for treating nervous system
XX disorders e.g. Huntington's, Parkinson's and Alzheimer's diseases.
XX XX
XX Claim 21; Page 53; 77pp; English.
XX XX
XX The fragment is that of an active region of the ependymin neuroactive
XX domain (gamma chain amino acids 30-36) effective in stimulating nerve
XX growth and elongation. It is 75% homologous to nerve growth factor amino
XX acids 10-18. It can be used to treat nerve injuries and to correct
XX genetic or systemic disorders, e.g. treatment of Huntington's,
XX Parkinson's or Alzheimer's diseases, or to pretreat nerve tissue before
XX transplantation. It can be administered in sustained release form and may
XX be coupled to a carrier which protects it against decomposition in the
XX stomach and blood stream after oral admin. and carries it across the
XX blood brain barrier, opt. with subsequent release of the free fragment in
XX the brain. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-
XX MAR-2003 to correct PA field.)
XX SQ Sequence 7 AA;
Query Match 53.8%; Score 21; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
   |||
Db 4 SYDS 7

RESULT 13
AAR89689
ID AAR89689 standard; peptide; 7 AA.
XX XX
XX AAR89689;
XX AC AAR89689;
DT 25-MAR-2003 (revised)
DT 02-SEP-1996 (first entry)
XX XX
XX Prostate specific antigen, semenogelin derived, cleavage substrate.
XX XX
XX Human; semenogelin I; sperm entrapping gel; ejaculation; protease;
XX gel structure; dissolution; prostate specific antigen; proteolysis;

```

KW chymotrypsin like specificity; peptide substrate; cleavage site; assay;
 KW determination; proteolytic activity; identification; inhibitor;
 KW cytotoxic agent; conjugated; treatment; prostate cancer.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT Cleavage-site 3..4 /note= "acylated"
 FT FT /note= "prostate specific antigen proteolytic cleavage site"
 FT Modified-site 7
 FT FT /note= "opt. C-terminally conjugated to the amino of the sugar moiety of doxorubicin"
 FT
 XX
 PN WO9600503-A1.
 XX
 PD 11-JAN-1996.
 XX
 PD 07-JUN-1995; 95WO-US008156.
 XX
 PR 28-JUN-1994; 94US-00267092.
 PR 15-MAR-1995; 95US-00404833.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI DefeoJones D, Feng D, Garsky VM, Jones RE, Oliff AI;
 XX
 DR WPI; 1996-077275/08.
 XX
 PT New peptide substrates cleaved by prostate-specific antigen - also
 PT cytotoxic conjugates for treating prostate cancer, and assay for
 PT determination of PSA activity.
 XX
 PS Example 3; Page 98; 142pp; English.
 XX
 CC Human semenogelin I (hSI) is one of the major proteins, including hSII
 CC and fibronectin, in the sperm entrapping gel formed at ejaculation. This
 CC gel structure undergoes dissolution via the action of prostate specific
 CC antigen (PSA), a protease with chymotrypsin like specificity, which
 CC proteolyzes the above major proteins. New substrates, including the
 CC present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage
 CC site, can be used in assays to determine the proteolytic activity of free
 CC PSA in a sample, and to identify cpds. which inhibit the proteolytic
 CC activity of PSA, they may also be conjugated, via a covalent bond or
 CC peptide linker, to a cytotoxic agent and used to treat prostate cancer.
 CC In a PSA hydrolysis assay, the percentage of the present peptide cleaved
 CC by YORK PSA after 4 hrs. was 98 %, and 95 % (partially soluble) when
 CC conjugated to doxorubicin. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;
 Query Match 53.8%; Score 21; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SYDSSNV 7
 Db ||| |:::
 1 SYQSSSL 7
 RESULT 14
 AAR89726
 ID AAR89726 standard; peptide; 7 AA.
 XX
 AC AAR89726;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-SEP-1996 (first entry)
 XX
 DE Prostate specific antigen, semenogelin derived, cleavage substrate.
 XX

KW Human; semenogelin I; sperm entrapping gel; ejaculation; protease;
 KW gel structure; dissolution; prostate specific antigen; proteolysis;
 KW chymotrypsin like specificity; peptide substrate; cleavage site; assay;
 KW determination; proteolytic activity; identification; inhibitor;
 KW cytotoxic agent; conjugated; treatment; prostate cancer.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT FT /note= "acylated"
 XX
 PN WO9600503-A1.
 XX
 PD 11-JAN-1996.
 XX
 PD 07-JUN-1995; 95WO-US008156.
 XX
 PR 28-JUN-1994; 94US-00267092.
 PR 15-MAR-1995; 95US-00404833.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI DefeoJones D, Feng D, Garsky VM, Jones RE, Oliff AI;
 XX
 DR WPI; 1996-077275/08.
 XX
 PT New peptide substrates cleaved by prostate-specific antigen - also
 PT cytotoxic conjugates for treating prostate cancer, and assay for
 PT determination of PSA activity.
 XX
 PS Claim 19; Page 115; 142pp; English.
 XX
 CC Human semenogelin I (hSI) is one of the major proteins, including hSII
 CC and fibronectin, in the sperm entrapping gel formed at ejaculation. This
 CC gel structure undergoes dissolution via the action of prostate specific
 CC antigen (PSA), a protease with chymotrypsin like specificity, which
 CC proteolyzes the above major proteins. New substrates, including the
 CC present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage
 CC site, can be used in assays to determine the proteolytic activity of free
 CC PSA in a sample, and to identify cpds. which inhibit the proteolytic
 CC activity of PSA, they may also be conjugated, via a covalent bond or
 CC peptide linker, to a cytotoxic agent and used to treat prostate cancer.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;
 Query Match 53.8%; Score 21; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SYDSSNV 7
 Db ||| |:::
 1 SYQSSSL 7
 RESULT 15
 AAW05566
 ID AAW05566 standard; peptide; 7 AA.
 XX
 AC AAW05566;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-DEC-1996 (first entry)
 XX
 DE Ependymin peptide fragment #11.
 XX
 KW Ependymin; nerve growth factor; glycoprotein; extracellular fluid; brain;
 KW cerebrospinal fluid; therapy; stroke recovery; neurodegenerative disease;
 KW neuron transplantation; memory loss; brain-penetration.
 XX
 OS Synthetic.
 XX

Wed Jun 9 06:02:34 2004

PN US55457119-A..
XX
XX PD 13-AUG-1996.
XX
XX PF 24-FEB-1994; 94US-00201046.
XX
XX PR 01-MAY-1990; 90US-00517159.
XX PR 14-MAY-1991; 91US-00700653.
XX
XX PA (NEUR-) NEUROMEDICA INC.
XX
XX PI Shashoua VE;
XX
XX DR WPI; 1996-383719/38.
XX
XX PT New ependymin peptide fragments - useful for promoting nerve growth.
XX
XX PS Claim 1; Col 23; 19pp; English.
XX
XX CC AAW05556-W05583 represent fragments of the nerve growth factor ependymin.
CC Ependymin is a glycoprotein dimer. The protein is synthesised by specific
CC cells which secrete and maintain a steady state concentration of the
CC protein in the extracellular and cerebrospinal fluids of the brain.
CC Ependymin is a nerve growth promoter, but it is not currently known how
CC it functions. These sequences promote nerve growth, and may be used as
CC therapy to enhance recovery after stroke, to counteract age-related
CC memory loss, or to treat neurodegenerative diseases. These sequences can
CC also be used for research purposes, such as in neuron transplantation
CC studies. Fatty acid conjugates of these peptides (using 16-22C fatty
CC acids) have an increased brain-penetration index, and may be used for the
CC same purposes. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 7 AA;

Query Match 53.8%; Score 21; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDS 4
|||
Db 4 SYDS 7

Search completed: June 8, 2004, 19:37:08
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:23:37 ; Search time 42 Seconds
(without alignments)
46.890 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38
Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62
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Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 49349

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	9	US-09-832-312-65
2	38	100.0	7	10	US-09-832-312-65
3	38	100.0	7	11	US-09-832-312-65
4	34	89.5	7	15	US-10-425-855-13
5	33	86.8	7	10	US-09-832-312-65
6	33	86.8	7	10	US-09-832-312-65
7	31	81.6	7	10	US-09-832-312-65
8	30	78.9	7	10	US-09-832-312-65
9	29	76.3	7	10	US-09-832-312-65
10	28	73.7	7	14	US-10-091-300-11
11	28	73.7	7	16	US-10-399-701-11
12	27	71.1	7	9	US-09-832-312-65
13	27	71.1	7	11	US-09-832-312-65
14	26	68.4	7	10	US-09-832-312-65
15	26	68.4	7	16	US-10-440-522-28

16	25	65.8	7	9	US-09-832-312-53
17	25	65.8	7	9	US-09-832-312-53
18	25	65.8	7	10	US-09-832-312-53
19	25	65.8	7	10	US-09-832-312-53
20	25	65.8	7	11	US-09-832-312-53
21	25	65.8	7	11	US-09-832-312-53
22	24	63.2	7	14	US-10-091-300-8
23	23	60.5	7	14	US-10-091-300-55
24	23	60.5	7	14	US-10-091-300-55
25	22	57.9	4	9	US-09-759-584-17
26	22	57.9	7	9	US-09-759-584-17
27	22	57.9	7	9	US-09-759-584-17
28	22	57.9	7	9	US-09-759-584-17
29	22	57.9	7	13	US-10-060-714-5
30	22	57.9	7	14	US-10-091-300-64
31	22	57.9	7	14	US-10-091-300-73
32	22	57.9	7	14	US-10-091-300-79
33	22	57.9	7	15	US-10-463-442-10
34	22	57.9	7	15	US-10-463-442-10
35	21	55.3	6	12	US-10-399-701-11
36	21	55.3	7	12	US-10-399-701-11
37	21	55.3	7	16	US-10-440-522-25
38	19	50.0	5	14	US-10-006-869-3201
39	19	50.0	5	15	US-10-395-032-3201
40	19	50.0	6	14	US-10-006-869-3202
41	19	50.0	6	15	US-10-395-032-3202
42	19	50.0	7	8	US-08-967-573A-19
43	19	50.0	7	8	US-08-967-573A-19
44	19	50.0	7	8	US-08-967-573A-21
45	19	50.0	7	9	US-09-761-962-34

ALIGNMENTS

RESULT 1
US-09-832-312-65
; Sequence 65, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ IDS NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-65

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
Db 1 EDNQRPS 7

RESULT 2
US-09-972-656-13
; Sequence 13, Application US/09972656

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; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-13

Query Match      100.0%; Score 38; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
   |||||
Db 1 EDNQRPS 7

RESULT 3
US-09-829-495-65
; Sequence 65, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-65

Query Match      100.0%; Score 38; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
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Db 1 EDNQRPS 7

RESULT 4
US-10-425-855-13
; Sequence 13, Application US/10425855
; Publication No. US20040005324A1
; GENERAL INFORMATION:
; APPLICANT: PILKINGTON, GLENN
; APPLICANT: GILMOUR, PAGE

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; APPLICANT: CHANOCK, ROBERT
; APPLICANT: CROWE, JAMES
; APPLICANT: MURPHY, BRIAN
; TITLE OF INVENTION: NEUTRALIZING MONOCLONAL ANTIBODIES TO RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS
; FILE REFERENCE: I8602.0007/P007-A
; CURRENT APPLICATION NUMBER: US/10/425,855
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/043,530
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: 60/003,931
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-855-13

Query Match      89.5%; Score 34; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 6
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Db 1 EDNQRPS 6

RESULT 5
US-09-972-656-14
; Sequence 14, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-14

Query Match      86.8%; Score 33; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
   |||||
Db 1 EDDQRPS 7

RESULT 6
US-09-972-656-20
; Sequence 20, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20

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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-20

Query Match      86.8%; Score 33; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRPS 7
Db 1 EDDQRPS 7

RESULT 7
US-09-563-222-24
; Sequence 24, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563.222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-24

Query Match      81.6%; Score 31; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRPS 7
Db 1 DDNKRPS 7

RESULT 8
US-09-791-153A-8
; Sequence 8, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791.153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-8

Query Match      78.9%; Score 30; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRPS 7
Db 1 EDSERPS 7

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-12

Query Match      76.3%; Score 29; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNQRPS 7
Db 1 EDKERPS 7

RESULT 9
US-09-972-656-12
; Sequence 12, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972.656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-12

Query Match      73.7%; Score 28; DB 14; Length 7;
Best Local Similarity 83.3%; Pred. No. 1e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNQRPS 7
Db 2 NNQRPS 7

RESULT 11
US-10-399-701-12
; Sequence 12, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAR AG
; TITLE OF INVENTION: Rekombinant anti-GPIIb/IIIa-antibodies as agents for
; FILE REFERENCE: 23600PMO DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 100 57 443.2
; PRIOR FILING DATE: 2000-11-20
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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
; OTHER INFORMATION: an optimized antibody against GPIIB/IIIA
US-10-399-701-12

Query Match          73.7%; Score 28; DB 16; Length 7;
Best Local Similarity 83.3%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY  2 DNQRPS 7
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Db   2 NNQRPS 7

RESULT 12
US-09-832-312-71
; Sequence 71, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-71

Query Match          71.1%; Score 27; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY  3 NQRPS 7
    :|||||
Db   3 NQRPS 7

RESULT 13
US-09-829-495-71
; Sequence 71, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Vallevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
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; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-71

Query Match          71.1%; Score 27; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY  3 NQRPS 7
    :|||||
Db   3 NQRPS 7

RESULT 14
US-09-563-222-18
; Sequence 18, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098,406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-18

Query Match          68.4%; Score 26; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0;

QY  1 EDNQRPS 7
    :|:|:|
Db   1 DNNKRPS 7

RESULT 15
US-10-440-522-28
; Sequence 28, Application US/10440522
; Publication No. US20040091494A1
; GENERAL INFORMATION:
; APPLICANT: PIER, GERALD B
; APPLICANT: PRESTON, MICHAEL J
; APPLICANT: CAVACINI, LISA
; APPLICANT: POSNER, MARSHALL
; TITLE OF INVENTION: P. AERUGINOSA MUCOID EXOPOLYSACCHARIDE SPECIFIC BINDING PEPTIDES
; FILE REFERENCE: B00801.70285.US
; CURRENT APPLICATION NUMBER: US/10/440,522
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/153,437
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/292,365
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-522-28
Query Match      68.4%; Score 26; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDNQRPS 7
      :|:|:|
Db      1 DNNKRPS 7
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Search completed: June 8, 2004, 19:30:05
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:28:12 ; Search time 21 Seconds
(without alignments)
32.064 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	52.6	7	2	SL6364
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7	13	34.2	7	2	A59489
8	12	31.6	3	3	RHTD70
9	12	31.6	3	3	RHPGT
10	12	31.6	3	3	RHSHT
11	12	31.6	3	3	A32971
12	12	31.6	3	3	A33802
13	12	31.6	5	2	UN0862
14	12	31.6	5	2	A26830
15	12	31.6	5	2	P50324
16	12	31.6	6	2	S71349
17	12	31.6	7	2	B44787
18	12	31.6	7	2	I48105
19	12	31.6	7	2	E33932
20	12	31.6	7	2	A39630
21	11	28.9	5	2	D60274
22	11	28.9	5	2	PT0535
23	11	28.9	5	2	PT0540
24	11	28.9	6	2	PC4127
25	11	28.9	6	2	A19780
26	11	28.9	6	2	B35640
27	11	28.9	6	2	PT0604
28	11	28.9	6	2	PT0599
29	11	28.9	6	2	PT0657

30 11 28.9 6 2 PT0726 T-cell receptor be
31 11 28.9 6 4 S15596 orf 3 rata 5'-regi
32 11 28.9 7 1 A61324 dermorphin - Rohde
33 11 28.9 7 2 A61081 tryptophyllin - bas
34 11 28.9 7 2 B39040 calsequestrin, fas
35 11 28.9 7 2 PT0602 T-cell receptor be
36 11 28.9 7 2 PT0526 T-cell receptor be
37 11 28.9 7 2 PT0543 T-cell receptor be
38 11 28.9 7 2 PT0676 T-cell receptor be
39 10 26.3 3 3 A43391 TRH-like tripeptid
40 10 26.3 5 2 PT0281 IG heavy chain CRD
41 10 26.3 6 2 A37765 hypothetical prote
42 10 26.3 6 2 A61140 sperm acrosomal pr
43 10 26.3 7 2 A44428 platelet aggregati
44 10 26.3 7 2 A28709 phosphonoacetaldeh
45 10 26.3 7 2 S38516 mabinlin II chain

ALIGNMENTS

RESULT 1

SL6364

opacity protein P.IIe - Neisseria gonorrhoeae (strain FA1090) (fragment)

N/Alternate names: outer membrane protein P.IIe

C/Species: Neisseria gonorrhoeae

A/Variety: strain FA1090

C/Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C/Accession: S16364

R/Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.

Infect. Immun. 55, 2026-2031, 1987

A/Title: Antigenic and structural differences among six proteins II expressed by a single

A/Reference number: S16360; MUID:87306843; PMID:3114142

A/Accession: S16364

A/Molecule type: protein

A/Residues: 1-7 <BAR>

A/Experimental source: strain FA1090

A/Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein

C/Superfamily: opacity protein

C/Keywords: cell surface component; transmembrane protein

F;1-7/Product: opacity protein P.IIe (fragment) #status experimental <MAT>

Query Match 52.6%; Score 20; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNQR 5

Db 3 EDNGR 7

RESULT 2

S16365

opacity protein P.IIf - Neisseria gonorrhoeae (strain FA1090) (fragment)

N/Alternate names: outer membrane protein P.IIf

C/Species: Neisseria gonorrhoeae

A/Variety: strain FA1090

C/Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C/Accession: S16365

R/Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.

Infect. Immun. 55, 2026-2031, 1987

A/Title: Antigenic and structural differences among six proteins II expressed by a single

A/Reference number: S16360; MUID:87306843; PMID:3114142

A/Accession: S16365

A/Molecule type: protein

A/Residues: 1-7 <BAR>

A/Experimental source: strain FA1090

A/Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein

C/Superfamily: opacity protein

C/Keywords: cell surface component; transmembrane protein

F;1-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>

Query Match 52.6%; Score 20; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNR 5
|||
Db 3 EDNR 7

RESULT 3
A41890
protein D - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A41890
R;Slettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.
J. Bacteriol. 174, 4094-4100, 1992
A;Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.
A;Reference number: A41890; MUID:92283767; PMID:1597424
A;Accession: A41890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <SLR>
A;Cross-references: GB:M81463

Query Match 50.0%; Score 19; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNR 4
|||
Db 1 EDNR 4

RESULT 4
A15398
choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)
C;Species: Alcaligenes sp.
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A15398
R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.
J. Biochem. 88, 197-203, 1980
A;Title: Identification and properties of the prosthetic group of choline oxidase from A
A;Reference number: A15398; MUID:81006769; PMID:6997283
A;Accession: A15398
A;Molecule type: protein
A;Residues: 1-7 <OHT>
C;Keywords: oxidoreductase

Query Match 34.2%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNORPS 7
|||
Db 1 DNPNS 6

RESULT 5
S71299
ICL2 protein - Parametium tetraurelia (fragment)
C;Species: Parametium tetraurelia
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C;Accession: S71299
R;Wadeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A;Title: Characterization of centrin genes in Parametium.
A;Reference number: S71299; MUID:96248429; PMID:8665928
A;Accession: S71299
A;Molecule type: protein
A;Residues: 1-7 <MAD>
A;Experimental source: strain d4-2

C;Genetics:
A;Genetic code: SGCS

Query Match 34.2%; Score 13; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QRP 6
|:|
Db 1 QRP 3

RESULT 6
PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0283
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0283
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 34.2%; Score 13; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QRP 6
|:|
Db 4 QRP 6

RESULT 7
A59489
protein kinase C inhibitor - rat (fragment)
C;Species: Rattus norvegicus
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C;Accession: A59489
R;Negoro, M.
submitted to the Protein Sequence Database, June 2003
A;Description: Purification of PKCI from rat liver.
A;Reference number: A59489
A;Accession: A59489
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NEG>
A;Experimental source: strain Wistar, liver
A;Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 34.2%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNR 4
|||
Db 4 EDDR 7

RESULT 8
RHDT0
thyroliberin - Bombina orientalis
C;Species: Bombina orientalis
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A;Reference number: A90919; MUID:76138399; PMID:815011

A;Accession: A90919

A;Molecule type: protein

A;Residues: 1-3 <YAS>

C;Superfamily: thyroliberin precursor

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.6%; Score 12; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6

Db 1 QHP 3

RESULT 9

RHPGT

thyroliberin - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A01415

R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A;Title: Structure of porcine thyrotropin releasing hormone.

A;Reference number: A90560; MUID:70136150; PMID:4984938

A;Accession: A01415

A;Molecule type: protein

A;Residues: 1-3 <NAI>

R;Bolex, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing h

A;Reference number: A90167; MUID:70039904; PMID:4982117

A;Contents: annotation

A;Note: biological activities and Rf values (in 17 chromatographic systems) of the synth

C;Superfamily: thyroliberin precursor

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.6%; Score 12; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6

Db 1 QHP 3

RESULT 10

RHSHT

thyroliberin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A93750; A01415

R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulat

A;Reference number: A93750

A;Accession: A93750

A;Molecule type: protein

A;Residues: 1-3 <DES>

R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A;Reference number: A93161; MUID:70163386; PMID:4985794

A;Contents: annotation

A;Note: physicochemical characteristics and biological activities of the natural and syn

C;Superfamily: thyroliberin precursor

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.6%; Score 12; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6

Db 1 QHP 3

RESULT 11

A92971

thyroliberin - eastern newt (tentative sequence)

C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A92971; A01415

R;Grimm-Jorgensen, Y.; McKelvy, J.P.

J. Neurochem. 23, 471-478, 1974

A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) bra

A;Reference number: A92971; MUID:75035605; PMID:4214528

A;Accession: A92971

A;Molecule type: protein

A;Residues: 1-3 <GRI>

A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrol

stidine, or glutamic acid

C;Superfamily: thyroliberin precursor

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.6%; Score 12; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6

Db 1 QHP 3

RESULT 12

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A33802

R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A;Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate comp

A;Reference number: A33802; MUID:89255196; PMID:2498305

A;Accession: A33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-3 <COC>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 31.6%; Score 12; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6

Db 1 QHP 3

RESULT 13

JN0862

peptidyl-dipeptidase A inhibitory peptide C112 - striped bonito

C;Species: Sarda orientalis (striped bonito)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C;Accession: JN0862

R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A;Reference number: JN0859; MUID:94080036; PMID:7764272
A;Accession: JN0862
A;Molecule type: protein
A;Residues: 1-5 <MAT>
A;Experimental source: intestine
A;Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converti
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 31.6%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6
||
Db 2 RP 3

RESULT 14
A26830
mitosis inhibiting peptide - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: A26830
R;Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A;Reference number: A26830; MUID:87298602; PMID:3619940
A;Accession: A26830
A;Molecule type: protein
A;Residues: 1-5 <REI>
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.6%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDN 3
||
Db 2 EDS 4

RESULT 15
PS0324
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 31.6%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRPS 7
||
Db 2 QAPT 5

Search completed: June 8, 2004, 19:34:12
Job time : 21 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:29:17 ; Search time 11 Seconds
(without alignments)
33.136 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38
Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	34.2	7	1	CHOX_ALCSP
2	12	31.6	3	1	THYL_PIG
3	12	31.6	7	1	FARB_CALVO
4	10	26.3	7	1	FAR4_PANRR
5	9	23.7	4	1	TUFT_HUMAN
6	9	23.7	6	1	OVN_LEPDE
7	9	23.7	7	1	TPFY_PACDA
8	9	23.7	7	1	TV51_LITRU
9	9	23.7	7	1	UF04_MOUSE
10	8	21.1	5	1	BLOA_CITFR
11	8	21.1	5	1	PRTC_PERAM
12	8	21.1	5	1	TRM3_ECOLI
13	8	21.1	6	1	ASP2_LACSN
14	8	21.1	6	1	TMOF_SARBU
15	8	21.1	7	1	FAR1_ASCSU
16	8	21.1	7	1	LANC_CARUI
17	7	18.4	3	1	LUXE_VIBFI
18	7	18.4	4	1	DCML_PSECH
19	7	18.4	4	1	RM01_YEAST
20	7	18.4	5	1	BPP7_BOTIN
21	7	18.4	5	1	BI03_LITRU
22	7	18.4	5	1	FAP2_PARNR
23	7	18.4	5	1	SUGA_ACHDO
24	7	18.4	5	1	TPIS_CANFA
25	7	18.4	5	1	UKA4_CHLTR
26	7	18.4	6	1	ACPH_RABIT
27	7	18.4	6	1	CIP1_MYTED
28	7	18.4	6	1	CIP2_MYTED
29	7	18.4	6	1	EI01_LITRU
30	7	18.4	6	1	TRP1_PSEPU
31	7	18.4	6	1	VP19_HSVIK
32	7	18.4	7	1	ALL3_CARMA
33	7	18.4	7	1	ALL4_CARMA

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34 7 18.4 7 1 ALL5_CARMA
35 7 18.4 7 1 CARP_MYTED
36 7 18.4 7 1 ET05_LITRU
37 7 18.4 7 1 FAR1_HELTI
38 7 18.4 7 1 FAR1_PROCL
39 7 18.4 7 1 GRFP_MOUSE
40 7 18.4 7 1 MNF1_LEPDE
41 7 18.4 7 1 UF03_MOUSE
42 7 18.4 7 1 UN06_PINPS
43 6 15.8 4 1 ACHL_ACHFU
44 6 15.8 4 1 FLRN_ANTEU
45 6 15.8 4 1 OCPI_OCTMI

P81808 carcinus ma
P10420 mytilus edu
P82101 litoria rub
P41871 helisoma tr
P38499 procambarus
P99025 mus musculus
P42984 leptinotars
P38641 mus musculus
P81675 pinus pinas
P35904 achatina fu
P58707 anthopleura
P58648 octopus min

ALIGNMENTS

RESULT 1
CHOX_ALCSP
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Oxidoreductase.
FT NON TER
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 34.2%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNQRPS 7
Db 1 DNPNHS 6

RESULT 2
THYL_PIG
ID THYL_PIG STANDARD; PRT; 3 AA.
AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thyroliberin (thyrotropin releasing hormone) (TRH) (Protirelin).
OS Sus scrofa (pig),
OS Ovis aries (sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106(1970).

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RN [2]
RP SYNTHESIS.
RC SPECIES=PIG;
RX MEDLINE=7003904; PubMed=4982117;
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
RL releasing hormone and pyroglutamyl-histidyl-proline amide.";
RN Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
RD Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
RL stimulating hormone releasing factor of ovine origin by means of mass
RN spectrometry.";
RN Org. Mass Spectrom. 5:221-228(1971).
RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RD Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic
RL TSH-releasing factor.";
RN Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RN Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RP SEQUENCE.
RC SPECIES=N. viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RL viridescens) brain in vitro. Isolation and characterization of
RN thyrotropin releasing factor.";
RN J. Neurochem. 23:471-478(1974).
RN [7]
RP FUNCTION.
RC "FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
RX in the anterior pituitary gland and as a neurotransmitter/
RL neuromodulator in the central and peripheral nervous systems.
RN PIR; A90919; RHDTDO.
RX PIR; A92971; A92971.
RN PIR; A93750; RHSHST.
RX Amidation; Pyrrolidone carboxylic acid.
RN MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
RX MOD_RES 3 3 AMIDATION.
RN SEQUENCE 3 AA; 380 MW; 7761FGB000000000 CRC64;

Query Match 31.6%; Score 12; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6
DB 1 QHP 3

RESULT 3
FARB CALVO
ID FARB CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

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OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RD Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RL neuropeptides (designated calliFMRamides) from the blowfly
RN Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
CC PIR; B44787; B44787.
RX Neuropeptide; Amidation.
RN MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 31.6%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3
DB 2 DN 3

RESULT 4
FAR4 PANRE
ID FAR4 PANRE STANDARD; PRT; 7 AA.
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF4 (KPNFIRF-amide).
RX Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RD Tim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RL KPNFIRamide, a novel FMRamide-related peptide from the free-living
RN nematode, Panagrellus redivivus."
RX Peptides 16:87-93(1995).
CC -1- FUNCTION: Myoactive; induces a rapid concentration-dependent
muscle tension increase.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
RX Neuropeptide; Amidation.
RN MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 26.3%; Score 10; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPS 7
DB 1 KPN 3

RESULT 5
TUFT HUMAN
ID TUFT HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Phagocytosis-stimulating peptide (Tuftsin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RA "The characteristics, isolation and synthesis of the phagocytosis
 RT stimulating peptide tuftsin.";
 RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RA "The physiological role of the lymphoid system. VI. The stimulatory
 RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 RT activity of human polymorphonuclear leucocyte.";
 RL Biochemistry 6:3386-3392 (1967).
 CC -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
 CC cell membrane of neutrophils in the blood. Leucokininase on the
 CC membrane releases the active peptide tuftsin from the gamma chain.
 CC Tuftsin is essential for maximum stimulation of the phagocytic
 CC activity of neutrophils.
 DR PIR; A02147; A02147.
 DR MIM; 191150; -.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006909; P:phagocytosis; NAS.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 RP 6
 :|
 DB 2 KP 3

RESULT 6
 OVM_LRPDE
 ID OVM_LRPDE STANDARD; PRT; 6 AA.
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Oviductal motility stimulating peptide (Leb-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=91271080; PubMed=2052497;
 RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
 RA Proost P., Torrekens S., de Loof A.;
 RA "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RT decemlineata.";
 RL Peptides 12:31-36 (1991).
 CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
 CC oviduct.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6
 FT SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 RP 6
 :|
 DB 4 KP 5

RESULT 7
 TPFY_PACDA
 ID TPFY_PACDA STANDARD; PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-1 (Pdt-1).
 OS Pachymedusa dactinolor (Giant mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Phyllomedusinae; Pachymedusa.
 OX NCBI_TaxID=75988;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
 RP PRO-7.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Shaw C.;
 RA "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA.";
 RL Submitted (SEP-2002) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD_RES 3
 FT MOD_RES 3 HYDROXYLATION.
 FT MOD_RES 7
 FT SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 RP 6
 :|
 DB 1 KP 2

RESULT 8
 TY51_LITRU
 ID TY51_LITRU STANDARD; PRT; 7 AA.
 AC P82065;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin 5.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RA "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963 (1996).
 CC -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
 CC -!- SUBCELLULAR LOCATION: Secreted.

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CC  -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC  -!- MASS SPECTROMETRY: MW=965; METHOD=FAB.
CC  Amphibian defense peptide; Amidation; Neuropeptide;
KW  Pyrrolidone carboxylic acid.
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  MOD RES 7 7 AMIDATION.
FT  MOD RES 7 7 7401E9D3676046B0 CRC64;
SQ  SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QRP 6
Db 1 QIP 3

RESULT 9
UF04_MOUSE STANDARD; PRT; 7 AA.
AC F38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (p46) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 46 kDa.
FT NON_TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6
Db 2 KP 3

RESULT 10
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BTOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8906280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).

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CC  -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC  oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC  dianiononanoate.
CC  -!- COFACTOR: Pyridoxal phosphate.
CC  -!- PATHWAY: Biotin biosynthesis.
CC  -!- SUBUNIT: Homodimer.
CC  -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC  aminotransferases.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
CC  EMBL; M21922; -; NOT ANNOTATED_CDS.
CC  PIR; I40697; I40697.
CC  InterPro; IPR005814; Aminotrans 3.
CC  PROSITE; PS00600; AA_TRANSFER_CLASS 3; PARTIAL.
CC  Biotin biosynthesis; Transferase; Aminotransferase;
KW  Pyridoxal phosphate.
FT NON_TER 5
FT SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ED 2
Db 4 DD 5

RESULT 11
PRCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT

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RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872661;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RL pericardial organs and the shore crab, Carcinus maenas.";
RC Peptides 7:67-72(1986).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
modulates visceral and skeletal muscle in many arthropods.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons and in
the crab pericardial organs.
CC PIR; A01644; KOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PS 7
Db | :
| :
4 PT 5

RESULT 12
TRM3 ECOLI
ID TRM3 ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TraM protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A. PubMed=2836369;
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
and traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the traM family.
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-----
DR EMBL; M20941; -; NOT ANNOTATED CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA4435000000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNQ 4

RT
RL
RN
RP
RC
RX
RA
RT
RL
RC
CC
CC
CC
CC
DR
DR
KW
SQ

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PS 7
Db | :
| :
4 PT 5

RESULT 13
ASP2 LACSN
ID ASP2 LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBI;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON TER 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDN 3
Db | :
| :
3 EYN 5

RESULT 14
TMOF SARBU
ID TMOF SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Ovary;
RX MEDLINE=94211930; PubMed=8159807;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT (Sarcophaga) bullata.";
RL Regul. Pept. 50:61-72(1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium after a blood meal.
KW Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PS 7

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Wed Jun 9 06:02:34 2004

Db 1: 2 PT 3

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RESULT 15
FAR1_ASCSU
ID FAR1_ASCSU STANDARD; PRT; 7 AA.
AC F31889;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=90180465; PubMed=2627377;
RA Cowden C., Stretton A.O.W., Davis R.E.;
RT "AF1, a sequenced bioactive neuropeptide isolated from the nematode
RT Ascaris suum.";
RL Neuron 2:1465-1473(1989).
CC -!- FUNCTION: Potent modulator of inhibitory motoneurons. Reduces the
CC input resistance and blocks slow oscillatory potentials in these
CC cells.
CC -!- TISSUE SPECIFICITY: Found in the nerve cords and a variety of
CC ganglia particularly in the anterior regions.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NQ 4
1:
Db 2 NE 3
```

Search completed: June 8, 2004, 19:34:36
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:33:13 ; Search time 38 Seconds
(without alignments)
58.122 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315519202 residues

Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	39.5	7	8	O98866
2	12	31.6	7	2	O50556
3	12	31.6	7	8	Q8MFY6
4	12	31.6	7	10	P93233
5	11	28.9	7	2	P83530
6	11	28.9	7	11	Q63668
7	11	28.9	7	15	Q07624
8	10	26.3	7	2	Q47477
9	9	23.7	5	2	P83073
10	9	23.7	7	10	Q49223
11	8	21.1	7	3	P83492
12	8	21.1	7	4	Q8NH7
13	8	21.1	7	6	Q28742
14	7	18.4	5	10	Q99007
15	7	18.4	5	13	P83308
16	7	18.4	6	5	P83569

17	7	18.4	7	2	Q8KMS9
18	7	18.4	7	8	P92214
19	7	18.4	7	8	P92393
20	7	18.4	7	8	P92403
21	7	18.4	7	8	P92427
22	7	18.4	7	8	P92430
23	7	18.4	7	8	P92221
24	7	18.4	7	8	P92425
25	7	18.4	7	8	P92381
26	7	18.4	7	8	P92387
27	7	18.4	7	8	P92210
28	7	18.4	7	8	P92440
29	7	18.4	7	8	P92218
30	7	18.4	7	8	P92390
31	7	18.4	7	8	P92372
32	7	18.4	7	8	P92442
33	7	18.4	7	8	P92226
34	7	18.4	7	8	P92385
35	7	18.4	7	8	P92421
36	7	18.4	7	12	Q66113
37	7	18.4	7	12	Q65578
38	7	18.4	7	13	Q42564
39	7	18.4	7	15	Q8JB81
40	6	15.8	4	11	Q08433
41	6	15.8	6	2	P83533
42	6	15.8	7	2	Q47505
43	6	15.8	7	2	Q34028
44	6	15.8	7	2	Q07354
45	6	15.8	7	2	Q8GL12

ALIGNMENTS

RESULT 1

O98866 ID O98866 PRELIMINARY; PRT; 7 AA.
AC O98866;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044 (1986).
DR EMBL; X03496; CAA27215.1; --
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 39.5%; Score 15; DB 8; Length 7;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NQRP 6
Db 1 NFRP 4

RESULT 2

O50556 ID O50556 PRELIMINARY; PRT; 7 AA.

ID	Q8MFY6	PRELIMINARY;	PRT;	7 AA.
AC	Q8MFY6	PRELIMINARY;	PRT;	7 AA.
DT	01-JUN-1998 (TrEMBLrel. 06, Created)			
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	GLYA (Fragment).			
DE	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)			
GN	LE-ACS1B.			
OS	Lycopodium esculentum (Tomato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4081;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97351561; PubMed=9207843;			
RA	Ceateker J.H., Olson D.C., Shiu O.Y., Yang S.F.;			
RT	"Differential induction of seven 1-aminocyclopropane-1-carboxylate			
RT	synthase genes by elicitor in suspension cultures of tomato			
RT	(Lycopodium esculentum).";			
RL	Plant Mol. Biol. 34:275-286 (1997).			
DR	EMBL; U75692; AAC49682.1; -;			
DR	GO: GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.			
DR	GO: GO:0016829; F:lyase activity; IEA.			
KW	lyase.			
FT	NON TER			
SQ	SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;			
Qy	Query Match 31.6%; Score 12; DB 2; Length 7;			
Db	Best Local Similarity 100.0%; Pred. No. 1e+06;			
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	3 NQRP 6			
Db	1 NQLP 4			
RESULT 3				
Q8MFY6	PRELIMINARY;	PRT;	7 AA.	
AC	Q8MFY6	PRELIMINARY;	PRT;	7 AA.
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	PSBA (Fragment).			
GN	PSBA.			
OS	Taraxacum (sect. Dioszegia) sp. 4310Hnew.			
OC	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;			
OC	Taraxacum.			
OX	NCBI_TaxID=154248;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUR=Leaf;			
RA	Mes T.H.M.;			
RT	"Reconstruction of the evolution of trnf pseudogenes.";			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY015477; AAK21591.1; -;			
DR	GO: GO:0009507; C:chloroplast; IEA.			
KW	Chloroplast.			
FT	NON TER			
SQ	SEQUENCE 7 AA; 675 MW; 687451B5A76DDB70 CRC64;			
Qy	Query Match 31.6%; Score 12; DB 8; Length 7;			
Db	Best Local Similarity 50.0%; Pred. No. 1e+06;			
	Matches 2; Conservative 1; Mismatches 1; Indels 1; Gaps 0;			
Qy	4 QRPS 7			
Db	1 EAPS 4			
RESULT 4				
Q8MFY6	PRELIMINARY;	PRT;	7 AA.	
AC	Q8MFY6	PRELIMINARY;	PRT;	7 AA.
DT	01-JUN-1997 (TrEMBLrel. 03, Created)			
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	GLYA (Fragment).			
DE	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)			
GN	LE-ACS1B.			
OS	Lycopodium esculentum (Tomato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4081;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97351561; PubMed=9207843;			
RA	Ceateker J.H., Olson D.C., Shiu O.Y., Yang S.F.;			
RT	"Differential induction of seven 1-aminocyclopropane-1-carboxylate			
RT	synthase genes by			

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Q63668
ID Q63668 PRELIMINARY; PRT; 7 AA.
AC Q63668;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF2 protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA MEDLINE=9539550; PubMed=7667072;
RA Mandon B., Bellanger A.C., Elalouf J.M.;
RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin
RT V2 receptor gene.";
RL pflugers Arch. 430:12-18(1995).
DR EMBL; X83264; CAA58237.1; -
SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;

Query Match 28.9%; Score 11; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PS 7
Db 6 PS 7

RESULT 7
Q07624
ID Q07624 PRELIMINARY; PRT; 7 AA.
AC Q07624;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE UORF1.
OS Rous sarcoma virus (strain Prague C).
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010967; PubMed=1327749;
RA Donze C., Spahr P.F.;
RT "Role of the open reading frames of Rous sarcoma virus leader RNA in
RT translation and genome packaging.";
RL EMBO J. 11:3747-3757(1992).
DR EMBL; X67587; CAA47862.1; -
SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 28.9%; Score 11; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PS 7
Db 4 PS 5

RESULT 8
Q47477
ID Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 26.3%; Score 10; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QR 5
Db 6 QR 7

RESULT 9
P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to Swiss-Prot.
FT NON_TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 23.7%; Score 9; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNQ 4
Db 2 KDTE 5

RESULT 10
O49223
ID O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HMG-1-like protein (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RX MEDLINE=91367679; PubMed=1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins.";

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RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047050; AAC03556.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match
Best Local Similarity 23.7%; Score 9; DB 10; Length 7;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDN 3
DB 5 DDD 7

RESULT 11
P83492 ID P83492 PRELIMINARY; PRT; 7 AA.
AC P83492;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-OCT-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
OS Bionectria ochroleuca (Glicocladium roseum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
OX NCBI_TaxID=29856;
[1]
RN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RP STRAIN=Gr87;
RC Zhao M., Zhang K.;
RA Submitted (DEC-2002) to Swiss-Prot.
RL FUNCTION: ACTS AS A SERINE PROTEASE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR InterPro; IPR000209; Peptidase S8.
DR PROSITE; PS00136; SUBTILASE_ASF; PARTIAL.
DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON TER 7
SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1AD80 CRC64;

Query Match
Best Local Similarity 21.1%; Score 8; DB 3; Length 7;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDN 3
DB 3 QSN 5

RESULT 12
Q8NH7 ID Q8NH7 PRELIMINARY; PRT; 7 AA.
AC Q8NH7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Mini-cistron.
GN NHE3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP

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RA Malakooti J., Ramaswamy K.;
RT "Molecular cloning and characterization of the human Na+/H+ exchanger
  NHE-3 gene promoter region.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282824; AAM33436.1; -.
SQ SEQUENCE 7 AA; 842 MW; 74072DC72D406F0 CRC64;

Query Match
Best Local Similarity 21.1%; Score 8; DB 4; Length 7;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PS 7
DB 4 PA 5

RESULT 13
Q28742 ID Q28742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
  ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
DR PIR; I46868; I46868.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match
Best Local Similarity 21.1%; Score 8; DB 6; Length 7;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNQ 4
DB 5 DEE 7

RESULT 14
Q99007 ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN AMY1 GENE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
  acid and abscisic acid in protoplasts prepared from mature barley
  aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
DR EMBL; X54643; CAA38455.1; -.

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FT  NON TER      5
SQ  SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match      18.4%; Score 7; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 NQ 4
      1
      |
Db      3 NK 4

RESULT 15
P83308
ID      P83308      PRELIMINARY;      PRT;      5 AA.
AC      P83308;
DT      01-JUN-2002 (TREMELrel. 21, Created)
DT      01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT      01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE      FMRamide-like neuropeptide (LPLRF-amide).
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE, AND SYNTHESIS.
RC      TISSUE=Brain;
RX      PubMed=6137771;
RA      Dockray G.J.; Reeve J.R. Jr.; Shively J.; Gayton R.J.; Barnard C.S.;
RT      "A novel active pentapeptide from chicken brain identified by
RT      antibodies to FMRamide.";
EL      Nature 305:328-330(1983).
CC      -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC      -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
DR      GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
KW      Neuropeptide; Amidation.
FT      MOD_RES      5      AMIDATION.
SQ      SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match      18.4%; Score 7; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 P 6
      1
      |
Db      2 P 2

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Search completed: June 8, 2004, 19:36:04
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:23:07 ; Search time 52 Seconds
(without alignments)
38.035 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 92273

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	4 AAB61297	Aab61297 Anti-TANG
2	38	100.0	7	6 ABU11263	Abu11263 Human TAN
3	34	89.5	7	2 AAU16592	Aau16592 Anti-RSV
4	31	81.6	7	5 AAU70344	Aau70344 Human lam
5	30	78.9	7	4 AAU08352	Aau08352 Antibody
6	29	76.3	7	6 ABP72113	Abp72113 Human IGE
7	28	73.7	7	2 AAU90304	Aau90304 Human ant
8	28	73.7	7	3 AAU95207	Aay95207 Anti-Plat
9	28	73.7	7	3 AAB39991	Aab39991 Anti-HIL1
10	28	73.7	7	5 AAU28860	Aae28860 Human KDR
11	28	73.7	7	5 AAU17796	Aao17796 CDR2 regi
12	28	73.7	7	6 ABJ26753	Abj26753 VEGF bind
13	28	73.7	7	7 ADD24404	Add24404 Human var
14	28	73.7	7	7 ADD80781	Add80781 Human var
15	27	71.1	7	2 AAU90337	Aaw90337 Human ant
16	27	71.1	7	4 AAB66404	Aab66404 Anti-TANG
17	27	71.1	7	6 ABU11269	Abu11269 Human TAN
18	26	68.4	7	5 AAU70338	Aau70338 Human lam
19	25	65.8	7	3 AAB39999	Aab39999 Anti-HIL1
20	25	65.8	7	3 AAB39990	Aab39990 Anti-HIL1
21	25	65.8	7	4 AAB61285	Aab61285 Anti-TANG
22	25	65.8	7	4 AAB61291	Aab61291 Anti-TANG
23	25	65.8	7	6 ABU11257	Abu11257 Human TAN
24	25	65.8	7	6 ABU11251	Abu11251 Human TAN
25	24	63.2	7	3 AAB39996	Aab39996 Anti-HIL1

26	24	63.2	7	5 AAE28857	Aae28857 Human KDR
27	24	63.2	7	6 ABJ26750	Abj26750 VEGF bind
28	24	63.2	7	7 ADD24401	Add24401 Human p1C
29	24	63.2	7	7 ADD80778	Add80778 Human var
30	23	60.5	7	3 AAY79089	Aay79089 Anti-fact
31	23	60.5	7	3 AAB39496	Aab39496 Anti-HIL-
32	23	60.5	7	3 AAB39504	Aab39504 Anti-HIL-
33	23	60.5	7	3 AAB39993	Aab39993 Anti-HIL1
34	23	60.5	7	3 AAB39992	Aab39992 Anti-HIL1
35	23	60.5	7	3 AAB40004	Aab40004 Anti-HIL1
36	23	60.5	7	3 AAB40002	Aab40002 Anti-HIL1
37	23	60.5	7	3 AAB40005	Aab40005 Anti-HIL1
38	23	60.5	7	3 AAB40006	Aab40006 Anti-HIL1
39	23	60.5	7	3 AAB40008	Aab40008 Anti-HIL1
40	23	60.5	7	3 AAB40001	Aab40001 Anti-HIL1
41	23	60.5	7	3 AAB39512	Aab39512 Anti-HIL-
42	23	60.5	7	3 AAB40003	Aab40003 Anti-HIL1
43	23	60.5	7	3 AAB39998	Aab39998 Anti-HIL1
44	23	60.5	7	3 AAB40007	Aab40007 Anti-HIL1
45	23	60.5	7	3 AAB40000	Aab40000 Anti-HIL1

ALIGNMENTS

RESULT 1

AAB61297	ID	AAB61297 standard; peptide; 7 AA.
XX	AC	AAB61297;
XX	DT	04-APR-2001 (first entry)
XX	DE	Anti-TANGO 268 scFv CDR, SEQ ID NO: 65.
XX	KW	Human; antibody; scFv; CDR; complementarity determining region;
KW	TANGO 268;	cardiant; cerebroprotective; cytostatic; anticoagulant;
KW	thrombolytic;	antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW	platelet membrane glycoprotein receptor;	bleeding disorder;
KW	blood vessel injury;	thrombotic disorder; haemorrhagic disorder; stroke;
KW	ischaemia;	cardiovascular disease; immunological disease; liver disorder;
KW	cancer.	
XX	OS	Homo sapiens.
XX	PN	WO200100810-A1.
XX	PD	04-JAN-2001.
XX	PF	30-JUN-2000; 2000WO-US018152.
XX	PR	30-JUN-1999; 99US-00145468.
PR	06-DEC-1999;	99US-00454824.
PR	14-FEB-2000;	2000US-00503387.
XX	PA	(MILL-) MILLENNIUM PHARM INC.
XX	PI	Busfield SJ, Villelial J, Jandrot-Perrus M, Vainchencker W;
PI	Gill DS,	Qian MD, Kingsbury G;
XX	DR	WPI; 2001-080877/09.
XX	PT	New genes encoding human platelet-expressed collagen receptor,
PT	glycoprotein VI, and its modulators, useful for preventing, treating and	
PT	diagnosing hemorrhagic disorders, thrombotic diseases and immunological	
PT	disorders.	
XX	PS	Claim 32; Page 102; 227pp; English.
XX	CC	The present sequence is given in a specification relating to an isolated
CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor	
CC	glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides	
CC	and polypeptides and their modulators, e.g. antisense nucleic acids,	

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 |||||
 Db 1 EDNQRPS 7

RESULT 2
 ABU11263
 ID ABU11263 standard; peptide; 7 AA.
 XX
 AC ABU11263;

06-FEB-2003 (first entry)

Human TANGO 268 VLCDR1 Peptide #3.

Human; mouse; variable heavy; VH; antigen; cancer;
 complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 TANGO 268; extracellular matrix; collagen; platelet release;
 proliferation; migration; embryogenesis; inflammation; thrombosis;
 degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 cardiovascular disease; angina pectoris; myocardial infarction;
 coronary restenosis; atherosclerosis; immunological disorder;
 developmental disorder; embryonic disorder; liver disorder;
 cerebral vascular disease; venous thromboembolism disease.

Homo sapiens.

WO200280968-A1.

17-OCT-2002.

09-APR-2002; 2002WO-US011122.

09-APR-2001; 2001US-00829495.

(MILL-) MILLENNIUM PHARM INC.

Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

Gill DS, Qian DM, Kingsbury G;

WPI; 2003-058477/05.

Novel substantially purified antibody immunospecifically binding to TANGO
 268 antigen, useful for treating bleeding disorders such as
 thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis.

Claim 11; Page 111; 236pp; English.

This invention relates to a novel purified antibody comprising a variable
 heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 |||||
 Db 1 EDNQRPS 7

RESULT 3

AAW16592

ID AAW16592 standard; peptide; 7 AA.

AC AAW16592;

30-NOV-1997 (first entry)

Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6 CDR2.

Respiratory syncytial virus; RSV; monoclonal antibody; CDR;
 complementarity determining region; pneumonia; bronchiolitis; diagnosis;
 therapy; vaccine; RSVF2-5.

Homo sapiens.

WO9710846-A1.

27-MAR-1997.

18-SRP-1996; 96WO-US014937.

18-SEP-1995; 95US-0003931P.

(INTR-) INTRACEL CORP.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Pilkington GR, Gilmour PS, Chanock RM, Crowe JE, Murphy BR;

WPI; 1997-202621/18.

Composition comprising respiratory syncytial virus antibody - useful for
 treatment or prophylaxis of active disease or infection.

Claim 8; Page 56; 71pp; English.

This peptide sequence comprises complementarity determining region 2
 (CDR2) of the light chain VL6 region of a novel neutralising human

CC monoclonal antibody to the respiratory syncytial virus (RSV). The
CC antibody, designated RSVF2-5 (ATCC 69909), selectively binds to an RSV F
CC glycoprotein epitope. DNA encoding RSVF2-5 Fd and light chain (see
CC AAT66556-57) was isolated from a phage library prepared from the RNA of
CC peripheral blood lymphocytes of an HIV-1 infected donor. A claimed
CC pharmaceutical preparation comprises a carrier and an antibody that
CC includes the RSVF2-5 VH3 CDR3 (AAW16584) and which may also include the
CC VH3 CDR2 (AAW16584) and/or CDR1 (AAW16582) or the entire Fd region
CC (AAW16594), CDR2, CDR1 (AAW16590) or entire light chain (AAW16588). The
CC preparation alternatively comprises a carrier and a vector that includes
CC a nucleotide sequence encoding the antibody. The preparations can be used
CC for the treatment or prophylaxis of active RSV disease or infection
CC (claimed), and may also be used for RSV detection. The antibody binds and
CC neutralises antigenic subgroups A and B of RSV with high efficiency
XX
SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORP 6
| | | | |
Db 1 EDNORP 6

RESULT 4
AAU70344
ID AAU70344 standard; peptide; 7 AA.

AC AAU70344;

XX 14-FEB-2002 (first entry)

DE Human lambda III light chain CDR2.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CDR2.

OS Homo sapiens.

XX WO200183806-A1.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014349.

XX 02-MAY-2000; 2000US-00563222.

XX (EPIC-) EPICYTE PHARM INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.

XX Disclosure; Page 14; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,

CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 7 AA;

Query Match 81.6%; Score 31; DB 5; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
: | | | |
Db 1 DDNKRPS 7

RESULT 5
AAU08352
ID AAU08352 standard; peptide; 7 AA.

XX AAU08352;

XX 17-DEC-2001 (first entry)

DE Antibody light chain variable region CDR2 #4.

XX Antibody; light chain; CDR2; complementarity determining region; OPGBP;
KW osteopathic; osteoprotein binding protein; osteoclast formation;
KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
KW steroid-induced osteoporosis.

OS Synthetic.

XX WO200162932-A1.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005973.

XX 23-FEB-2000; 2000US-00511139.

XX 22-FEB-2001; 2001US-00791153.

XX (AMGE-) AMGEN INC.

XX Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;

XX WPI; 2001-557706/62.

XX Antibodies that bind antagonistically to osteoprotein binding protein,
XX useful for treating osteoporosis, metastasis of cancer to bone,
XX rheumatoid arthritis, hypercalcaemia of malignancy and steroid-induced
XX osteoporosis.

XX Claim 14; Page 129; 239pp; English.

XX The invention relates to an antibody or antigen binding domain (or
CC fragment, variant or derivative), which binds to an osteoprotein
CC binding protein (OPGBP) and which is an antagonistic antibody. The
CC antibody or antigen binding domain may be administered to inhibit
CC osteoclast formation or activation, inhibit bone resorption in a mammal,
CC prevent or treat loss of bone mass in a mammal and to prevent or treat
CC tumour cell growth in bone. The loss of bone mass results from
CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC present sequence is an antibody light chain variable region
CC complementarity determining region, CDR2, which can be incorporated into
CC an antibody/antigen binding domain of the invention

XX

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SQ      Sequence 7 AA;
Query Match      78.9%; Score 30; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. NO. 1.4e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNQRP 7
        ||:||||
Db       1 EDSRPS 7

RESULT 6
ABP72113
ID      ABP72113 standard; peptide; 7 AA.
XX
AC      ABP72113;
XX
DT      27-JUN-2003 (first entry)
XX
DE      Human IgE receptor antibody variable light domain CDR2.
XX
KW      Human; antibody; variable light domain; IgE receptor; IgE; CDR2;
KW      anti-allergic; allergy.
XX
OS      Homo sapiens.
XX
PN      WO2003008584-A1.
XX
PD      30-JAN-2003.
XX
PF      18-JUL-2002; 2002WO-JP007283.
XX
PR      19-JUL-2001; 2001JP-00219990.
XX
PA      (KAGA ) CHEVO-SERO-THERAPEUTIC RES INST.
XX
PI      Sugimura K, Nakashima T, Torikai M;
XX
DR      WPI; 2003-229579/22.
XX
PT      Antibodies and antibody fragments inhibiting binding of human IgE to its
PT      receptor and gene fragments encoding them for treatment of allergic
PT      disease.
XX
PS      Claim 7; Page 13; 29pp; Japanese.
XX
CC      The invention relates to novel gene fragments encoding an antibody
CC      fragment which contains the variable regions of the heavy and/or light
CC      chains of a human anti-IgE receptor antibody, which binds to human IgE
CC      receptor and is able to inhibit the binding of human IgE to its receptor.
CC      The polypeptides of the invention have anti-allergic activity, and are
CC      useful in the treatment of allergic diseases induced by binding of IgE to
CC      its receptor. The present sequence represents CDR2 of the variable light
CC      domain of the human IgE receptor antibody of the invention
XX
SQ      Sequence 7 AA;
Query Match      76.3%; Score 29; DB 6; Length 7;
Best Local Similarity 71.4%; Pred. NO. 1.4e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNQRP 7
        ||:||||
Db       1 EDSKRP 7

RESULT 7
AAW90304
ID      AAW90304 standard; protein; 7 AA.
XX
AC      AAW90304;
XX
DT      07-SEP-1999 (first entry)
XX
XX
DE      Anti-platelet glycoprotein Ib human H1b-2 VL CDR2.
XX
KW      Variable light chain; single chain antibody; scFv; human; H1b-2;
KW      glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW      antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW      complementarity determining region.
XX
OS      Homo sapiens.
XX
PN      WO200026667-A1.
XX
XX
DE      Human anti-GPIIb/IIIa auto-antibody light chain protein CDR2 region 2.
XX
KW      Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
KW      blood platelet membrane protein; predisposition; prevention; treatment;
KW      autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
KW      thrombocyte; cardiac infarction; pulmonary embolism; light chain.
XX
OS      Homo sapiens.
XX
PN      WO9855619-A1.
XX
PD      10-DEC-1998.
XX
PF      05-JUN-1998; 98WO-EP003397.
XX
PR      06-JUN-1997; 97DE-01023904.
PR      12-DEC-1997; 97DE-01055227.
PR      08-MAY-1998; 98DE-01020663.
XX
PA      (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX
PI      Berchtold P, Escher RFA;
XX
DR      WPI; 1999-105496/09.
XX
PT      Nucleic acid encoding human autoantibodies against platelet glycoprotein
PT      IIb/IIIa - used for diagnosis, treatment and prevention of autoimmune
PT      thrombocytopenic purpura and for modulation of fibrinogen binding.
XX
PS      Claim 6b; Page 6; 93pp; German.
XX
CC      This invention describes novel nucleic acid fragments that encode human
CC      auto-antibodies and anti-idiotypic antibodies against blood platelet
CC      membrane protein, GPIIb/IIIa. The products of the invention are used for
CC      diagnosis (including monitoring and determining predisposition),
CC      prevention and treatment of autoimmune thrombocytopenic purpura (AITP)
CC      and also for modulating binding of fibrinogen to thrombocytes
CC      (particularly to dissolve thrombi and/or prevent their formation, e.g. in
CC      cases of cardiac infarction or pulmonary embolism). Unlike murine
CC      antibodies, human antibodies (hAb) do not induce adverse side effects and
CC      persist for longer in vivo than small peptides. AAW90293-W90337 represent
CC      antibody fragments used in the method of the invention
XX
SQ      Sequence 7 AA;
Query Match      73.7%; Score 28; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. NO. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNQRP 7
        :|||||
Db       2 NNQRP 7

RESULT 8
AAV95207
ID      AAV95207 standard; peptide; 7 AA.
XX
AC      AAV95207;
XX
DT      29-AUG-2000 (first entry)
XX
DE      Anti-platelet glycoprotein Ib human H1b-2 VL CDR2.
XX
KW      Variable light chain; single chain antibody; scFv; human; H1b-2;
KW      glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW      antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW      complementarity determining region.
XX
OS      Homo sapiens.
XX
PN      WO200026667-A1.
XX

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XX 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US025495.
 XX 30-OCT-1998; 98US-0106275P.
 XX (MILL/) MILLER J L.
 XX Miller JL;
 XX WPI; 2000-365744/31.
 XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT Ib alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 XX Claim 20; Fig 6; 89pp; English.
 XX The present sequence is that of complementarity determining region 2
 CC (CDR2) of the light chain variable region (VL) of human single chain
 CC antibody (scFv) HIB-2 (see AAY95209), which is directed against platelet
 CC glycoprotein Ib (GPIb). The HIB series of scFv was isolated from a human
 CC synthetic VH and VL scFv library on the basis of their binding to
 CC platelet GPIb. Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by *Escherichia coli*, the HIB scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL
 CC chain, including CDR fragments, are also claimed
 XX Sequence 7 AA;
 SQ
 Query Match 73.7%; Score 28; DB 3; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNQRP 7
 Db :|||
 2 NNQRP 7
 RESULT 9
 AAB39991
 ID AAB39991 standard; peptide; 7 AA.
 AC AAB39991;
 XX 05-FEB-2001 (first entry)
 XX Anti-hIL2 antibody light chain CDR2 amino acid sequence SEQ ID 507.
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX antisclerotic; neuroprotective; antipsoriatic; antistomatitic; cardiant;
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US007946.
 XX 25-MAR-1999; 99US-0126603P.

XX (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX Claim 33; Fig 2G; 377pp; English.
 XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAB61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antarthritic; antisclerotic; antinflammatory;
 CC neuroprotective; antipsoriatic; antistomatitic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX Sequence 7 AA;
 SQ
 Query Match 73.7%; Score 28; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNQRPS 7
 Db :|||
 1 ENDQRPS 7
 RESULT 10
 AAE28860
 ID AAE28860 standard; peptide; 7 AA.
 XX AAE28860;
 XX 27-DEC-2002 (first entry)
 XX Human KDR (VEGFR-2) Fab light chain CDR2 from D1F7 clone.
 XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
 XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 XX breast; VEGFR; heart; EGFR; complementarity determining region; therapy;
 XX invasiveness; CDR.
 XX Homo sapiens.
 XX WO200270008-A1.
 XX 12-SEP-2002.
 XX 04-MAR-2002; 2002WO-US006762.
 XX 02-MAR-2001; 2001US-00798689.

XX (IMCL-) IMCLONE SYSTEMS INC.
 PA (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 XX WPI; 2002-691738/74.
 DR
 XX Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists.
 XX
 PS Example 9; Page 78; 151pp; English.
 XX
 CC The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumours. The inhibition or
 CC reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancerous and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) fab antibody light chain complementarity determining
 CC region (CDR) peptide
 XX
 SQ Sequence 7 AA;
 Query Match 73.7%; Score 28; DB 5; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNQRPS 7
 Db :|||||
 2 NNQRPS 7
 RESULT 11
 ID AAO17796
 AC AAO17796 standard; peptide; 7 AA.
 XX
 XX AAO17796;
 DT 15-AUG-2002 (first entry)
 XX
 DE CDR2 region of antibody for glycoprotein IIb/IIIa receptor #4.
 XX
 CC CDR2; complementarity determining region 2; antibody; metastatic;
 KW glycoprotein IIb/IIIa; GPIIb/IIIa; angiogenesis; cancer; cytostatic;
 KW antiangiogenic; vasotropic; intimal hyperplasia; vascular occlusion.
 XX
 OS Unidentified.
 XX
 PN DE10057443-A1.
 XX
 PD 23-MAY-2002.
 XX
 XX 20-NOV-2000; 2000DE-01057443.
 XX
 PR 20-NOV-2000; 2000DE-01057443.
 XX
 PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
 XX
 PI Peter B, Escher RF;
 XX
 XX WPI; 2002-472625/51.
 DR

XX Use of specific antibodies, or individual chains, for treating tumors and
 PT vascular occlusions, by inhibition of the gpIb/IIIa receptor.
 XX
 PS Claim 6; Page 10; 10pp; German.
 XX
 CC The present invention relates to the use of heavy or light chains or
 CC their functional derivatives or fragments, having specific CDR
 CC (complementarity determining region) sequences of antibodies. The
 CC peptides can be used for the combined inhibition of the binding of
 CC fibrinogen to thrombocytes and of vitronectin to endothelial cells, the
 CC inhibition of angiogenesis, the inhibition of tumour metastasis and/or
 CC the inhibition of intimal hyperplasia after vascular injury. They are
 CC useful for prevention and treatment of vascular occlusion and for
 CC treating tumours. The present sequence is a CDR2 region of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 73.7%; Score 28; DB 5; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNQRPS 7
 Db :|||||
 2 NNQRPS 7
 RESULT 12
 ID ABJ26753 standard; peptide; 7 AA.
 XX
 XX ABJ26753;
 DT 01-MAY-2003 (first entry)
 XX
 DE VEGF binding related peptide SEQ ID No 63.
 XX
 CC Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KW leukaemia cell; vascular endothelial growth factor; tumour;
 KW bispecific antigen-binding protein; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003002144-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 26-JUN-2002; 2002WO-US020332.
 XX
 PR 26-JUN-2001; 2001US-0301299P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Zhu Z;
 XX
 XX WPI; 2003-201468/19.
 DR
 XX
 PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a second
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
 PT treating tumors.
 XX
 PS Claim 14; Page 26; 98pp; English.
 XX
 CC The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells and
 CC migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a human peptide relating to the

CC bispecific antibodies that bind to the VEGF receptors of the invention

XX

QQ Sequence 7 AA;

Query Match 73.7%; Score 28; DB 6; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7

DB 2 NNORPS 7

RESULT 13

ADD24404

ID ADD24404 standard; peptide; 7 AA.

XX

AC ADD24404;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human IgG1 heavy chain variable region CDR-H3 #2.

XX

KW tumour; vascular endothelial growth factor receptor; VEGFR;

KW epidermal growth factor receptor; EGFR; cancer; human; IgG1;

KW immunoglobulin.

XX

OS Homo sapiens.

XX

PN US2003108545-A1.

XX

PD 12-JUN-2003.

XX

PF 04-MAR-2002; 2002US-00091300.

XX

PR 10-FEB-1994; 94US-00196041.

PR 20-OCT-1994; 94US-00326552.

PR 07-JUN-1995; 95US-00476533.

PR 03-SEP-1996; 96US-00706804.

PR 07-JAN-1997; 97US-00779450.

PR 10-NOV-1997; 97US-00967113.

PR 22-SEP-1999; 99US-00401163.

PR 02-MAR-2001; 2001US-00798689.

XX

PA (ROCK/) ROCKWELL P.

PA (GOLD/) GOLDSTEIN N I.

XX

PI Rockwell P, Goldstein NI;

XX

WPI; 2003-801265/75.

XX

PT Inhibiting tumor growth by administering to a human a vascular

PT endothelial growth factor receptor (VEGFR) antagonist and epidermal

PT growth factor receptor (EGFR) antagonist.

XX

Example 9; SEQ ID NO 11; 90pp; English.

PS

CC The invention relates to a method of inhibiting tumour growth comprising

CC administering to a human a vascular endothelial growth factor receptor

CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)

CC antagonist. The method is useful for inhibiting tumour growth. The

CC present sequence is used in the exemplification of the invention.

XX

Sequence 7 AA;

Query Match 73.7%; Score 28; DB 7; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7

DB 2 NNORPS 7

RESULT 14

ADD80781

ID ADD80781 standard; peptide; 7 AA.

XX

AC ADD80781;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human variable light chain CDR2 KDR antibody SEQ ID NO:11.

XX

KW human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;

KW tumour; angiogenesis.

XX

OS Homo sapiens.

XX

PN WO2003075840-A2.

XX

PD 18-SEP-2003.

XX

PF 04-MAR-2003; 2003WO-US006459.

XX

PR 04-MAR-2002; 2002US-0361783P.

XX

PA (IMCL-) IMCLONE SYSTEMS INC.

XX

PI Zhu Z;

XX

WPI; 2003-779032/73.

XX

PT New human anti-KDR antibody, useful for preparing a composition for

PT reducing tumor growth and inhibiting angiogenesis.

XX

Example 1; SEQ ID NO 11; 49pp; English.

PS

CC The invention relates to a novel isolated human antibody or its fragment

CC binds selectively to KDR. An antibody of the invention has cytostatic

CC activity, and may have a use in gene therapy. The antibody is anti-KDR

CC antibody. The antibody is useful for preparing a composition for reducing

CC tumour growth and inhibiting angiogenesis. The present sequence is used

CC in the exemplification of the invention.

XX

Sequence 7 AA;

Query Match 73.7%; Score 28; DB 7; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7

DB 2 NNORPS 7

RESULT 15

AAW90337

ID AAW90337 standard; protein; 7 AA.

XX

AC AAW90337;

XX

DT 07-SEP-1999 (first entry)

XX

DE Human anti-idiotypic antibody light chain protein CDR2 region 2.

XX

KW Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;

KW blood platelet membrane protein; predisposition; prevention; treatment;

KW autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombi;

KW thrombocyte; cardiac infarction; pulmonary embolism; light chain; CDR2.

XX

OS Homo sapiens.

XX

PN WO9855619-A1.

XX

PD 10-DEC-1998.

```

XX PF 05-JUN-1998; 98WO-EP003397.
XX PR 06-JUN-1997; 97DE-01023904.
XX PR 12-DEC-1997; 97DE-01055227.
XX PR 08-MAY-1998; 98DE-01020663.
XX PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX PI Berchtold P, Escher RFA;
XX DR WPI; 1999-105496/09.
XX PT
XX PT Nucleic acid encoding human autoantibodies against platelet glycoprotein
XX PT IIb/IIIa - used for diagnosis, treatment and prevention of autoimmune
XX PT thrombocytopaenic purpura and for modulation of fibrinogen binding.
XX PS Claim 10; Page 10; 93pp; German.
XX CC
XX CC This invention describes novel nucleic acid fragments that encode human
XX CC auto-antibodies and anti-idiotypic antibodies against blood platelet
XX CC membrane protein, GPIIb/IIIa. The products of the invention are used for
XX CC diagnosis (including monitoring and determining predisposition), (A1TP)
XX CC prevention and treatment of autoimmune thrombocytopaenic purpura
XX CC and also for modulating binding of fibrinogen to thrombocytes
XX CC (particularly to dissolve thrombi and/or prevent their formation, e.g. in
XX CC cases of cardiac infarction or pulmonary embolism). Unlike murine
XX CC antibodies, human antibodies (hAb) do not induce adverse side effects and
XX CC persist for longer in vivo than small peptides. AAW90293-W90337 represent
XX CC antibody fragments used in the method of the invention
XX SQ Sequence 7 AA;

```

```

Query Match 71.1%; Score 27; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDNORPS 7
Db ||: |||
1 EDSYRPS 7

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Search completed: June 8, 2004, 19:29:11
 Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:21:16 ; Search time 23 Seconds
(without alignments)
29.180 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	62.9	13	1	US-07-988-925-4
2	39	62.9	13	2	US-08-362-780-4
3	28	45.2	13	4	US-09-383-667-13
4	27	43.5	13	4	US-09-524-435-10
5	25	40.3	10	4	US-09-149-476-706
6	25	40.3	13	4	US-09-524-435-8
7	24	38.7	13	3	US-08-895-530-17
8	23.5	37.9	11	1	US-07-942-245-495
9	23.5	37.9	11	1	US-08-024-253-16
10	23.5	37.9	11	4	US-09-649-063-16
11	23	37.1	11	1	US-07-942-245-497
12	23	37.1	11	2	US-08-637-759B-380
13	23	37.1	11	2	US-08-476-176B-53
14	23	37.1	11	3	US-08-871-355A-380
15	23	37.1	11	3	US-08-127-721A-53
16	23	37.1	11	3	US-08-485-246A-53
17	23	37.1	11	3	US-09-191-906A-6
18	23	37.1	11	3	US-08-341-555-6
19	23	37.1	11	4	US-09-201-945-380
20	23	37.1	11	4	US-09-680-201-6
21	23	37.1	12	2	US-08-372-197-3
22	23	37.1	12	3	US-09-258-754-91
23	23	37.1	12	3	US-09-191-906A-13
24	23	37.1	12	3	US-09-042-107-91
25	23	37.1	12	4	US-09-722-250D-91
26	23	37.1	12	4	US-09-680-201-13
27	23	37.1	13	1	US-07-979-966A-3

28	23	37.1	13	3	US-08-505-250-10	Sequence 10, Appl
29	23	37.1	13	4	US-08-505-250-10	Sequence 10, Appl
30	22	35.5	7	4	US-09-708-606-21	Sequence 21, Appl
31	22	35.5	9	4	US-09-644-600-89	Sequence 89, Appl
32	22	35.5	9	4	US-09-654-600A-89	Sequence 89, Appl
33	22	35.5	9	4	US-09-601-729-243	Sequence 243, App
34	22	35.5	10	1	US-07-842-349-3	Sequence 3, Appli
35	22	35.5	10	4	US-09-443-199C-1219	Sequence 1219, Ap
36	22	35.5	11	1	US-07-923-724-21	Sequence 21, Appl
37	22	35.5	11	2	US-08-609-426A-21	Sequence 12, Appl
38	22	35.5	11	4	US-08-817-832B-12	Sequence 5, Appli
39	22	35.5	12	1	US-08-244-646-5	Sequence 9, Appli
40	22	35.5	12	1	US-08-408-120-9	Sequence 18, Appl
41	22	35.5	13	1	US-08-264-093-18	Sequence 16, Appl
42	22	35.5	13	3	US-09-196-293-16	Sequence 16, Appl
43	22	35.5	13	4	US-09-711-546-16	Sequence 14, Appl
44	21	33.9	5	1	US-08-064-111C-14	Sequence 12, Appl
45	21	33.9	6	2	US-08-865-203-12	

ALIGNMENTS

RESULT 1
US-07-988-925-4
; Sequence 4, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L
; APPLICANT: Clark, Michael R
; APPLICANT: Gorman, Scott D
; APPLICANT: Rutledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye PC
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,925
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206422.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB92/01933
; FILING DATE: 21-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-925-4
Query Match 62.9%; Score 39; DB 1; Length 13;

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Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
Db 1 TLSSGNIENYV 12

RESULT 2
US-08-362-780-4
; Sequence 4, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Rutledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-4

Query Match 62.9%; Score 39; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
Db 1 TLSSGNIENYV 12

RESULT 3
US-09-383-667-13
; Sequence 13, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte

; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-13

Query Match 45.2%; Score 28; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
Db 3 STSNIGNYV 12

RESULT 4
US-09-524-435-10
; Sequence 10, Application US/09524435
; Patent No. 6365366
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: T2K Kinase Assays
; FILE REFERENCE: T00-003
; CURRENT APPLICATION NUMBER: US/09/524,435
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-524-435-10

Query Match 43.5%; Score 27; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 GSIASNYV 12
Db 4 GSIRASFV 11

RESULT 5
US-09-149-476-706
; Sequence 706, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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[illegible]

Query Match 40.3%; Score 25; DB 4; Length 10;
Best Local Similarity 30.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
: | : | : | :
Db 1 NDGRVVSNFI 10

RESULT 6
US-09-524-435-8
; Sequence 8, Application US/09524435
; Patent No. 6365366
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: T2K Kinase Assays
; FILE REFERENCE: T00-003
; CURRENT APPLICATION NUMBER: US/09/524,435
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-524-435-8

Query Match 40.3%; Score 25; DB 4; Length 10;
Best Local Similarity 30.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
: | : | : | :
Db 1 NDGRVVSNFI 10

RESULT 6
US-09-524-435-8
; Sequence 8, Application US/09524435
; Patent No. 6365366
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: T2K Kinase Assays
; FILE REFERENCE: T00-003
; CURRENT APPLICATION NUMBER: US/09/524,435
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-524-435-8

Query Match 40.3%; Score 25; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 GSIASNYV 12
: | : | : | :
Db 4 GSLAASFV 11

RESULT 7
US-08-895-590-17
; Sequence 17, Application US/08895590
; Patent No. 6207410
; GENERAL INFORMATION:
; APPLICANT: Hall, Linda M.
; APPLICANT: Ren, Dejian
; APPLICANT: Zheng, Wei
; APPLICANT: Dubald, Manuel Marcel Paul
; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,590
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/374,888
; APPLICATION NUMBER: US/08/374,888
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm M.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 022650-263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-590-17

Query Match 38.7%; Score 24; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GSIASNY 11
: | : | : | :
Db 7 GSADSNY 13

RESULT 8
US-07-942-245-495
; Sequence 495, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.

```
/
/ TITLE OF INVENTION: SURFACE RESIDUE VENEREERING OF RODENT
/
/ TITLE OF INVENTION: ANTIBODIES
/
/ NUMBER OF SEQUENCES: 522
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: United States
/ ZIP: 20037-3202
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: HP 9000/700 Workstation
/ OPERATING SYSTEM: UNIX
/ SOFTWARE: In house
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/942,245
/ FILING DATE: 09-SEP-1992
/ CLASSIFICATION: 530
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 293-7060
/ TELEFAX: (202) 293-7860
/ TELEX: 6491103
/
/ INFORMATION FOR SEQ ID NO: 495:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
/ US-07-942-245-495
/
/ Query Match 37.9%; Score 23.5; DB 1; Length 11;
/ Best Local Similarity 54.5%; Pred. No. 3e+02;
/ Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
/
/ Qy 2 RSSGSIASNYV 12
/ |:|:|:|
/ Db 1 RASGNI-HNYL 10
/
/ RESULT 9
/ US-08-024-253-16
/ Sequence 16, Application US/08024253
/ Patent No. 5785968
/
/ GENERAL INFORMATION:
/ APPLICANT: KIMACHI, Kazuhiko
/ APPLICANT: MAEDA, Hiroaki
/ APPLICANT: NISHIYAMA, Kiyoto
/ APPLICANT: TOKIYOSHI, Sachio
/ APPLICANT: TOHYA, Yukinobu
/ APPLICANT: MIKAMI, Takeshi
/
/ TITLE OF INVENTION: ANTI-PELINE CALCIVIRUS RECOMBINANT
/
/ TITLE OF INVENTION: ANTIPODY AND GENE FRAGMENT ENCODING THE SAME
/
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
/ STREET: 1233 20th Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20036-8218
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/024,253
/ FILING DATE: 19930301
/ CLASSIFICATION: 424
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/ INFORMATION FOR SEQ ID NO: 492:
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
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/ US-07-942-245-495
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/ ATTORNEY/AGENT INFORMATION:
/ NAME: CANTOR, Herbert I.
/ REGISTRATION NUMBER: 24,392
/ REFERENCE/DOCKET NUMBER: P-500-23744
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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-0400
/ TELEFAX: (202) 835-0605
/ TELEX: 440706 WEGER
/
/ INFORMATION FOR SEQ ID NO: 16:
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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/ US-08-024-253-16
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/ Query Match 37.9%; Score 23.5; DB 1; Length 11;
/ Best Local Similarity 54.5%; Pred. No. 3e+02;
/ Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
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/ Qy 2 RSSGSIASNYV 12
/ |:|:|:|
/ Db 1 RASGNI-HNYL 10
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/ RESULT 10
/ US-09-649-063-16
/ Sequence 16, Application US/09649063
/ Patent No. 6600022
/
/ GENERAL INFORMATION:
/ APPLICANT: TORIGOE, Kakuji
/ USHIO, Shimpel
/ KUNIKATA, Toshio
/ KURIMOTO, Masashi
/
/ TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
/
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/649,063
/ FILING DATE: 29-Aug-2000
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/996,140
/ FILING DATE: <Unknown>
/
/ APPLICATION NUMBER: JP 52,526/1997
/ FILING DATE: 21-FEB-1997
/
/ APPLICATION NUMBER: JP 163,490/1997
/ FILING DATE: 6-JUN-1997
/
/ APPLICATION NUMBER: JP 215,490/1997
/ FILING DATE: 28-JUL-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: TORIGOE=2
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/
/ INFORMATION FOR SEQ ID NO: 16:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
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FRAGMENT TYPE: Internal fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-649-063-16

Query Match 37.9%; Score 23.5; DB 4; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 RSSGSIASNV 12
|:|:|:|:
Db 1 RASGNI-HNYL 10

RESULT 11
US-07-942-245-497
; Sequence 497, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 497:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-497

Query Match 37.1%; Score 23; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RSSGSIASN 10
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Db 1 RASQSIGNN 9

RESULT 12
US-08-637-759B-380
; Sequence 380, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst

STREET: 2900 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GH95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 380:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-380

Query Match 37.1%; Score 23; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GSIASNY 11
|:|:|:|:
Db 2 GNVASAY 8

RESULT 13
US-08-476-176B-53
; Sequence 53, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-53

Query Match 37.1%; Score 23; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RSSGSIASN 10
Db 1 RASQSIGN 9

RESULT 14

US-08-871-355A-380
Sequence 380, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPNs 101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 380:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-380

Query Match 37.1%; Score 23; DB 3; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GSIASNY 11
Db 2 GNVASAY 8

RESULT 15

US-08-127-721A-53
Sequence 53, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-127-721A-53

Query Match 37.1%; Score 23; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RSSGSIASN 10
Db 1 RASQSIGN 9

Search completed: June 8, 2004, 19:24:08
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:22:32 ; Search time 41 Seconds
(without alignments)
89.205 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 176922

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	62	100.0	13	11	US-09-829-495-64
3	55	88.7	13	10	US-09-972-656-2
4	54	87.1	13	10	US-09-972-656-3
5	50	80.6	13	10	US-09-972-656-1
6	50	80.6	13	15	US-10-425-855-11
7	47	75.8	13	10	US-09-972-656-9
8	39	62.9	13	9	US-09-736-371B-8
9	39	62.9	13	13	US-10-060-714-4
10	39	62.9	13	15	US-10-463-442-8
11	34	54.8	13	14	US-10-001-934-12
12	34	54.8	13	15	US-10-279-633-68
13	34	54.8	13	15	US-10-279-633-78
14	34	54.8	13	15	US-10-279-633-84
15	34	54.8	13	15	US-10-275-046-18

16	34	54.8	13	15	US-10-275-046-20	Sequence 20, Appl
17	32	51.6	13	14	US-10-001-934-7	Sequence 7, Appl
18	32	51.6	13	15	US-10-279-633-99	Sequence 99, Appl
19	32	51.6	13	15	US-10-275-046-51	Sequence 51, Appl
20	31	50.0	13	15	US-10-279-633-69	Sequence 69, Appl
21	31	50.0	13	15	US-10-279-633-97	Sequence 97, Appl
22	31	50.0	13	16	US-10-440-522-27	Sequence 27, Appl
23	30	48.4	13	14	US-10-001-934-13	Sequence 13, Appl
24	30	48.4	13	14	US-10-001-934-14	Sequence 14, Appl
25	30	48.4	13	14	US-10-001-934-30	Sequence 30, Appl
26	30	48.4	13	15	US-10-275-046-30	Sequence 34, Appl
27	30	48.4	13	15	US-10-275-046-35	Sequence 35, Appl
28	30	48.4	13	15	US-10-275-046-39	Sequence 39, Appl
29	29	46.8	12	9	US-09-828-708-38	Sequence 38, Appl
30	29	46.8	12	9	US-09-828-708-40	Sequence 40, Appl
31	29	46.8	12	9	US-09-828-708-41	Sequence 41, Appl
32	29	46.8	12	9	US-09-828-708-42	Sequence 42, Appl
33	29	46.8	12	10	US-09-563-222-11	Sequence 11, Appl
34	29	46.8	12	12	US-10-379-741-8	Sequence 8, Appl
35	29	46.8	12	14	US-10-001-934-62	Sequence 62, Appl
36	29	46.8	12	15	US-10-374-932-8	Sequence 8, Appl
37	29	46.8	12	15	US-10-338-366-20	Sequence 20, Appl
38	29	46.8	12	15	US-10-275-046-19	Sequence 19, Appl
39	28	45.2	12	12	US-09-948-939-24	Sequence 24, Appl
40	28	45.2	13	14	US-10-001-934-16	Sequence 16, Appl
41	28	45.2	13	14	US-10-001-934-28	Sequence 28, Appl
42	28	45.2	13	15	US-10-279-633-64	Sequence 64, Appl
43	28	45.2	13	15	US-10-279-633-77	Sequence 77, Appl
44	28	45.2	13	15	US-10-279-633-85	Sequence 85, Appl
45	28	45.2	13	15	US-10-279-633-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1

US-09-832-312-64
; Sequence 64, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-64

Query Match 100.0%; Score 62; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13

DB 1 TRSSGSIASNYVQ 13

RESULT 2

US-09-829-495-64
; Sequence 64, Application US/09829495

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; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-829-495-64

Query Match      100.0%; Score 62; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
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Db      1 TRSSGSIASNYVQ 13

RESULT 3
US-09-972-656-2
; Sequence 2, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-2

Query Match      88.7%; Score 55; DB 10; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
      |||||
Db      1 TGSSGSIASNYVQ 13

RESULT 4
US-09-972-656-3
; Sequence 3, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-1

Query Match      80.6%; Score 50; DB 10; Length 13;
Best Local Similarity 84.8%; Pred. No. 0.031;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
      |||||
Db      1 TGSSGSIASNYVQ 13

RESULT 5
US-09-972-656-1
; Sequence 1, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-1

Query Match      87.1%; Score 54; DB 10; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.006;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
      |||||
Db      1 TRSSGSIASNYVQ 13

RESULT 6
US-10-425-855-11
; Sequence 11, Application US/10425855
; Publication No. US20040005324A1
; GENERAL INFORMATION:
; APPLICANT: PILKINGTON, GLENN
; APPLICANT: GILMOUR, PAGE
; APPLICANT: CHANOCK, ROBERT
; APPLICANT: CROWE, JAMES
; APPLICANT: MURPHY, BRIAN
; TITLE OF INVENTION: NEUTRALIZING MONOCLONAL ANTIBODIES TO RESPIRATORY
; FILE REFERENCE: 18602.0007/P007-A
; CURRENT APPLICATION NUMBER: US/10/425,855
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/043,530
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: 60/003,931
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
```



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; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-855-11
Query Match      80.6%; Score 50; DB 15; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.031;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 13
   ||: |||||
Db 1 TRAGRIASNYV 13

RESULT 7
US-09-972-656-9
; Sequence 9, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Wei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-9
Query Match      75.8%; Score 47; DB 10; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
   |||||: |||
Db 1 TGSSGSIANNYV 12

RESULT 8
US-09-736-371B-8
; Sequence 8, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus
US-09-736-371B-8
Query Match      62.9%; Score 39; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
   |||||: |||
Db 1 TLSSGNIENNYV 12

US-09-972-656-9
Query Match      62.9%; Score 39; DB 13; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
   |||||: |||
Db 1 TLSSGNIENNYV 12

US-10-060-714-4
; Sequence 4, Application US/10060714
; Publication No. US20020147312A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Pat
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HYBRID ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10448-039001
; CURRENT APPLICATION NUMBER: US/10/060,714
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/265,914
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-060-714-4
Query Match      62.9%; Score 39; DB 13; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
   |||||: |||
Db 1 TLSSGNIENNYV 12

RESULT 10
US-10-463-442-8
; Sequence 8, Application US/10463442
; Publication No. US20040006216A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/10/463,442
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/736,371
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus
US-10-463-442-8
Query Match      62.9%; Score 39; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
   |||||: |||
Db 1 TLSSGNIENNYV 12

RESULT 11
US-10-001-934-12
; Sequence 12, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: Nagy, Zoltan
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
```

; TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-12

Query Match 54.8%; Score 34; DB 14; Length 13;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
|||:||||
Db 3 SSSNIGSNYV 12

RESULT 12
US-10-279-633-68
; Sequence 68, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-68

Query Match 54.8%; Score 34; DB 15; Length 13;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
|||:||||
Db 3 SSSNIGSNYV 12

RESULT 13
US-10-279-633-78
; Sequence 78, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-78

Query Match 54.8%; Score 34; DB 15; Length 13;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
|||:||||
Db 1 TGSSSNIGNNYV 12

RESULT 14
US-10-279-633-84
; Sequence 84, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-84

Query Match 54.8%; Score 34; DB 15; Length 13;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
|||:||||
Db 1 TGSSSNIGNNYV 12

RESULT 15
US-10-275-046-18
; Sequence 18, Application US/10275046
; Publication No. US20040019187A1
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-DR specific polypeptide
US-10-275-046-18

Query Match 54.8%; Score 34; DB 15; Length 13;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
|||:||||
Db 3 SSSNIGSNYV 12

Search completed: June 8, 2004, 19:28:05

Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:19:41 ; Search time 20 Seconds
(without alignments)
62.524 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSTASNYVQ 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78.*

2: PIR1.*

3: PIR2.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	38.7	11	2 S60294	tubulin 2 beta-3 c
2	23	37.1	13	2 S47365	T-cell antigen rec
3	22	35.5	13	2 S32473	lymnaDpamide 3 - g
4	21	33.9	9	2 PT0238	Ig heavy chain CRD
5	21	33.9	13	2 S47390	T-cell antigen rec
6	20	32.3	9	2 PT0231	Ig heavy chain CDR
7	20	32.3	12	2 I39390	acetylcholine rece
8	20	32.3	12	2 S25039	Ig heavy chain V r
9	20	32.3	13	2 S47372	T-cell antigen rec
10	20	32.3	13	2 S47374	T-cell antigen rec
11	19	30.6	9	2 G41946	T-cell receptor ga
12	19	30.6	11	2 PH0941	T-cell receptor be
13	19	30.6	11	2 A34243	H-hyosophorin - Ja
14	19	30.6	12	2 PH1188	T-cell receptor al
15	18	29.0	8	2 S45651	probable Na+-trans
16	18	29.0	9	2 PC7078	unidentified 48.7K
17	18	29.0	12	2 A34858	protenase E - bla
18	18	29.0	12	2 PH1189	T-cell receptor al
19	18	29.0	12	2 PH1172	T-cell receptor al
20	18	29.0	12	2 PH1175	T-cell receptor al
21	18	29.0	13	2 S38736	lipid transfer pro
22	18	29.0	13	2 PT0305	Ig heavy chain CRD
23	18	29.0	13	2 E61458	Ig kappa chain V-I
24	18	29.0	13	2 S47380	T-cell antigen rec
25	18	29.0	13	4 I70075	glycophorin B (mis
26	17	27.4	10	2 A59272	peptide-N4-(N-acet
27	17	27.4	11	2 S35490	type II site-speci
28	17	27.4	11	2 S23373	T-cell receptor al
29	17	27.4	12	2 S28215	Glucan endo-1,3-be

ALIGNMENTS

RESULT 1

S60294

tubulin 2 beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jun-2002

C:Accession: S60294

R:Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue

Insect Mol. Biol. 2: 39-48, 1993

A:Title: In Drosophila Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expression

A:Reference number: S60292; MUID:97242543; PMID:9087542

A:Accession: S60294

A:Molecule type: mRNA

A:Residues: 1-11 <CHA>

A:Cross-references: EMBL:X60393

C:Genetics:

A:Gene: FlyBase:beta-Tub60D

A:Cross-references: FlyBase:FBgn0003888

Query Match 38.7%; Score 24; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSG 5

Db 5 TRSSG 9

RESULT 2

S47365

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce

A:Reference number: S47355

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: EMBL:Z35690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:Z35679;

A:Accession: S47375

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LE2>

A:Cross-references: EMBL:Z35700; NID:g527493; PIDN:CAA84769.1; PID:g527494

A:Accession: S47379

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LE3>

A:Cross-references: EMBL:Z35708; NID:g527509; PIDN:CAA84777.1; PID:g527510

A:Accession: S47396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:Z35674; NID:g527527; PIDN:CAA84743.1; PID:g527528
A:Accession: S47397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:Z35675; NID:g527529; PIDN:CAA84744.1; PID:g527530
A:Accession: S47398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:Z35676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C:Keywords: T-cell receptor

Query Match 37.1%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 SGIASNYVQ 13
: ||| :
Db 2 ASSIRSYEQ 11

RESULT 3
S32473
Lymnaeidae 3 - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C:Accession: S32473
R:Johnsen, A.H.; Renfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A:Title: Lymnaeidae, a new family of neuropeptides from the pond snail, Lymnaea stagnalis
A:Reference number: S32471; MUID:93238777; PMID:8477756
A:Accession: S32473
A:Molecule type: protein
A:Residues: 1-13 <JOH>
A:Cross-references: PIDN:AAB26364.1; PID:g299831
A:Experimental source: ganglia
C:Keywords: amidated carboxyl end; neuropeptide
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 35.5%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RSSGSIASNY 11
: ||| :
Db 4 RISGSAPSD 13

RESULT 4
PT0238
Ig heavy chain CDR3 region (clone 2-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0238
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0238
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 21; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SNYV 12
: ||| :
Db 1 SNYV 4

RESULT 5
S47390
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47390
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35703; NID:g527499; PIDN:CAA84772.1; PID:g527500
C:Keywords: T-cell receptor

Query Match 33.9%; Score 21; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSSGSI 7
: ||| :
Db 6 RSSGEL 11

RESULT 6
PT0231
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0231
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0231
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.3%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIA 8
: ||| :
Db 2 THSSGWVS 9

RESULT 7
I39390
acetylcholine receptor (alternative exon 5b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
C:Accession: I39390
R:Milovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Taroni, P.; Clementi, F.; Ro
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
A:Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A:Reference number: I39390; MUID:94071933; PMID:8250918
A:Accession: I39390
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:U18973; NID:g441143; PIDN:AAA86792.1; PID:g441144
C:Keywords: alternative splicing; neurotransmitter receptor

```
Query Match      32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SGSIASNYVQ 13
       :|:|:|
Db      3 SCSVTQGVQ 12

RESULT 8
S25039
IG heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C;Accession: S25039
R;Jacob, J.; Kelseo, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A;Reference number: S25024
A;Accession: S25039
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-12 <JAC>
A;Cross-references: EMBL:X67391; NID:G50119; PIDN:CAA47803.1; PID:e51597; PID:G1333874
C;Keywords: heterotetramer; immunoglobulin

Query Match      32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 RSSGSIASNY 11
       :|:|:|
Db      2 RSGGLDGMNY 11

RESULT 9
S47372
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47372
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number: S47355
A;Accession: S47372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35697; NID:G527485; PIDN:CAA84766.1; PID:G527486
C;Keywords: T-cell receptor

Query Match      32.3%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SGSIASNYVQ 13
       :|:|:|
Db      2 ASSIRSAVEQ 11

RESULT 10
S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C;Accession: S47374; S47399; S47364
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number: S47355
A;Accession: S47374
A;Status: preliminary
```

```
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35699; NID:G527491; PIDN:CAA84768.1; PID:G527492; EMBL:Z35689;
A;Accession: S47399
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE2>
A;Cross-references: EMBL:Z35677; NID:G527533; PIDN:CAA84746.1; PID:G527534
C;Keywords: T-cell receptor

Query Match      32.3%; Score 20; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      4 SGSIASNYVQ 13
       :|:|:|
Db      2 ASSMRSSVEQ 11

RESULT 11
G41946
T-cell receptor gamma chain (2t.23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: G41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: G41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-9 <WHE>
C;Keywords: T-cell receptor

Query Match      30.6%; Score 19; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 SSGSIASNY 11
       :|:|:|
Db      1 SYGSYSSGF 9

RESULT 12
PH0941
T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0941
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0941
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match      30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4 SGSIASNYVQ 13
       :|:|:|
Db      2 ASSAVSSVEQ 11

RESULT 13
A34243
H-hyosophorin - Japanese flounder (fragment)
C;Species: Paralichthys olivaceus (Japanese flounder)
```

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Feb-1999
C/Accession: A34243
R;Seko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.
J. Biol. Chem. 264, 15922-15929, 1989
A/Title: Structural studies of fertilization-associated carbohydrate-rich glycoproteins
of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide unit
A/Reference number: A34243; MUID:89380184; PMID:2777771
A/Accession: A34243
A/Molecule type: protein
A/Residues: 1-11 <SEK>
A/Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GSIAAS 10
Db 2 GSVGGN 7

RESULT 14
PHI188
T-cell receptor alpha chain V region (Cw3/Cas11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PHI188
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PHI188
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 30.6%; Score 19; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIAS 9
Db 4 SAGGFAS 10

RESULT 15
S45651
probable Na+-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment)
C/Species: Acetobacterium woodii
C/Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C/Accession: S45651
R;Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A/Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A/Reference number: S45648; MUID:94307271; PMID:8033902
A/Accession: S45651
A/Molecule type: protein
A/Residues: 1-8 <REI>
A/Experimental source: DSM 1030
C/Keywords: hydrolase

Query Match 29.0%; Score 18; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IASNY 11
Db 3 VASKY 7

Search completed: June 8, 2004, 19:23:01
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:15:41 ; Search time 11 Seconds
(without alignments)

61.537 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 597

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	22	35.5	13	1	NP3_LYMST	P80180 Lymnaea sta
2	19	30.6	13	1	PROX_ORYSA	P83647 oryza sativ
3	18	29.0	13	1	ITB5_BOVIN	P80747 bos taurus
4	18	29.0	13	1	SA2A_ONCMY	P82238 oncorhynch
5	17	27.4	11	1	T2P1_PROVU	P31031 proteus vul
6	17	27.4	12	1	PVK2_PERAM	P81555 periplaneta
7	16	25.8	10	1	HTF_HELZE	P16353 heliothis z
8	16	25.8	11	1	ASLI_BACSE	P83146 bacteroides
9	16	25.8	11	1	RS30_ONCMY	P83328 oncorhynch
10	16	25.8	13	1	MP1_MICOC	P81532 microplitis
11	16	25.8	13	1	NP1_LYMST	P80178 Lymnaea sta
12	16	25.8	13	1	NP2_LYMST	P80179 Lymnaea sta
13	16	25.8	13	1	NP4_LYMST	P80181 Lymnaea sta
14	16	25.8	13	1	NP5_LYMST	P80182 Lymnaea sta
15	15	24.2	9	1	OXYT_EUFRE	P42995 bufo regula
16	15	24.2	9	1	OXYT_CYPCA	P23879 cyprinus ca
17	15	24.2	9	1	OXYT_RABIT	P32878 oryctolagus
18	15	24.2	9	1	OXYV_SQUAC	P43000 squalus aca
19	15	24.2	9	1	XYLA_STRSQ	P19149 streptomyce
20	15	24.2	10	1	PAR2_PENMO	P83317 penaeus mon
21	15	24.2	12	1	FAR7_PENMO	P83322 penaeus mon
22	15	24.2	13	1	SA2B_ONCMY	P82239 oncorhynch
23	14	22.6	10	1	COXO_THUOB	P80982 thunnus obe
24	14	22.6	10	1	GS09_BACSU	P80243 bacillus su
25	14	22.6	10	1	PSBF_CAPAN	Q03367 capsicum an
26	14	22.6	10	1	RRLP_PHODY	P35946 plocium dis
27	14	22.6	12	1	FIFI_SAREU	P83349 sarcophaga
28	14	22.6	13	1	CF1_APLCA	Q10998 aplysia cal
29	13	21.0	7	1	FAR4_PANFE	P41875 panagrellus
30	13	21.0	8	1	AKH_MELML	P25423 melolontha
31	13	21.0	8	1	ALL7_CARMA	P81609 carcinus ma
32	13	21.0	9	1	PAR3_MACRS	P82276 macrobrachi
33	13	21.0	9	1	HUTU_KLEAE	P12381 kiebsiella

34	13	21.0	10	1	SPI_HALRO	Q10997 halocynthia
35	13	21.0	11	1	COXA_CANFA	P99501 canis famli
36	13	21.0	11	1	PVK1_PERAM	P41837 periplaneta
37	12	19.4	5	1	PSK_DAUCA	P58261 daucus caro
38	12	19.4	7	1	MNP1_LEPDE	P42984 leptinotars
39	12	19.4	9	1	DSIP_RABIT	P01158 oryctolagus
40	12	19.4	9	1	FAR8_MACRS	P83281 macrobrachi
41	12	19.4	9	1	THYF_PIG	P01255 sus scrofa
42	12	19.4	9	1	YBFR_AZOVI	P25825 azotobacter
43	12	19.4	10	1	AEGL_AGRAE	P83465 agropybe ae
44	12	19.4	10	1	AH3_ERUSE	P29261 prunus sero
45	12	19.4	10	1	COXO_RAT	P80432 rattus norv

ALIGNMENTS

RESULT 1
NP3_LYMST
ID NP3_LYMST STANDARD; PRT; 13 AA.
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-DP-amide 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnaeidaeFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32473; S32473.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
FT UNSURE 12 12
SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;
Query Match 35.5%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 RSSGSIASNY 11
| | | | | : :
Db 4 RISGSASFSD 13
RESULT 2
PROX_ORYSA
ID PROX_ORYSA STANDARD; PRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable profilin LP04 (Fragments).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Indica-IR64; TISSUE=Panicle;
RA Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RL Submitted (JUL-2003) to Swiss-Prot.

CC -!- FUNCTION: Binds to actin and affects the structure of the
 CC cytoskeleton. At high concentrations, profilin prevents the
 CC polymerization of actin, whereas it enhances it at low
 CC concentrations. By binding to PIP2, it inhibits the formation of
 CC IP3 and DG (By similarity).
 CC -!- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
 CC actin in a 1:1 ratio.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.4, its MW is: 14.0 KDa.
 CC -!- SIMILARITY: Belongs to the profilin family.
 DR PROSITE; PS00414; PROFILIN; PARTIAL.
 KW Actin-binding; Cytoskeleton; Multigene family.
 FT NON_TER 1 1
 FT NON_CONS 5 6
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1362 MW; 0A3022EE0E52C68B CRC64;
 SQ
 Query Match 30.6%; Score 19; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 GSASNYVQ 13
 ||:|:
 D 2 GSAYMVQ 10
 ||:|:
 RESULT 3
 ITB5_BOVIN STANDARD; PRT; 13 AA.
 ID ITB5_BOVIN STANDARD; PRT; 13 AA.
 AC P80747;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integrin beta-5 (Fragment).
 GN ITGB5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=9729977; PubMed=9154926;
 RA Andersen M.H., Berglund L., Rasmussen J.T., Petersen T.E.;
 RT "Bovine PAS-6/7 binds alpha v beta 5 integrins and anionic
 RT phospholipids through two domains.";
 RL Biochemistry 36:5441-5446(1997).
 CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
 CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
 CC ASSOCIATES WITH ALPHA-V.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the integrin beta chain family.
 DR InterPro; IPR001169; Integrin beta C.
 DR PROSITE; PS00243; INTEGRIN BETA; PARTIAL.
 KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
 KW Repeat.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1299 MW; 844197D005B9B865 CRC64;
 SQ
 Query Match 29.0%; Score 18; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SSGSIAS 9
 :|||:
 D 5 TSGSATS 11
 :|||:
 RESULT 4
 SA2A_ONCMY STANDARD; PRT; 13 AA.
 ID SA2A_ONCMY

AC P82238;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Salmocidin 2A (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE AND FUNCTION.
 RC TISSUE=Serum;
 RA Henry M.A.; Secombes C.J.;
 RT "Purification and partial characterization of antibacterial peptides
 RT from rainbow trout, Oncorhynchus mykiss.";
 RL Submitted (DEC-1999) to Swiss-Prot.
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma serum.
 KW Antibiotic.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1416 MW; 5PFB792AFC645873 CRC64;
 SQ
 Query Match 29.0%; Score 18; DB 1; Length 13;
 Best Local Similarity 30.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 4 SGIASNYVQ 13
 ||:|:
 D 1 SGFVLGYTK 10
 ||:|:
 RESULT 5
 T2P1_PROVU STANDARD; PRT; 11 AA.
 ID T2P1_PROVU STANDARD; PRT; 11 AA.
 AC P31031;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
 DE (R.PvuI) (Fragment).
 GN PVUIR.
 OS Proteus vulgaris.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Proteus.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13315;
 RX MEDLINE=93087186; PubMed=1454536;
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
 RT "Cloning and characterization of genes for the PvuI restriction and
 RT modification system.";
 RL Nucleic Acids Res. 20:5743-5747(1992).
 CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
 CC CLEAVES AFTER T-4.
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -----
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 CC -----
 DR EMBL; L04163; AAA25660.1; -.
 DR PIR; S35490; S35490.
 DR REBASE; 1541; PvuI.
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.
 FT NON_TER 1 1

```
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;
Query Match 27.4%; Score 17; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SNY 11
Db 7 SNY 9

RESULT 6
PVK2 PERAM
ID PVK2 PERAM STANDARD; PRT; 12 AA.
AC P81555;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-2 (Pea-PVK-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TSSUR=Abdominal perisymphathetic organs;
RC MEDLINE=98326577; PubMed=9663444;
RA Predel R., Rapus J., Eckert M., Holman G.M., Nachman R.J., Wang Y.,
RA Penzlin H.;
RT "Isolation of periviscerokinin-2 from the abdominal perisymphathetic
RT organs of the American cockroach, Periplaneta americana.";
RL Peptides 19:801-809(1998).
CC -!- FUNCTION: Myoactive peptide; has excitatory actions on the
CC hyperneural muscle.
CC -!- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1190 MW; 2F4D8EE1EB05728 CRC64;
Query Match 27.4%; Score 17; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SSGSIA 8
Db 3 SSGIIS 8

RESULT 7
HTF HELZE
ID HTF HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (HeZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
SEQUENCE.
RP TISSUE=Corpora cardiaca;
RA MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
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CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RFCH family.
DR PIR; A31571; A31571.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;
Query Match 25.8%; Score 16; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TRSSG 5
Db 3 TRSSG 7

RESULT 8
ASL1 BACSE
ID ASL1 BACSE STANDARD; PRT; 11 AA.
AC P33146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RP STEAIN-HJ-15;
RC MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;
Query Match 25.8%; Score 16; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NYV 12
Db 1 NYI 3

RESULT 9
RS30 ONCMY
ID RS30 ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Skin mucus;
RC MEDLINE=22142142; PubMed=12147245;
RX Fernandes J.M.O., Smith V.J.;
RA "A novel antimicrobial function for a ribosomal peptide from rainbow
RT trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -|- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -|- MASS SPECTROMETRY: MW=6676.6; METHOD=WALDI.
CC -|- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON TER 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GSIA 8
Db ||:|
4 GSIA 7

RESULT 10
NP1 MICOC STANDARD; PRT; 13 AA.
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MP1 protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgastrinae; Microplitis.
OX NCBI_TaxID=99573;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RA Takahashi M., Quicke D.L.J.;
RL Submitted (OCT-1998) to Swiss-Prot.
CC -|- TISSUE SPECIFICITY: Salivary glands.
CC -|- DEVELOPMENTAL STAGE: LARVAL.
FT NON CONS 10 11
SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 NVV 12
Db ||:
10 NVI 12

RESULT 11
NP1 LYMST STANDARD; PRT; 13 AA.
AC P80178;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea stagnalis 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;

RN SEQUENCE.
RP TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32471; S32471.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RSSGSIASNY 11
Db ||:|:
4 RISSAFAFDF 13

RESULT 12
NP2 LYMST STANDARD; PRT; 13 AA.
AC P80179;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-DP-amide 2.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32472; S32472.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
FT UNSURE 8 8
SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5A5A5 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RSSGSIASNY 11
Db ||:|:
4 RISSAFAFDF 13

RESULT 13
NP4 LYMST STANDARD; PRT; 13 AA.
AC P80181;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-DP-amide 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;

```
RN SEQUENCE.
RP TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Chauvet J., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
DR PIR; S32474; S32474.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RSSGSIASNY 11
Db 4 RISSAFSDF 13

RESULT 14
NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnae-DF-amide 5.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_taxID=6523;
RN [1]
RP SEQUENCE.
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
DR PIR; S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RSSGSIASNY 11
Db 4 RISSAFSDF 13

RESULT 15
OXIT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Ser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
OX NCBI_taxID=8390;
RN [1]
```

```
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin)",
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 24.2%; Score 15; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YVQ 13
Db 2 YIQ 4

Search completed: June 8, 2004, 19:21:36
Job time : 11 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:18:46 ; Search time 39 Seconds
(without alignments)
105.173 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	32.3	12	Q13695	Q13695 homo sapien
2	19	30.6	10	Q8BHN2	Q8bhn2 mus musculus
3	18	29.0	11	Q96QP8	Q96qf8 homo sapien
4	18	29.0	12	Q8KI49	Q8kt49 fischerella
5	18	29.0	12	O05328	O05328 sphingomona
6	18	29.0	13	Q8GBU2	Q8gbu2 vibrio harv
7	18	29.0	13	Q14461	Q14461 homo sapien
8	17	27.4	9	Q28112	Q28112 bos taurus
9	17	27.4	10	P81899	P81899 prunus dulc
10	17	27.4	11	P82699	P82699 leucophaea
11	17	27.4	11	P82700	P82700 leucophaea
12	17	27.4	11	Q9UEX7	Q9uex7 homo sapien
13	17	27.4	11	Q9TOR6	Q9tor6 bacterioph
14	17	27.4	11	Q7ZZI9	Q7zzi9 motacilla f
15	17	27.4	11	Q7ZZI6	Q7zzi6 motacilla f
16	17	27.4	12	Q7ZZI3	Q7zzi3 motacilla f

17	17	27.4	13	4	Q9UE87	Q9ue87 homo sapien
18	17	27.4	13	4	Q9UEB3	Q9ueb3 homo sapien
19	17	27.4	13	8	Q8WGC2	Q8wgc2 isocheles p
20	17	27.4	13	11	P97622	P97622 rattus norv
21	17	27.4	13	13	Q7ZZJ6	Q7zzj6 anthus prat
22	17	27.4	13	13	Q7ZZJ5	Q7zzj5 motacilla c
23	17	27.4	13	13	Q7ZZJ4	Q7zzj4 motacilla c
24	17	27.4	13	13	Q7ZZJ3	Q7zzj3 motacilla f
25	17	27.4	13	13	Q7ZZJ1	Q7zzj1 motacilla f
26	17	27.4	13	13	Q7ZZJ0	Q7zzj0 motacilla f
27	17	27.4	13	13	Q7ZZI8	Q7zzi8 motacilla f
28	17	27.4	13	13	Q7ZZI7	Q7zzi7 motacilla f
29	17	27.4	13	13	Q7ZZI5	Q7zzi5 motacilla f
30	17	27.4	13	13	Q7ZZI4	Q7zzi4 motacilla f
31	17	27.4	13	13	Q7ZT29	Q7zt29 motacilla c
32	17	27.4	13	13	Q7ZT28	Q7zt28 motacilla f
33	16	25.8	8	2	P83531	P83531 lactobacill
34	16	25.8	8	5	Q94623	Q94623 manduca sex
35	16	25.8	8	8	Q8WGC7	Q8wgc7 petiolithe
36	16	25.8	8	13	Q8GUJ35	Q8jj35 ficedula hy
37	16	25.8	9	12	Q88612	Q88612 middelburg
38	16	25.8	10	15	Q9QKJ0	Q9qk10 human immu
39	16	25.8	11	2	O56972	O56972 versinia pe
40	16	25.8	11	5	P82698	P82698 leucophaea
41	16	25.8	11	7	O77913	O77913 oreochromis
42	16	25.8	11	11	Q9ZIH5	Q9zih5 mus musculu
43	16	25.8	12	2	Q46747	Q46747 escherichia
44	16	25.8	12	10	Q9SQF8	Q9sqf8 pinus taeda
45	16	25.8	12	15	Q9ICE5	Q9ice5 human immu

ALIGNMENTS

RESULT 1

Q13695	Q13695	PRELIMINARY;	PRT;	12 AA.
ID	Q13695			
AC	Q13695;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Acetylcholine receptor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Thymus;			
RX	MEDLINE=94071933; PubMed=8250918;			
RA	Mihovilovic M., Mai Y., Herbstreith M., Rubboli F., Tarroni P.,			
RA	Clementi P., Roses A.D.;			
RT	"Splicing of an anti-sense Alu sequence generates a coding sequence			
RT	variant for the alpha-3 subunit of a neuronal acetylcholine			
RT	receptor.";			
RL	Biochem. Biophys. Res. Commun. 197:137-144 (1993).			
DR	EMBL; L18973; AAA86792.1; -.			
DR	PIR; I39390; I39390.			
KW	Receptor.			
FT	NON TER			
SQ	SEQUENCE 12 AA; 1282 MW; 8B0B423A6FC1B2D5 CRC64;			

Query Match 32.3%; Score 20; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SGSIASNYVQ 13

Db 3 SCSVTQNGVQ 12

RESULT 2

Q8BHN2
ID Q8BHN2 PRELIMINARY; PRT; 10 AA.
AC Q8BHN2; 10 AA.
DT 01-MAR-2003 (TtEMBLrel. 23, Created)
DT 01-MAR-2003 (TtEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TtEMBLrel. 24, Last annotation update)
DE Methylentetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv, and BALB/c;
RX MEDLINE=2257759; PubMed=12370778;
RA Tran P., Leclerc D., Chan M., Pal A., Hion-Tim F., Wu Q., Goyette P.,
RA Artigas C., Milos R., Rozen R.;
RT "Multiple transcription start sites and alternative splicing in the
RT methylentetrahydrofolate reductase gene result in two enzyme
RT isoforms";
RL Mamm. Genome 13:483-492(2002).
DR EMBL; AY046557; AAL17641.1; -;
DR EMBL; AF398931; AAN40867.1; -;
DR MGD; MGI:106639; Mthfr.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1007 MW; 01695CB8640DDB14 CRC64;
Query Match 30.6%; Score 19; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 RSSGS 6
DB 6 RGS GS 10
RESULT 3
Q96QF8
ID Q96QF8 PRELIMINARY; PRT; 11 AA.
AC Q96QF8; 11 AA.
DT 01-DEC-2001 (TtEMBLrel. 19, Created)
DT 01-DEC-2001 (TtEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TtEMBLrel. 19, Last annotation update)
DE Agrin (Fragment).
GN AGRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liyanage Y., Vincent A.C., Beeson D.M.W.;
RT "Cloning, expression and functional studies on human neural agrin
RT isoforms; y028 inserts in spinal cord and a small cell lung cancer
RT line.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Liyanage Y.;
RT Thesis (1999), Department of Clinical Medicine, University of Oxford,
RL Oxford, United Kingdom.
DR EMBL; AJ309206; CAC42508.1; -;
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1126 MW; 59E0B33DD865BAA7 CRC64;
Query Match 29.0%; Score 18; DB 4; Length 11;
Best Local Similarity 44.4%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 TRSSGS 9
ID TRSSGS 9
DB TRSSGS 9

Db 3 TLDGALHS 11
RESULT 4
Q8KT49
ID Q8KT49 PRELIMINARY; PRT; 12 AA.
AC Q8KT49; 12 AA.
DT 01-OCT-2002 (TtEMBLrel. 22, Created)
DT 01-OCT-2002 (TtEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TtEMBLrel. 22, Last annotation update)
DE Red capping linker protein (Fragment).
GN CPD.
OS Fischerella sp. PCC 7603.
OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.
OX NCBI_TaxID=70809;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7603;
RA Zhu J.P., Wu D., Zhao K.H., Scheer H.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506031; AAM69290.1; -;
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1268 MW; 730838103CA7376B CRC64;
Query Match 29.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRSSG 5
DB 8 TRAAG 12
RESULT 5
O05328
ID O05328 PRELIMINARY; PRT; 12 AA.
AC O05328; 12 AA.
DT 01-JUL-1997 (TtEMBLrel. 04, Created)
DT 01-JUL-1997 (TtEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TtEMBLrel. 24, Last annotation update)
DE Catechol 2,3-dioxygenase (Fragment).
GN PHNE.
OS Sphingomonas chungbukensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=56193;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ77;
RX MEDLINE=97242176; PubMed=9125165;
RA Shin H.J., Kim S.J., Kim Y.C.;
RT "Sequence analysis of the phnd gene encoding 2-hydroxymuconic
RT semialdehyde hydrolase in Pseudomonas sp. strain DJ77";
RL Biochem. Biophys. Res. Commun. 232:288-291(1997).
DR EMBL; U83881; AAC45092.1; -;
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KM Dioxigenase.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1277 MW; 2981743D4D0042C8 CRC64;
Query Match 29.0%; Score 18; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 SGSIASNYV 12
DB 4 TGVIRPGYV 12
RESULT 6
Q8GBU2
ID Q8GBU2 PRELIMINARY; PRT; 13 AA.
AC Q8GBU2;


```

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LuxR (Fragment).
GN LUXR.
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B392;
RX MEDLINE=96417856; PubMed=8820647;
RA Miyamoto C.M.; Chatterjee J., Swartzman E., Saittner R., Meighen E.A.;
RT "The role of lux autoinducer in regulating luminescence in Vibrio
RL harveyi; control of luxR expression.";
RL Mol. Microbiol. 19:767-775(1996).
DR EMBL; S83266; AAN86705.1; -.
FT NON TER 13
SQ SEQUENCE 13 AA; 1473 MW; 52B85F99702E7403 CRC64;

Query Match 29.0%; Score 18; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GSIA 8
Db |||||
2 GSIA 5

RESULT 7
Q14461 PRELIMINARY; PRT; 13 AA.
AC Q14461; Q14842;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glycophorin B (Fragment).
GN GYPB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding
RT human glycophorin variant Sta. Similarity to the crossing-over point
RT in haptoglobin-related genes.";
RT J. Biol. Chem. 265:9259-9263(1990).
RN [2]
RP SEQUENCE OF 1-9 FROM N.A.
RA Cartton J.P.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=90005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
BLanchard C.D.;
RT "Molecular analysis of glycophorin A and B gene structure and
RT expression in homozygous Miltenberger class V (Mi. V) human
RT erythrocytes.";
RT Eur. J. Biochem. 184:337-344(1989).
DR EMBL; M33505; AAA53152.1; -.
DR EMBL; X15824; CAA33822.1; -.
DR EMBL; I70075; I70075.
FT NON TER 1
SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;

Query Match 29.0%; Score 18; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy 2 RSSGSIASNY 11
| : |||
Db 3 RDNLISIVSLY 12

RESULT 8
Q28112 PRELIMINARY; PRT; 9 AA.
AC Q28112;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase (Fragment).
GN GENE B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93387464; PubMed=8397106;
RA Vidal H., Crepin K.M., Rider M.H., Hue L., Rousseau G.G.;
RT "Cloning and expression of novel isoforms of 6-phosphofructo-2-
RT kinase/fructose-2,6-bisphosphatase from bovine heart.";
RL FEBS Lett. 330:329-333(1993).
DR EMBL; X74564; CAA52652.1; -.
DR GO; GO:0016301; F:Kinase activity; IEA.
KW Kinase.
FT NON TER 9
SQ SEQUENCE 9 AA; 837 MW; 859CA5BDC7644865 CRC64;

Query Match 27.4%; Score 17; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SGSIASN 10
| : |||
Db 2 SGNPASS 8

RESULT 9
P81899 PRELIMINARY; PRT; 10 AA.
AC P81899;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large
DE chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX PubMed=9523720;
RA Altmann F., Paschinger K., Dalik T., Vorauer K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT amidase A and its N-glycans.";
RL Eur. J. Biochem. 252:118-123(1998).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -!- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -!- MASS SPECTROMETRY: MW=54182; METHOD=MALDI.

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DR PIR; A59272; A59272.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000224; F:peptide-N4-(N-acetyl-beta-glucosaminyl)aspa. . .; IEA.
KW Hydrolase; Glycoprotein.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;

Query Match 27.4%; Score 17; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IASNY 11
   :|||
Db 1 LASGY 5

RESULT 10
P82699 PRELIMINARY; PRT; 11 AA.
AC P82699;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-2 (LEM-PVK-2).
OS Leucophaea cinerea (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach),
OS Blaberus craniifer,
OS Blaptica dubia, and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
RN NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RX MEDLINE=20307624; PubMed=10849006;
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
DE Human leucocyte antigen B (Fragment).
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1102.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1103 MW; 2F4D9FFD85B05728 CRC64;

Query Match 27.4%; Score 17; DB 5; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSIA 8
   ||||
Db 2 SGLIS 7

RESULT 11
P82700 PRELIMINARY; PRT; 11 AA.
AC P82700;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-3 (LEM-PVK-3).
OS Leucophaea cinerea (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach),
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
RN NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RX MEDLINE=20307624; PubMed=10849006;
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
DE Human leucocyte antigen B (Fragment).
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FFD7605698 CRC64;

Query Match 27.4%; Score 17; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSI 7
   ||||
Db 2 SSGMI 6

RESULT 12
Q9UEX7 PRELIMINARY; PRT; 11 AA.
AC Q9UEX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Human leucocyte antigen B (Fragment).
GN HLA-A*03.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX MEDLINE=20307624; PubMed=10849006;
RP SEQUENCE FROM N.A.
RA Fae I., Kriks D., Cernava B., Fischer G.F.;
RT "A novel HLA-A*03 allele.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ252283; CAB65736.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;

Query Match 27.4%; Score 17; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGSIA 8
   ||||
Db 1 SGALA 5

RESULT 13
Q9TOR6 PRELIMINARY; PRT; 11 AA.
AC Q9TOR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ner protein (Fragment).
OS Bacteriophage Mu.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC Mu-like viruses.
RN NCBI_TaxID=10677;

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RN SEQUENCE FROM N.A.
RP MEDLINE=85153064; PubMed=6099259;
RA Krause H.M., Higgins N.P.;
RT "On the Mu repressor and early DNA intermediates of transposition.";
RL Cold Spring Harb. Symp. Quant. Biol. 49:827-834(1984).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=92356834; PubMed=1386645;
RA Alazard R., Betermier M., Chandler M.;
RT "Escherichia coli integration host factor stabilizes bacteriophage Mu
repressor interactions with operator DNA in vitro.";
RL Mol. Microbiol. 6:1707-1714(1992).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=92356835; PubMed=1386646;
RA Gama M.J., Tousseint A., Higgins N.P.;
RT "Stabilization of bacteriophage Mu repressor-operator complexes by the
Escherichia coli integration host factor protein.";
RL Mol. Microbiol. 6:1715-1722(1992).
DR EMBL; M10192; AAA32371.2; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1006 MW; 89978F816766987A CRC64;

Query Match 27.4%; Score 17; DB 9; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GSIA 8
|||
Db 8 GSVA 11

RESULT 14

Q7ZZI9 PRELIMINARY; PRT; 11 AA.
AC Q7ZZI9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Chromo-helicase-DNA binding protein (Fragment).
GN CHD1Z.
OS Motacilla flava iberiae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Motacillidae; Motacilla.
CX NCBI_TaxID=228287;
RN [1]
RP SEQUENCE FROM N.A. TISSUE=Muscle;
RA Odeen A., Bjorklund M.;
RT "Dynamics in the evolution of sexual traits: losses and gains,
radiation and convergence in yellow wagtails (Motacilla flava).";
RL Mol. Ecol. 0:0-0(2003).
DR EMBL; AY259492; AAP20752.1; -.
DR GO; GO:0004386; F:helicase activity; IEA.
KW Helicase.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1243 MW; 3B0D1082733045B8 CRC64;

Query Match 27.4%; Score 17; DB 13; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RSSGSI 7
|
Db 1 RLDGSI 6

RESULT 15

Q7ZZI6 PRELIMINARY; PRT; 11 AA.
ID Q7ZZI6
AC Q7ZZI6;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Chromo-helicase-DNA binding protein (Fragment).
GN CHD1Z.
OS Motacilla flava pygmaea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Motacillidae; Motacilla.
CX NCBI_TaxID=228290;
RN [1]
RP SEQUENCE FROM N.A.
RA Odeen A., Bjorklund M.;
RT "Dynamics in the evolution of sexual traits: losses and gains,
radiation and convergence in yellow wagtails (Motacilla flava).";
RL Mol. Ecol. 0:0-0(2003).
DR EMBL; AY259495; AAP20755.1; -.
DR GO; GO:0004386; F:helicase activity; IEA.
KW Helicase.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1243 MW; 3B0D1082733045B8 CRC64;

Query Match 27.4%; Score 17; DB 13; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RSSGSI 7
|
Db 1 RLDGSI 6

Search completed: June 8, 2004, 19:22:28

Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:15:05 ; Search time 53 seconds
(without alignments)
69.304 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A: Geneseq_29Jan04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	13	4	AAB61296 Anti-TANG
2	62	100.0	13	6	ABU11262 Human TAN
3	50	80.6	13	2	AAW16590 Anti-RSV
4	39	62.9	13	2	AAR23736 Ligand CD
5	39	62.9	13	2	AAR50108 CDR (d)
6	39	62.9	13	3	AAY68804 Amino aci
7	39	62.9	13	5	ABG31465 Rat immun
8	39	62.9	13	6	ABP98797 Rat anti-
9	34	54.8	12	5	AAU81251 Human trk
10	34	54.8	13	3	AAY95206 Anti-plat
11	34	54.8	13	5	AAU83780 MS-GPC-8
12	34	54.8	13	5	AAU83736 MS-GPC-8
13	34	54.8	13	5	AAU83721 MS-GPC-8
14	34	54.8	13	5	AAU83739 MS-GPC-8
15	34	54.8	13	5	AAU83742 MS-GPC-8
16	34	54.8	13	5	AAU83727 MS-GPC-8
17	34	54.8	13	5	AAU83724 MS-GPC-10
18	34	54.8	13	5	AAU83730 MS-GPC-8
19	34	54.8	13	5	AAU83745 MS-GPC-8
20	34	54.8	13	5	AAU83715 MS-GPC-1
21	34	54.8	13	5	AAU83733 MS-GPC-8
22	34	54.8	13	5	AAU83778 MS-GPC-8
23	34	54.8	13	5	ABBS7489 HLA-DR-sp
24	34	54.8	13	5	ABBS7501 HLA-DR-sp
25	34	54.8	13	5	ABBS7507 HLA-DR-sp

26	34	54.8	13	5	ABBS7513 HLA-DR-sp
27	34	54.8	13	5	ABBS7516 HLA-DR-sp
28	34	54.8	13	5	ABBS7519 HLA-DR-sp
29	34	54.8	13	5	ABBS7492 HLA-DR-sp
30	34	54.8	13	5	ABBS7510 HLA-DR-sp
31	34	54.8	13	5	ABBS7504 HLA-DR-sp
32	34	54.8	13	5	ABBS7483 HLA-DR-sp
33	34	54.8	13	5	ABBS7486 HLA-DR-sp
34	34	54.8	13	5	ABBS7466 HLA-DR-sp
35	34	54.8	13	6	ABR01562 Human ant
36	32	51.6	13	5	AAU83766 MS-GPC-8
37	32	51.6	13	5	AAU83794 MS-GPC-8
38	32	51.6	13	5	AAU83775 MS-GPC-8
39	32	51.6	13	5	AAU83800 MS-GPC-8
40	32	51.6	13	5	ABBS7549 HLA-DR-sp
41	32	51.6	13	5	ABBS7540 HLA-DR-sp
42	32	51.6	13	5	ABBS7463 Antibody
43	31	50.0	10	4	AAG87787 Saccharom
44	31	50.0	10	4	AAG87786 Saccharom
45	31	50.0	12	4	AAB81967 Gangliosi

ALIGNMENTS

RESULT 1
AAB61296
ID AAB61296 standard; peptide; 13 AA.
XX
AC AAB61296;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 64.
XX
KW Human; antibody; scFv; CDR; complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200100810-A1.
XX
PD 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US018152.
XX
PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
XX
DR WPI; 2001-080877/09.

XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.

XX Claim 32; Page 102; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 62; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 Db 1 TRSSGSIASNYVQ 13

RESULT 2

ABU11262

ID ABU11262 standard; peptide; 13 AA.

XX AC ABU11262;

DT 06-FEB-2003 (first entry)

XX DE Human TANGO 268 VLCDRI Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX OS Homo sapiens.

XX PN WO200280968-A1.

XX PD 17-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011122.

XX PR 09-APR-2001; 2001US-00829495.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX PI Gill DS, Qian DM, Kingsbury G;

XX DR WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX PS Claim 10; Page 11; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 62; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 Db 1 TRSSGSIASNYVQ 13

RESULT 3

AAW16590

ID AAW16590 standard; peptide; 13 AA.

XX AC AAW16590;

XX 30-NOV-1997 (first entry)

DE Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6 CDR1.

XX Respiratory syncytial virus; RSV; monoclonal antibody; CDR;
 KW complementarity determining region; pneumonia; bronchiolitis; diagnosis;
 KW therapy; vaccine; RSVF2-5.

XX OS Homo sapiens.

XX PN WO9710846-A1.

XX PD 27-MAR-1997.

XX PF 18-SEP-1996; 96WO-US014937.

XX PR 18-SEP-1995; 95US-0003931P.

XX PA (INTR-) INTRACEL CORP.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Pilkington GR, Gilmour PS, Chanock RM, Crowe JE, Murphy BR;

XX DR WPI; 1997-202621/18.

XX Composition comprising respiratory syncytial virus antibody - useful for
 PT treatment or prophylaxis of active disease or infection.

XX Claim 9; Page 54; 71pp; English.

XX This peptide sequence comprises complementarity determining region 1
 CC (CDR1) of the light chain VL6 region of a novel neutralising human

CC monoclonal antibody to the respiratory syncytial virus (RSV). The
 CC antibody, designated RSVF2-5 (ATCC 6909), selectively binds to an RSV F
 CC glycoprotein epitope. DNA encoding RSVF2-5 Fd and light chain (see
 CC AAW6556-57) was isolated from a phage library prepared from the RNA of
 CC peripheral blood lymphocytes of an HIV-1 infected donor. A claimed
 CC pharmaceutical preparation comprises a carrier and an antibody that
 CC includes the RSVF2-5 VH3 CDR3 (AAW16586) and which may also include the
 CC VH3 CDR2 (AAW16584) and/or CDR1 (AAW16582) or the entire Fd region
 CC (AAW16580), or is an Fab fragment and includes the RSVF2-5 VL6 CDR3
 CC (AAW16594), CDR2 (AAW16592), CDR1 or entire light chain (AAW16588). The
 CC preparation alternatively comprises a carrier and a vector that includes
 CC a nucleotide sequence encoding the antibody. The preparations can be used
 CC for the treatment or prophylaxis of active RSV disease or infection
 CC (claimed), and may also be used for RSV detection. The antibody binds and
 CC neutralises antigenic subgroups A and B of RSV with high efficiency
 XX
 SQ Sequence 13 AA;

Query Match 80.6%; Score 50; DB 2; Length 13;
 Best Local Similarity 76.9%; Pred. NO. 0.016;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 ||:|||||
 Db 1 TRAGRIASNYVQ 13

RESULT 4

AAR23736
 ID AAR23736 standard; protein; 13 AA.

XX AC AAR23736;

DT 27-OCT-1992 (first entry)

DE Ligand CDR (d).

KW Complementarity determining region; heavy chain variable domain;
 KW antigen binding site.

OS Synthetic.

PN WO9206193-A.

XX PD 16-APR-1992.

PF 04-OCT-1991; 91WO-GB001726.

XX 05-OCT-1990; 90GB-00021679.

XX (GORM/) GORMAN S D.

PI Gorman SD, Routledge EG, Waldmann H;

XX WPI; 1992-150879/18.

DR N-PSDB; AAQ24340.

XX Ligands and antibodies with binding affinity for CD3 antigen - for
 PT treatment of immunosuppression e.g. in graft rejection, and cancer, esp.
 PT lymphoid malignancies.

PS Disclosure; Page 4; 49pp; English.

XX The sequence given is a complementarity determining region (CDR)
 CC designated CDR(d). CDR's are found in the variable domains of light and
 CC heavy chains which form the antigen binding site, and act as connectors
 CC between the four framework regions. It has been noted that there seem to
 CC be no characteristic features which distinguish human from mouse or rat
 CC CDR's and they are therefore immunologically identical. The CDR described
 CC is used in a ligand with a binding affinity for the human CD3 antigen
 CC within the framework regions of the heavy chain variable domain along
 CC with the CDR's described in AAR23737 and AAR23738

XX

SQ Sequence 13 AA;

Query Match 62.9%; Score 39; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
 |||||:
 Db 1 TLSSGNIENNV 12

RESULT 5

AAR50108
 ID AAR50108 standard; peptide; 13 AA.

XX AC AAR50108;

XX 25-MAR-2003 (revised)

DT 27-APR-1994 (first entry)

DE CDR (d).

KW Antibody; glycosylation; IgG; binding affinity; CD3; antigen; CDR;
 KW complementarity determining region; heavy chain; light chain;
 KW variable domain; immunosuppressant; T-cell; mitogenesis; cytokine; graft;
 KW rejection; cancer; proliferation.

OS Synthetic.

PN WO9319196-A1.

XX PD 30-SEP-1993.

PF 21-OCT-1992; 92WO-GB001933.

XX 24-MAR-1992; 92GB-00006422.

XX (BOLT/) BOLT S L.

PA (CLAR/) CLARK M R.

PA (GORM/) GORMAN S D.

PA (ROUT/) ROUTLEDGE E G.

XX (WALD/) WALDMANN H.

PI Bolt SL, Clark MR, Gorman SD, Routledge EG, Waldmann H;

XX WPI; 1993-320762/40.

XX Aglycosylated IgG antibody against human CD3 antigen - for preventing
 PT graft rejection and treating cancer, and does not induce T cell
 PT proliferation and cytokine prodn.

XX Claim 3; Page 25; 41pp; English.

XX An aglycosylated IgG antibody having a binding affinity for the human CD3
 CC antigen complex comprises at least one CDR selected from the amino acid
 CC sequences given in AAR50105-R50110. The heavy and light chain variable
 CC domains of an aglycosylated antibody is given in AAR41721- AAR41722. The
 CC antibodies are useful as immunosuppressants. Unlike glycosylated
 CC antibodies, they do not induce T-cell mitogenesis nor do they cause high
 CC level release of cytokines. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 13 AA;

Query Match 62.9%; Score 39; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYV 12
 |||||:
 Db 1 TLSSGNIENNV 12

RESULT 6

AAY68804
 ID AAY68804 standard; peptide; 13 AA.
 XX AC AAY68804;
 XX DT 16-MAY-2000 (first entry)
 XX DE Amino acid sequence of CDR (d) of an anti-CD3 IgG antibody.
 XX DE Complementarity determining region; CDR; rat; immunoglobulin G; IgG;
 KW CD3 antigen complex; chimeric antibody; immunosuppression;
 KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.
 XX
 OS Rattus sp.
 XX
 PN WO200005268-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-GB002380.
 XX
 PR 21-JUL-1998; 98GB-00015909.
 XX
 PA (BTGI-) BTG INT LTD.
 XX
 PI Waldmann H, Frewin M;
 XX
 DR WPI; 2000-182655/16.
 DR N-PSDB; AAZ60593.
 XX
 XX New humanized anti-CD3 antibodies, used for treating cancer or for
 PT immunosuppression and preventing graft rejection.
 XX
 PS Claim 1; Page 38; 56pp; English.
 XX
 CC AAY68801-06 represent complementarity determining regions (CDRs) of a rat
 CC immunoglobulin G (IgG) antibody which is specific for the CD3 antigen
 CC complex. The CDR regions are used to produce chimeric human/rodent anti-
 CC CD3 antibodies, which have a rodent CD3 light chain variable region and a
 CC human heavy chain variable region. The anti-CD3 antibodies can render T-
 CC cells non-functional by antibody blockade of the CD3 antigen-T-cell
 CC receptor (TCR) complex. They can be used for immunosuppression,
 CC particularly for the control of graft rejection. The antibodies can also
 CC enhance or re-direct T-cell responses to antigens. They can be used in
 CC the treatment of cancer
 XX
 SQ Sequence 13 AA;
 Query Match 62.9%; Score 39; DB 3; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSGTASNYV 12
 | | | | | : | | |
 Db 1 TLSSGNIENNYV 12
 RESULT 7
 ABG31465
 ID ABG31465 standard; peptide; 13 AA.
 XX AC ABG31465;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Rat immunoglobulin light chain variable region CDR sequence #1.
 XX
 KW Hybrid antibody; anti-CD3 hybrid antibody; humanised antibody;
 KW complementarity determining region; CDR-grafted; immunoglobulin; Ig;
 KW framework region; PR; immune disorder; T-cell mediated disorder;
 KW transplant rejection; autoimmune disorder; diabetes mellitus;
 KW juvenile rheumatoid arthritis; osteoarthritis; psoriatic arthritis;
 KW multiple sclerosis; encephalomyelitis; myasthenia gravis;

KW systemic lupus erythematosus; autoimmune thyroiditis; dermatitis;
 KW cancer disorder; lymphoma; leukaemia; cytostatic; antidiabetic;
 KW antiarthritic; antiinflammatory; dermatological; immunosuppressive;
 KW antithyroid; rat; light chain variable region.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200262850-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US003925.
 XX
 PR 02-FEB-2001; 2001US-0265914P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI O'keefe T, Rao P;
 XX
 DR WPI; 2002-627524/67.
 DR N-PSDB; ABSS3548.
 XX
 XX New hybrid and anti-CD3 hybrid antibody molecules comprising at least one
 PT light and/or heavy variable regions useful for treating or preventing
 PT cancer or immune disorders, e.g. diabetes, arthritis, multiple sclerosis,
 PT lupus, dermatitis.
 XX
 PS Claim 22; Page 77; 84pp; English.
 XX
 CC The present invention relates to methods of producing hybrid antibody
 CC molecules e.g. a hybrid anti-CD3 antibody. The hybrid antibody comprises
 CC (i) a humanised, or complementarity determining region (CDR)-grafted,
 CC light chain variable region comprising 1, 2 or preferably all 3 CDRs from
 CC a donor immunoglobulin (Ig) (e.g. a rodent (mouse or rat)
 CC immunoglobulin), and a light chain variable framework region (FR), and,
 CC (ii) a chimeric heavy chain variable region comprising 1, 2 or preferably
 CC all 3 CDRs from a donor Ig, and 1, 2, 3 or preferably all 4 heavy chain
 CC variable FRs. The hybrid antibody molecules are useful for treating or
 CC preventing immune or T-cell mediated disorders (e.g. transplant
 CC rejection, or autoimmune disorders such as diabetes mellitus, rheumatoid
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 CC arthritis, multiple sclerosis, encephalomyelitis, myasthenia gravis,
 CC systemic lupus erythematosus, autoimmune thyroiditis, and dermatitis),
 CC and cancer disorders (e.g. lymphoma, leukaemia). ABG31462-ABG31467
 CC represent rat immunoglobulin heavy/light chain variable region CDRs used
 CC to construct an anti-CD3 hybrid antibody
 XX
 SQ Sequence 13 AA;
 Query Match 62.9%; Score 39; DB 5; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSGTASNYV 12
 | | | | | : | | |
 Db 1 TLSSGNIENNYV 12
 RESULT 8
 ABP98797
 ID ABP98797 standard; peptide; 13 AA.
 XX AC ABP98797;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Rat anti-human CD3 antibody light chain CDR1.
 XX
 KW rat; human; CD3; antibody; CDR; complementarity determining region;
 KW antiinflammatory; antirheumatic; antiarthritic; antipsoriatic;
 KW osteopathic; vaccine; inflammation; inflammatory synovitis;
 KW rheumatoid arthritis; ankylosing spondylitis; psoriatic arthritis;
 KW osteoarthritis.


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XX OS Rattus sp.
XX PN WO2003026692-A2.
XX PD 03-APR-2003.
XX PF 26-SEP-2002; 2002WO-GB004358.
XX PR 26-SEP-2001; 2001GB-00023156.
XX RA (ISIS-) ISIS INNOVATION LTD.
XX PI Isaacs J, Waldmann H, Hale G;
XX DR WPI; 2003-357419/34.
XX SQ Sequence 13 AA;
Query Match 62.9%; Score 39; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSGSGIASNYV 12
Db 1 TLSSGNIENNV 12

RESULT 9
AAU81251
ID AAU81251 standard; peptide; 12 AA.
XX AC AAU81251;
XX DT 09-APR-2002 (first entry)
XX DE Human trkC antibody light chain CDR1 of variable region #3.
XX KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
XX KW trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
XX KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
XX KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
XX KW nerve cell injury; blood cell disorder; leukopenia; eosinopenia; wound;
XX KW basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
XX KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
XX KW cellular degeneration; gene therapy.
XX OS Homo sapiens.
XX PN WO200198361-A2.
XX PD 27-DEC-2001.

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XX PF 22-JUN-2001; 2001WO-US020153.
XX PR 22-JUN-2000; 2000US-0213141P.
XX PD 05-OCT-2000; 2000US-0238319P.
XX RA (GETH ) GENENTECH INC.
XX PF Devaux B, Hongo JS, Presta LG, Shelton DL;
XX DR WPI; 2002-130790/17.
XX SQ Sequence 12 AA;
Query Match 54.8%; Score 34; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSSGSIASNYV 12
Db 1 RASQSVSSNYL 11

RESULT 10
AAV95206
ID AAV95206 standard; peptide; 13 AA.
XX AC AAV95206;
XX DT 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human HIB-2 VL CDR1.
XX KW Variable light chain; single chain antibody; scFv; human; HIB-2;
XX KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX KW antithrombotic; thrombus; therapy; diagnostic; CDR1;
XX KW complementarity determining region.
XX OS Homo sapiens.
XX PN WO200026667-A1.
XX PD 11-MAY-2000.
XX PF 29-OCT-1999; 99WO-US025495.
XX PR 30-OCT-1998; 98US-0106275P.
XX RA (MILL/) MILLER J L.
XX PD Miller JL;

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Novel anti-trkC agonist monoclonal antibody useful for treating neurodegenerative disease, shows no significant cross-reactivity with trkA/trkB, and recognizes epitope in domain 5 of trkC.

Claim 13; Fig 11; 121pp; English.

The invention relates to an anti-trkC agonist monoclonal antibody which shows no significant cross-reactivity with trkA or trkB, and recognizes an epitope in domain 5 of trkC. The antibodies of the invention are effective in the treatment of cisplatin- or pyridoxine-induced neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre sensory neuropathy, neurodegenerative disease including amyotrophic lateral sclerosis, nerve cell injuries, disorders of insufficient blood cells such as leukopenia including eosinopenia, basopenia, lymphopenia, monocytopenia, neutropenia, Alzheimer's disease, Parkinson's disease, Huntington's disease and tumours. The sequences are also useful for inducing angiogenesis for treating wounds, ulcers and diabetic complications of sickle cell disease; for treating cardiac ischaemia and cerebrovascular disorders and in the diagnosis of diseases involving cellular degeneration. Sequences AAU81229-AAU81284 represent human and mouse anti-trkC agonist monoclonal antibodies and antibody fragments of the invention

XX WPI; 2000-365744/31.
 XX
 XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT IB alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 XX
 XX Claim 19; Fig 6; 89pp; English.
 PS
 XX The present sequence is that of complementarity determining region 1
 CC (CDR1) of the light chain variable region (VL) of human single chain
 CC antibody (scFv) HIB-2 (see AAY95209), which is directed against platelet
 CC glycoprotein IB (GP1b). The HIB series of scFv was isolated from a human
 CC synthetic VH and VL scFv library on the basis of their binding to
 CC platelet GP1b. Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by *Escherichia coli*, the HIB scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GP1b alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL
 CC chain, including CDR fragments, are also claimed
 XX
 XX Sequence 13 AA;

Query Match 54.8%; Score 34; DB 3; Length 13;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
 || : |||||
 Db 3 SSSNIGSNV 12

RESULT 11
 AAU83780
 ID AAU83780 standard; peptide; 13 AA.
 XX
 XX AAU83780;
 XX
 XX 08-MAY-2002 (first entry)
 DT
 XX MS-GPC-8 optimised light chain variable region CDR1 sequence #2.
 DE
 XX Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS

WO200187337-A1.
 XX
 XX 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US015625.
 XX
 XX 12-MAY-2000; 2000EP-00110065.
 PR 06-OCT-2000; 2000US-0238492P.
 XX
 XX (GPCR-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 PA
 XX Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;

XX WPI; 2002-075288/10.
 DR
 XX
 XX Polypeptide compositions which bind to cell surface epitopes, which in
 PT multivalent form kills lymphoid tumor cells and in monovalent form causes
 PT immunosuppression or inhibits activation of lymphocytes.
 XX
 XX Example 4; Page 68; 150pp; English.

XX The invention relates to a composition which includes a polypeptide or a
 CC multivalent polypeptide comprising one or more antibody-based antigen -
 CC binding domain of human composition with binding specificity for an
 CC antigen expressed on surface of a human cell, especially HLA-DR (human
 CC leukocyte antigen DR), where treating cells expressing HLA-DR with the
 CC multivalent polypeptide causes or leads to killing of cells without need
 CC of cytotoxic entities or immunological mechanisms. Also included are the
 CC nucleic acid encoding the polypeptide, a vector comprising the nucleic
 CC acid and a host cell harbouring vector or nucleic acid. The polypeptide
 CC (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
 CC and the host cell are useful for preparing a pharmaceutical preparation
 CC for the treatment of cell proliferative disorders, disorders involving
 CC transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
 CC lymphoma, B cell lymphoma, B cell acute lymphoid leukaemia, Burkitt's
 CC lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid
 CC leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic
 CC myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid
 CC leukaemia, disorders involving unwanted activation of the cells of the
 CC immune system, such as lymphoid cells expressing MHC class II, rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 CC antigen is useful for suppressing activation or proliferation of a cell
 CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 CC cell of the immune system, such as expressing HLA-DR, the interaction of
 CC the cell of the immune system with another cell, immunosuppressing a
 CC patient and for killing a cell expressing an antigen, HLA-DR on the
 CC surface of the cell, where neither cytotoxic entities nor immunological
 CC mechanisms are needed to cause or lead to the killing. The killing is
 CC dependent on the action of non-caspase proteases and/or cannot be
 CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a
 CC complementarity determining region (CDR) based on the human antigen
 CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 CC either the native sequence or have been optimised/mutated to alter their
 CC antigen binding capabilities
 XX
 XX Sequence 13 AA;

Query Match 54.8%; Score 34; DB 5; Length 13;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
 || : |||||
 Db 3 SSSNIGSNV 12

RESULT 12
 AAU83736
 ID AAU83736 standard; peptide; 13 AA.
 XX
 XX AAU83736;
 XX
 XX 08-MAY-2002 (first entry)
 DT
 XX MS-GPC-8-10 light chain variable region CDR1 sequence.
 DE
 XX Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW

KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200187337-A1.
 XX
 XX 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US015625.
 XX
 XX 12-MAY-2000; 2000EP-00110065.
 XX
 XX 06-OCT-2000; 2000US-0238492P.
 XX
 XX (GPCB-) GPC BIOTECH AG.
 XX (MORP-) MORPHOSYS AG.
 XX
 XX Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
 XX WPI, 2002-075288/10.
 XX
 XX Polypeptide compositions which bind to cell surface epitopes, which in
 XX multivalent form kills lymphoid tumor cells and in monovalent form causes
 XX immunosuppression or inhibits activation of lymphocytes.
 XX
 XX Example 4; Page 66; 150pp; English.
 XX
 XX The invention relates to a composition which includes a polypeptide or a
 XX multivalent polypeptide comprising one or more antibody-based antigen -
 XX binding domain of human composition with binding specificity for an
 XX antigen expressed on surface of a human cell, especially HLA-DR (human
 XX leukocyte antigen DR), where treating cells expressing HLA-DR with the
 XX multivalent polypeptide causes or leads to killing of cells without need
 XX of cytotoxic entities or immunological mechanisms. Also included are the
 XX nucleic acid encoding the polypeptide, a vector comprising the nucleic
 XX acid and a host cell harbouring vector or nucleic acid. The polypeptide
 XX (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
 XX and the host cell are useful for preparing a pharmaceutical preparation
 XX for the treatment of cell proliferative disorders, disorders involving
 XX transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
 XX lymphoma, B cell lymphoma, hairy cell leukaemia, acute myeloid
 XX leukaemia, T cell lymphoma, hairy cell leukaemia, acute myeloid
 XX leukaemia, chronic lymphoid leukaemia or multiple myeloid
 XX leukaemia, disorders involving unwanted activation of the cells of the
 XX immune system, such as lymphoid cells expressing MHC class II, rheumatoid
 XX arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
 XX insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 XX erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
 XX host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 XX cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 XX antigen is useful for suppressing activation or proliferation of a cell
 XX of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 XX cell of the immune system, such as expressing HLA-DR, the interaction of
 XX the cell of the immune system with another cell, immunosuppressing a
 XX patient and for killing a cell expressing an antigen, HLA-DR on the
 XX surface of the cell, where neither cytotoxic entities nor immunological
 XX mechanisms are needed to cause or lead to the killing. The killing is
 XX dependent on the action of non-caspase proteases and/or cannot be
 XX inhibited by zVAD-fmk or zBVD-fmk. The present sequence is a
 XX complementarity determining region (CDR) based on the human antigen
 XX binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 XX either the native sequence or have been optimised/mutated to alter their
 XX antigen binding capabilities
 XX
 XX Sequence 13 AA;

Query Match 54.8%; Score 34; DB 5; Length 13;
 Best Local Similarity 70.0%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SSGSIASNYV 12
 |||:|||||
 Db 3 SSSNIGSNV 12
 RESULT 13
 AAU83721
 ID AAU83721 standard; peptide; 13 AA.
 XX
 XX AC AAU83721;
 XX
 XX DT 08-MAY-2002 (first entry)
 XX
 XX DE MS-GPC-8 light chain variable region CDR1 sequence.
 XX
 XX KW Human; antibody-based antigen: HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.
 XX
 XX OS Homo sapiens.
 XX WO200187337-A1.
 XX
 XX PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US015625.
 XX
 XX 12-MAY-2000; 2000EP-00110065.
 XX 06-OCT-2000; 2000US-0238492P.
 XX
 XX (GPCB-) GPC BIOTECH AG.
 XX (MORP-) MORPHOSYS AG.
 XX
 XX Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
 XX WPI, 2002-075288/10.
 XX
 XX Polypeptide compositions which bind to cell surface epitopes, which in
 XX multivalent form kills lymphoid tumor cells and in monovalent form causes
 XX immunosuppression or inhibits activation of lymphocytes.
 XX
 XX Example 4; Page 66; 150pp; English.
 XX
 XX The invention relates to a composition which includes a polypeptide or a
 XX multivalent polypeptide comprising one or more antibody-based antigen -
 XX binding domain of human composition with binding specificity for an
 XX antigen expressed on surface of a human cell, especially HLA-DR (human
 XX leukocyte antigen DR), where treating cells expressing HLA-DR with the
 XX multivalent polypeptide causes or leads to killing of cells without need
 XX of cytotoxic entities or immunological mechanisms. Also included are the
 XX nucleic acid encoding the polypeptide, a vector comprising the nucleic
 XX acid and a host cell harbouring vector or nucleic acid. The polypeptide
 XX (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
 XX and the host cell are useful for preparing a pharmaceutical preparation
 XX for the treatment of cell proliferative disorders, disorders involving
 XX transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
 XX lymphoma, B cell lymphoma, hairy cell leukaemia, acute myeloid
 XX leukaemia, T cell lymphoma, hairy cell leukaemia, acute myeloid
 XX leukaemia, chronic lymphoid leukaemia or multiple myeloid
 XX leukaemia, disorders involving unwanted activation of the cells of the
 XX immune system, such as lymphoid cells expressing MHC class II, rheumatoid
 XX arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
 XX insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 XX erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
 XX host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 XX cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 XX antigen is useful for suppressing activation or proliferation of a cell
 XX of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 XX cell of the immune system, such as expressing HLA-DR, the interaction of
 XX the cell of the immune system with another cell, immunosuppressing a
 XX patient and for killing a cell expressing an antigen, HLA-DR on the
 XX surface of the cell, where neither cytotoxic entities nor immunological
 XX mechanisms are needed to cause or lead to the killing. The killing is
 XX dependent on the action of non-caspase proteases and/or cannot be
 XX inhibited by zVAD-fmk or zBVD-fmk. The present sequence is a
 XX complementarity determining region (CDR) based on the human antigen
 XX binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 XX either the native sequence or have been optimised/mutated to alter their
 XX antigen binding capabilities
 XX
 XX Sequence 13 AA;

CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 CC antigen is useful for suppressing activation or proliferation of a cell
 CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 CC cell of the immune system, such as expressing HLA-DR, the interaction of
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 CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 CC either the native sequence or have been optimised/mutated to alter their
 CC antigen binding capabilities

XX Sequence 13 AA;

Query Match 54.8%; Score 34; DB 5; Length 13;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 3 SSGSIASNYV 12

Db ||:|||||
 3 SSSNIGSNV 12

RESULT 14

AAU83739

ID AAU83739 standard; peptide; 13 AA.

XX

AC AAU83739;

XX

DT 08-MAY-2002 (first entry)

XX

DE MS-GPC-8-17 light chain variable region CD1 sequence.

XX

KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.

OS Homo sapiens.

OS Synthetic.

XX

PN WC200187337-A1.

XX

PD 22-NOV-2001.

XX

PF 14-MAY-2001; 2001WO-US015625.

XX

PR 12-MAY-2000; 2000EP-00110065.

XX

PR 06-OCT-2000; 2000US-0238492P.

XX

PA (GPCB-) GPC BIOTECH AG.

XX

PA (MORP-) MORPHOSYS AG.

XX

PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;

XX

DR WPI; 2002-075288/10.

XX

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 CC antigen expressed on surface of a human cell, especially HLA-DR (human
 CC leukocyte antigen DR), where treating cells expressing HLA-DR without need
 CC multivalent polypeptide causes or leads to killing of cells with the
 CC of cytotoxic entities or immunological mechanisms. Also included are the
 CC nucleic acid encoding the polypeptide, a vector comprising the nucleic
 CC acid and a host cell harbouring vector or nucleic acid. The polypeptide
 CC (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
 CC and the host cell are useful for preparing a pharmaceutical preparation
 CC for the treatment of cell proliferative disorders, disorders involving
 CC transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
 CC lymphoma, B cell lymphoma, B cell acute lymphoid leukaemia, Burkitt's
 CC leukaemia, T cell lymphoma, hairy cell leukaemia, acute myeloid
 CC myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid
 CC leukaemia, disorders involving unwanted activation of the cells of the
 CC immune system, such as lymphoid cells expressing MHC class II, rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
 CC antigen is useful for suppressing activation or proliferation of a cell
 CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
 CC cell of the immune system, such as expressing HLA-DR, the interaction of
 CC the cell of the immune system with another cell, immunosuppressing a
 CC patient and for killing a cell expressing an antigen, HLA-DR on the
 CC surface of the cell, where neither cytotoxic entities nor immunological
 CC mechanisms are needed to cause or lead to the killing. The killing is
 CC dependent on the action of non-caspase proteases and/or cannot be
 CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a
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 CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
 CC either the native sequence or have been optimised/mutated to alter their
 CC antigen binding capabilities

XX Sequence 13 AA;

Query Match 54.8%; Score 34; DB 5; Length 13;

Best Local Similarity 70.0%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12

Db ||:|||||
 3 SSSNIGSNV 12

RESULT 15

AAU83742

ID AAU83742 standard; peptide; 13 AA.

XX

AC AAU83742;

XX

DT 08-MAY-2002 (first entry)

XX

DE MS-GPC-8-18 light chain variable region CD1 sequence.

XX

KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200187337-A1.

XX

PD 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015625.
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XX 12-MAY-2000; 2000EP-00110065.
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XX (GPCB-) GPC BIOTECH AG.
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PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
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XX WPI; 2002-075288/10.
XX
XX Polypeptide compositions which bind to cell surface epitopes, which in
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XX Example 4; Page 66; 150pp; English.
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CC antigen expressed on surface of a human cell, especially HLA-DR (human
CC leukocyte antigen DR), where treating cells expressing HLA-DR with the
CC multivalent polypeptide causes or leads to killing of cells without need
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CC nucleic acid encoding the polypeptide, a vector comprising the nucleic
CC acid and a host cell harbouring vector or nucleic acid. The polypeptide
CC (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
CC and the host cell are useful for preparing a pharmaceutical preparation
CC for the treatment of cell proliferative disorders, disorders involving
CC transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
CC lymphoma, B cell lymphoma, B cell acute lymphoid leukemia, Burkitt's
CC lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid
CC leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic
CC myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid
CC leukaemia, disorders involving unwanted activation of the cells of the
CC immune system, such as lymphoid cells expressing MHC class II, rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
CC antigen is useful for suppressing activation or proliferation of a cell
CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
CC cell of the immune system, such as expressing HLA-DR, the interaction of
CC the cell of the immune system with another cell, immunosuppressing a
CC patient and for killing a cell expressing an antigen, HLA-DR on the
CC surface of the cell, where neither cytotoxic entities nor immunological
CC mechanisms are needed to cause or lead to the killing. The killing is
CC dependent on the action of non-caspase proteases and/or cannot be
CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a
CC complementarity determining region (CDR) based on the human antigen
CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
CC either the native sequence or have been optimised/mutated to alter their
CC antigen binding capabilities
XX
SQ Sequence 13 AA;

Query Match 54.8%; Score 34; DB 5; Length 13;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSGSIASNYV 12
||:|
DB 3 SSSNIGSNV 12

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 19:12:15 ; Search time 23 Seconds
(without alignments)
31.425 Million cell updates/sec

Title: US-09-610-118-63
Perfect score: 80
Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 136113

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	38.8	14	1	US-08-433-318A-109
2	31	38.8	14	1	US-08-433-318A-172
3	31	38.8	14	2	US-08-922-048-109
4	31	38.8	14	2	US-08-922-048-172
5	31	38.8	14	4	US-09-111-681C-125
6	31	38.8	14	4	US-09-111-681C-188
7	31	38.8	14	5	PCT-US96-06270-109
8	31	38.8	14	5	PCT-US96-06270-172
9	30	37.5	10	1	US-08-190-788A-13
10	30	37.5	10	1	US-08-383-474B-145
11	30	37.5	10	1	US-08-465-391A-140
12	30	37.5	10	2	US-08-464-538B-140
13	30	37.5	10	2	US-08-463-076E-190
14	30	37.5	10	4	US-09-428-082B-758
15	30	37.5	11	2	US-08-726-136-13
16	30	37.5	11	3	US-09-103-434-13
17	30	37.5	11	3	US-09-687-594-13
18	30	37.5	14	1	US-08-433-318A-107
19	30	37.5	14	1	US-08-433-318A-170
20	30	37.5	14	2	US-08-922-048-107
21	30	37.5	14	2	US-08-922-048-170
22	30	37.5	14	4	US-09-111-681C-123
23	30	37.5	14	4	US-09-111-681C-186
24	30	37.5	14	5	PCT-US96-06270-107
25	30	37.5	14	5	PCT-US96-06270-170
26	28	35.0	9	4	US-09-289-942A-4
27	28	35.0	9	4	US-09-289-942A-5

28	28	35.0	10	1	US-08-485-508-22	Sequence 22, Appl
29	28	35.0	14	1	US-07-756-250-14	Sequence 14, Appl
30	28	35.0	14	1	US-08-433-318A-105	Sequence 105, App
31	28	35.0	14	1	US-08-433-318A-168	Sequence 168, App
32	28	35.0	14	2	US-08-922-048-105	Sequence 105, App
33	28	35.0	14	2	US-08-922-048-168	Sequence 168, App
34	28	35.0	14	4	US-09-111-681C-121	Sequence 121, App
35	28	35.0	14	4	US-09-111-681C-184	Sequence 184, App
36	28	35.0	14	5	PCT-US96-06270-105	Sequence 105, App
37	28	35.0	14	5	PCT-US96-06270-168	Sequence 168, App
38	27	33.8	6	1	US-08-433-318A-9	Sequence 9, Appli
39	27	33.8	6	2	US-08-922-048-9	Sequence 9, Appli
40	27	33.8	6	4	US-09-315-304B-1593	Sequence 1593, Ap
41	27	33.8	6	4	US-09-111-681C-25	Sequence 25, Appl
42	27	33.8	6	4	US-09-350-325-43	Sequence 43, Appl
43	27	33.8	6	4	US-09-350-641C-1593	Sequence 1593, Ap
44	27	33.8	6	5	PCT-US96-06270-9	Sequence 9, Appli
45	27	33.8	10	1	US-08-433-318A-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-08-433-318A-109
; Sequence 109, Application US/08433318A
; Patent No. 5663144
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 5663144+1s
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,318A
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-433-318A-109

Query Match 38.8%; Score 31; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
|:|:| | |

Db 3 DQWEYCYP 11

RESULT 2

US-08-433-318A-172

; Sequence 172, Application US/08433318A

; Patent No. 5663144

; GENERAL INFORMATION:

; APPLICANT: Greene, Mark I.

; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND

; TITLE OF INVENTION: METHODS OF USING THE SAME

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 5663144ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WORDPERFECT 6

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,318A

; FILING DATE: 03-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,318A

; FILING DATE: 03-MAY-1995

; NAME: Mark DeLuca

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: UPN-2106

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 172:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-433-318A-172

Query Match 38.8%; Score 31; DB 1; Length 14;

Best Local Similarity 55.6%; Pred. No. 78;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9

Db 3 DQWEYCYP 11

RESULT 3

US-08-922-048-109

; Sequence 109, Application US/08922048

; Patent No. 5919764

; GENERAL INFORMATION:

; APPLICANT: Greene, Mark I.

; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND

; TITLE OF INVENTION: METHODS OF USING THE SAME

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 5919764ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WORDPERFECT 6

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/922,048

; FILING DATE: 03-MAY-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,318

; FILING DATE: 03-MAY-1995

; NAME: Mark DeLuca

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: UPN-2106

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 172:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-922-048-109

Query Match 38.8%; Score 31; DB 1; Length 14;

Best Local Similarity 55.6%; Pred. No. 78;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9

Db 3 DQWEYCYP 11

RESULT 4

US-08-922-048-172

; Sequence 172, Application US/08922048

; Patent No. 5919764

; GENERAL INFORMATION:

; APPLICANT: Greene, Mark I.

; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND

; TITLE OF INVENTION: METHODS OF USING THE SAME

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 5919764ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: WORDPERFECT 6

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/922,048

; FILING DATE: 03-MAY-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,318

; FILING DATE: 03-MAY-1995

; NAME: Mark DeLuca

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: UPN-2106

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 172:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-922-048-109

Query Match 38.8%; Score 31; DB 2; Length 14;

Best Local Similarity 55.6%; Pred. No. 78;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9

Db 3 DQWEYCYP 11


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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-922-048-172

Query Match 38.8%; Score 31; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
Db 3 DQWEWYCYP 11

RESULT 5
US-09-111-681C-125
; Sequence 125, Application US/09111681C
; Patent No. 6417168
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: O'Rourke, Donald M.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Park, Byeong Woo
; TITLE OF INVENTION: Compositions And Methods Of Treating Tumors
; FILE REFERENCE: UPN3458
; CURRENT APPLICATION NUMBER: US/09/111,681C
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/076,788
; PRIOR FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-111-681C-125

Query Match 38.8%; Score 31; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
Db 3 DQWEWYCYP 11

RESULT 6
US-09-111-681C-188
; Sequence 188, Application US/09111681C
; Patent No. 6417168
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: O'Rourke, Donald M.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Park, Byeong Woo
; TITLE OF INVENTION: Compositions And Methods Of Treating Tumors
; FILE REFERENCE: UPN3458
; CURRENT APPLICATION NUMBER: US/09/111,681C
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/076,788
; PRIOR FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-111-681C-188

Query Match 38.8%; Score 31; DB 5; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
Db 3 DQWEWYCYP 11

RESULT 7
PCT-US96-06270-109
; Sequence 109, Application PC/TUS9606270
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Zhang, Xin
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,318
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark DeLuca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2748
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-06270-109

Query Match 38.8%; Score 31; DB 5; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
Db 3 DQWEWYCYP 11

RESULT 8
PCT-US96-06270-172
; Sequence 172, Application PC/TUS9606270
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Zhang, Xin
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; OTHER INFORMATION: Synthetic Sequence
PCT-US96-06270-172
```

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06270
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Mark DeLuca

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2748

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 14

TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: peptide
PCT-US96-06270-172

Query Match 38.8%; Score 31; DB 5; Length 14;
Best Local Similarity 55.8%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
|:|:|:|
Db 3 DQWEWYCYP 11

RESULT 9
US-08-190-788A-140
Sequence 140, Application US/08190788A
Patent No. 5608035
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies N.V.
STREET: 4001 Miranda Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788A
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-190-788A-140

Query Match 37.5%; Score 30; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|:|:|:|
Db 3 WQPYATP 9

RESULT 10
US-08-383-474B-145
Sequence 145, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-145

Query Match 37.5%; Score 30; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|: |||
DB 3 WQPYATP 9

RESULT 11
US-08-465-391A-140
; Sequence 140, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465.391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-140

Query Match 37.5%; Score 30; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|: |||
DB 3 WQPYATP 9

RESULT 12
US-08-464-538B-140
; Sequence 140, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464.538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-538B-140

Query Match 37.5%; Score 30; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|: |||
DB 3 WQPYATP 9

RESULT 13
US-08-463-076E-190
; Sequence 190, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor

NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-190

Query Match 37.5%; Score 30; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|:|:|
Db 3 WQPYATP 9

RESULT 14
US-09-428-082B-758
Sequence 758, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patent in version 3.1
SEQ ID NO: 758
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-758

Query Match 37.5%; Score 30; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
|:|:|

Db 3 WQPYATP 9
RESULT 15
US-08-726-136-13
Sequence 13, Application US/08726136
Patent No. 5811286
GENERAL INFORMATION:
APPLICANT: ROBERT D. FALLON
APPLICANT: MARK S. PAYNE
APPLICANT: MARK J. NELSON
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS ENCODING
STEREOSPECIFIC NITRILE HYDRATASE AND AMIDASE ENZYMES AND
TITLE OF INVENTION: RECOMBINANT ORGANISMS EXPRESSING THOSE ENZYMES USEFUL FOR
THE PRODUCTION OF CHIRAL AMIDES AND ACIDS
TITLE OF INVENTION: THE PRODUCTION OF CHIRAL AMIDES AND ACIDS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,136
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004914
FILING DATE: OCTOBER 6, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9677
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-726-136-13

Query Match 37.5%; Score 30; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
|:|:|
Db 2 DLWDDYLEP 10

Search completed: June 8, 2004, 19:15:38
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:13:40 ; Search time 42 Seconds
(without alignments)

93.780 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

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Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 185969

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	80	100.0	14	11	US-09-829-495-63
3	34	42.5	14	10	US-09-880-748-3128
4	34	42.5	14	12	US-10-293-418-3128
5	31	38.8	14	13	US-10-100-952-125
6	31	38.8	14	13	US-10-100-952-188
7	30	37.5	10	10	US-09-880-748-3117
8	30	37.5	10	12	US-10-609-217-758
9	30	37.5	10	12	US-10-632-388-758
10	30	37.5	10	12	US-10-651-723-758
11	30	37.5	10	12	US-10-293-418-3117
12	30	37.5	10	12	US-10-645-761-758
13	30	37.5	10	16	US-10-666-696-758
14	30	37.5	10	16	US-10-653-048-758
15	30	37.5	14	13	US-10-100-952-123

16	30	37.5	14	13	US-10-100-952-186	Sequence 186, App
17	29	36.2	9	10	US-09-932-165-8	Sequence 8, Appli
18	29	36.2	9	10	US-09-932-165-437	Sequence 437, App
19	29	36.2	9	10	US-09-932-165-615	Sequence 615, App
20	29	36.2	10	10	US-09-932-165-501	Sequence 501, App
21	29	36.2	10	10	US-09-932-165-712	Sequence 712, App
22	29	36.2	11	14	US-10-119-528-74	Sequence 74, Appli
23	29	36.2	12	10	US-09-870-498A-4	Sequence 4, Appli
24	29	36.2	13	15	US-10-285-335-18	Sequence 18, Appli
25	28.5	35.6	10	10	US-09-880-748-3178	Sequence 3178, Ap
26	28.5	35.6	10	12	US-10-293-418-3178	Sequence 3178, Ap
27	28	35.0	9	12	US-10-014-340-272	Sequence 272, App
28	28	35.0	14	13	US-10-100-952-121	Sequence 121, App
29	28	35.0	14	13	US-10-100-952-184	Sequence 184, App
30	27	33.8	6	13	US-10-100-952-25	Sequence 25, Appli
31	27	33.8	6	14	US-10-347-562-43	Sequence 43, Appli
32	27	33.8	6	14	US-10-351-641-1583	Sequence 1583, Ap
33	27	33.8	9	14	US-10-116-788A-25	Sequence 25, Appli
34	27	33.8	10	13	US-10-100-952-157	Sequence 157, App
35	27	33.8	11	13	US-10-100-952-141	Sequence 141, App
36	27	33.8	14	10	US-09-983-802-326	Sequence 326, App
37	27	33.8	14	12	US-09-973-278-321	Sequence 321, App
38	27	33.8	14	12	US-09-984-490-326	Sequence 326, App
39	27	33.8	14	13	US-10-100-952-119	Sequence 119, App
40	27	33.8	14	13	US-10-100-952-124	Sequence 124, App
41	27	33.8	14	13	US-10-100-952-133	Sequence 133, App
42	27	33.8	14	13	US-10-100-952-182	Sequence 182, App
43	27	33.8	14	13	US-10-100-952-187	Sequence 187, App
44	27	33.8	14	13	US-10-100-952-196	Sequence 196, App
45	26	32.5	5	14	US-10-190-082-233	Sequence 233, App

ALIGNMENTS

RESULT 1
US-09-832-312-63
; Sequence 63, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-63

Query Match 100.0%; Score 80; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFDV 14
Db 1 DKWEAYITPGAFDV 14

RESULT 2
US-09-829-495-63
; Sequence 63, Application US/09829495

Publication No. US20040001826A1
GENERAL INFORMATION:
APPLICANT: Busfield SJ
APPLICANT: Villevall J
APPLICANT: Jandrot-Perrus M
APPLICANT: Vainchenker W
APPLICANT: Gill DS
APPLICANT: Qian MD
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/829,495
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-829-495-63

Query Match 100.0%; Score 80; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGADV 14
DB 1 DKWEAYITPGADV 14

RESULT 3
US-09-880-748-3128
Sequence 3128, Application US/09880748
Publication No. US2003005993A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3128
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-3128

Query Match 42.5%; Score 34; DB 10; Length 14;
Best Local Similarity 38.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 KWEAYITPGADV 14
DB 2 EWEDIVVGSADF 14

RESULT 4
US-10-293-418-3128
Sequence 3128, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3128
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-3128

Query Match 42.5%; Score 34; DB 12; Length 14;
Best Local Similarity 38.5%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 KWEAYITPGADV 14
DB 2 EWEDIVVGSADF 14

RESULT 5
US-10-100-952-125
Sequence 125, Application US/10100952
Publication No. US20020165193A1
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: O'Rourke, Donald M.
APPLICANT: Murali, Ramachandran
APPLICANT: Park, Byeong Woo
TITLE OF INVENTION: Compositions And Methods Of Treating Tumors
FILE REFERENCE: UPN3458
CURRENT APPLICATION NUMBER: US/10/100,952
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/111,681
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: 60/076,788
PRIOR FILING DATE: 1998-03-04
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn version 3.1
SEQ ID NO 125
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-100-952-125

Query Match 38.8%; Score 31; DB 13; Length 14;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 DKWEAYITP 9
   :|||
Db 3 DQWEYCYP 11

RESULT 6
US-10-952-188
; Sequence 189, Application US/10100952
; Publication No. US2002015193A1
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: O'Rourke, Donald M.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Park, Byoung Woo
; TITLE OF INVENTION: Compositions And Methods Of Treating Tumors
; FILE REFERENCE: US/10/100,952
; CURRENT APPLICATION NUMBER: US/10/100,952
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/111,681
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/076,788
; PRIOR FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-100-952-188

Query Match 38.8%; Score 31; DB 13; Length 14;
Best Local Similarity 55.6%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
   :|||
Db 3 DQWEYCYP 11

RESULT 7
US-09-880-748-3117
; Sequence 3117, Application US/09880748
; Publication No. US2003059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3117
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3117

Query Match 37.5%; Score 30; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 ITGAPDV 14
   :|||
Db 3 LTGGAFDI 10

RESULT 8
US-10-609-217-758
; Sequence 758, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-758

Query Match 37.5%; Score 30; DB 12; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
   :|||
Db 3 WQPYATP 9

RESULT 9
US-10-632-388-758
; Sequence 758, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-758

Query Match 37.5%; Score 30; DB 12; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3 WEAYITP 9
|: |||
Db 3 WQPYATP 9

RESULT 10

US-10-651-723-758
; Sequence 758, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-758

Query Match 37.5%; Score 30; DB 12; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WEAYITP 9
|: |||
Db 3 WQPYATP 9

RESULT 11

US-10-293-418-3117
; Sequence 3117, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3117
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3117

Query Match 37.5%; Score 30; DB 12; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ITPGAPDV 14
|: |||||
Db 3 LTGGAFDI 10

RESULT 12

US-10-645-761-758
; Sequence 758, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-645-761-758

Query Match 37.5%; Score 30; DB 12; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WEAYITP 9
|: |||
Db 3 WQPYATP 9

RESULT 13

US-10-666-696-758
; Sequence 758, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


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; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-666-696-758
Query Match      37.5%; Score 30; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 WEAYITP 9
      | : | | |
Db      3 WQPYATP 9

RESULT 14
US-10-653-048-758
; Sequence 758, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-653-048-758
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Query Match      37.5%; Score 30; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 WEAYITP 9
      | : | | |
Db      3 WQPYATP 9
```

```
RESULT 15
US-10-100-952-123
; Sequence 123, Application US/10100952
; Publication No. US20020165193A1
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: O'Rourke, Donald M.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Park, Byeong Woo
; TITLE OF INVENTION: Compositions And Methods Of Treating Tumors
; FILE REFERENCE: UPN3458
; CURRENT APPLICATION NUMBER: US/10/100,952
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/111,681
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/076,788
; PRIOR FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
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US-10-100-952-123
Query Match      37.5%; Score 30; DB 13; Length 14;
Best Local Similarity 55.6%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 DKWEAYITP 9
      | | | | |
Db      3 DNWEWYCYP 11

Search completed: June 8, 2004, 19:19:36
Job time : 42 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 19:11:20 ; Search time 21 Seconds
(without alignments)
64.128 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80
Sequence: 1 DKWEAYTPGAPDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2095

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	31.2	11	2 S78026	ribosomal protein
2	23	28.7	10	2 PH0944	T-cell receptor be
3	22	27.5	13	2 A60379	factor X activator
4	22	27.5	14	2 PH1347	Ig heavy chain DJ
5	21	26.2	10	2 S63696	DNA polymerase - y
6	21	26.2	12	2 S43957	Ig mu chain V regi
7	20	25.0	10	1 RHFGG	gonadoliberin - pi
8	20	25.0	10	1 RHSHG	gonadoliberin - sh
9	20	25.0	10	1 RHAQ1	gonadoliberin I -
10	20	25.0	14	2 PH1305	Ig heavy chain DJ
11	20	25.0	14	2 PH1306	Ig heavy chain DJ
12	19	23.8	12	2 I40663	bma protein - Clos
13	19	23.8	13	2 A46463	preabsorbing antig
14	19	23.8	13	2 PS0453	36K protein 3124 -
15	19	23.8	13	2 PQ0700	unidentified 6.3/4
16	18	22.5	8	2 A33995	adipokinetic hormo
17	18	22.5	8	2 S5310	adipokinetic hormo
18	18	22.5	8	2 A58620	adipokinetic hormo
19	18	22.5	9	2 D57444	neuropeptide Grb-A
20	18	22.5	10	2 B33995	hypotrehalosemic h
21	18	22.5	10	2 S59625	beta-galactosidase
22	18	22.5	10	2 PH0664	T-cell receptor be
23	18	22.5	10	2 PH0916	T-cell receptor be
24	18	22.5	10	2 PQ0783	NADH2 dehydrogenas
25	18	22.5	11	2 S33300	probable substance
26	18	22.5	12	2 A40763	sucrose-6-phosphat
27	18	22.5	12	2 A35585	cytokinin-binding
28	18	22.5	13	2 B58533	CD61 homolog - cha
29	18	22.5	13	2 S47368	T-cell antigen rec

30 18 22.5 14 2 PC2373 probable IMP dehyd
31 18 22.5 14 2 A39239 actin 8 - slime mo
32 18 22.5 14 2 PT0294 Ig heavy chain CRD
33 17.5 21.9 13 2 PC4391 cysteine proteinas
34 17 21.2 5 2 PT0308 Ig heavy chain CRD
35 17 21.2 6 2 A31283 dihydrofolate redu
36 17 21.2 6 2 B31263 dihydrofolate redu
37 17 21.2 9 2 PT0562 T-cell receptor be
38 17 21.2 10 2 S23370 T-cell receptor al
39 17 21.2 10 2 F49033 T-cell receptor ga
40 17 21.2 10 2 PT0213 T-cell receptor al
41 17 21.2 11 2 S07203 uperolein - frog (
42 17 21.2 11 2 S45698 gamma-MSH-like pro
43 17 21.2 11 2 PH1343 Ig heavy chain DJ
44 17 21.2 12 2 G49215 urcase (EC 3.5.1.5
45 17 21.2 12 2 S01122 photosystem II 3.7

ALIGNMENTS

RESULT 1

S78026
ribosomal protein Yml29, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C:Species: Saccharomyces cerevisiae
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C:Accession: S78026
R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma
Eur. J. Biochem. 245, 449-456, 1997
A>Title: Identification and characterization of the genes for mitochondrial ribosomal pr
A:Reference number: S78018; MUID:97296414; PMID:9151978
A:Accession: S78026
A:Molecule type: protein
A:Residues: 1-11 <KIT>
C:Genetics:
A:Genome: nuclear
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 31.2%; Score 25; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 BAYTTP 9
DB 3 BAYTTP 8

RESULT 2

PH0944
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0944
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0944
A:Molecule type: mRNA
A:Residues: 1-10 <COL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon GAC for residue 9 as Glu
C:Keywords: T-cell receptor

Query Match 28.7%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TPGAFD 13
DB 4 SPGGYD 9

RESULT 3

A60379
factor X activator - aspic viper (fragment)
C/Species: Vipera aspis (aspic viper)
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 18-Jun-1993
C/Accession: A60379
R/Komori, Y.; Nikai, T.; Sugihara, H.
Int. J. Biochem. 22, 1053-1060, 1990
A/Title: Isolation and characterization of factor X activator from the venom of Vipera a
A/Reference number: A60379; MUID:91130643; PMID:2282962
A/Accession: A60379
A/Molecule type: protein
A/Residues: 1-13 <KOM>
A/Note: the source is designated as Vipera aspis aspis
C/Keywords: venom

Query Match 27.5%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WEAY 6
| : : : |
Db 8 WSAY 11

RESULT 4

PH1347
Ig heavy chain DJ region (clone C100-103A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1347
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DUH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1347
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
C/Keywords: heterotetramer; immunoglobulin

Query Match 27.5%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAYITPCA 11
| : : : |
Db 4 EDFITPCA 11

RESULT 5

S63696
DNA polymerase - yeast (Kluyveromyces marxianus var. lactis) killer plasmid pGKL2 (fragm
C/Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C/Accession: S63696
R/Takeda, M.; Hiraishi, H.; Takesako, T.; Tanase, S.; Gunge, N.
Yeast 12, 241-246, 1996
A/Title: The terminal protein of the linear DNA plasmid pGKL2 shares an N-terminal domai
A/Reference number: S63696; MUID:97060015; PMID:8904336
A/Accession: S63696
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <TAK>
A/Note: the source is designated as Kluyveromyces lactis

Query Match 26.2%; Score 21; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWE 4
| : : : |
Db 3 KWE 5

RESULT 6

S43957
Ig mu chain V region (clone 3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C/Accession: S43957
R/Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.
Nucleic Acids Res. 22, 1389-1393, 1994
A/Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A/Reference number: S43956; MUID:94248036; PMID:8190629
A/Accession: S43957
A/Molecule type: DNA
A/Residues: 1-12 <WAG>
C/Keywords: immunoglobulin

Query Match 26.2%; Score 21; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GAFDV 14
| : : : |
Db 4 GPFDV 8

RESULT 7

RH9GG
gonadoliberin - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
C/Accession: A01411
R/Baba, Y.; Matsuo, H.; Schally, A.V.
Biochem. Biophys. Res. Commun. 44, 459-463, 1971
A/Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the
A/Reference number: A90172; MUID:72114303; PMID:4946067
A/Accession: A01411
A/Molecule type: protein
A/Residues: 1-10 <BAB>
R/Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 822-827, 1971
A/Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase meth
A/Reference number: A90176; MUID:72065376; PMID:4942726
A/Contents: annotation; synthesis
A/Note: the synthetic and natural hormones have the same physicochemical and biological
R/Baba, Y.; Arimura, A.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 483-487, 1971
A/Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
A/Reference number: A90175; MUID:72117544; PMID:4946275
A/Contents: annotation
A/Note: Trp-3 appears to be essential for biological activity
C/Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and f
C/Superfamily: gonadoliberin
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 20; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 WEAYITPG 10
| : : : |
Db 3 WSYGLRPG 10

RESULT 8

RHSHG
gonadoliberin - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
C/Accession: A93780; A01411
R/Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; B
Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972

A;Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor
 A;Reference number: A93780; MUID:72094314; PMID:4550508
 A;Accession: A93780
 A;Molecule type: protein
 A;Residues: 1-10 <BUR>
 A;Note: the natural and synthetic hormones have the same biological activity
 C;Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle stimulating hormones
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 WEAVITPG 10
 | : ||
 Db 3 WSYGLRPG 10

RESULT 9
 BHAQ1
 gonadoliberin I - American alligator
 N;Alternate names: gonadotropin-releasing hormone I
 C;Species: Alligator mississippiensis (American alligator)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
 C;Accession: A60066
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson, R.; Regl. Fept. 33, 105-116, 1991
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of the American alligator
 A;Reference number: A60066; MUID:91352338; PMID:1882082
 A;Accession: A60066
 A;Molecule type: protein
 A;Residues: 1-10 <LOV>
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 WEAVITPG 10
 | : ||
 Db 3 WSYGLRPG 10

RESULT 10
 PH1305
 Ig heavy chain DJ region (clone C85-1B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1305
 R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1305
 A;Molecule type: DNA
 A;Residues: 1-14 <WAS>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 YITPGA 11
 | : ||
 Db 6 YTTTGA 11

RESULT 11
 PH1306
 Ig heavy chain DJ region (clone C96-100) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1306
 R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1306
 A;Molecule type: DNA
 A;Residues: 1-14 <WAS>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 YITPGA 11
 | : ||
 Db 6 YTTTGA 11

RESULT 12
 I40663
 bma protein - Clostridium cochlearium (fragment)
 C;Species: Clostridium cochlearium
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
 C;Accession: I40663; S47465
 R;Zelizer, O.; Bearix, B.; Leutbecher, U.; Buckel, W.
 Eur. J. Biochem. 226, 577-585, 1994
 A;Title: Characterization of the coenzyme-B12-dependent glutamate mutase from Clostridium cochlearium
 A;Reference number: I40659; MUID:95094816; PMID:7880251
 A;Accession: I40663
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-12 <RES>
 C;Cross-references: EMBL:X80997; NID:9530005; PIDN:CAAS6924.1; PID:9530010
 C;Genetics:
 A;Gene: bma

Query Match 23.8%; Score 19; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TPGA 11
 | : ||
 Db 9 TPGS 12

RESULT 13
 A46463
 preabsorbing antigen (PA-Ag) - Streptococcus sp. (fragment)
 C;Species: Streptococcus sp.
 C;Date: 18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
 C;Accession: A46463
 R;Yoshizawa, N.; Oshima, S.; Sagel, I.; Shimizu, J.; Treser, G.
 J. Immunol. 148, 3110-3116, 1992
 A;Title: Role of a streptococcal antigen in the pathogenesis of acute poststreptococcal glomerulonephritis
 A;Reference number: A46463; MUID:92251171; PMID:1578137
 A;Accession: A46463
 A;Molecule type: protein
 A;Residues: 1-13 <YOS>
 A;Cross-references: PIDN:AAB22148.1; PID:9249161
 A;Note: sequence extracted from NCBI backbone (NCBIP:100561)

Query Match 23.8%; Score 19; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 EAYITPGAFD 13
 | : ||

Db 4 EAASAPGDD 13

RESULT 14

PS0453
36K protein 3124 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C;Accession: PS0453
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0453
A;Molecule type: protein
A;Residues: 1-13 <TSU>
A;Experimental source: leaf, chlorophyll, stem
A;Note: molecular weight 36k, pI 6.1

Query Match 23.8%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGAF 12
|||
Db 7 PGXF 10

RESULT 15

PQ0700
unidentified 6.3/40K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0700
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696
A;Accession: PQ0700
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <KOM>

Query Match 23.8%; Score 19; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GAFDV 14
|||
Db 7 GAIDI 11

Search completed: June 8, 2004, 19:15:03
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:07:39 ; Search time 12 Seconds
(without alignments)
60.749 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 673

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	35.0	10	GON1_CHEPR	P80677 chelyosoma
2	23	28.7	14	MCR2_METTM	P58816 methanobact
3	22	27.5	10	GON1_CLUPA	P81749 clupea pall
4	21	26.2	12	UP01_CABEL	P55954 caenorhabdi
5	21	26.2	13	E121_LITRU	P82097 litoria rub
6	20	25.0	10	GON1_ALLMI	P37041 alligator m
7	20	25.0	10	AUL1_LITRA	P82386 litoria ran
8	20	25.0	13	AUL2_LITRA	P82387 litoria ran
9	19	23.8	10	CATB_SHEEP	P83205 ovis aries
10	19	23.8	10	ESTA_SCHGA	P81012 schizaphis
11	19	23.8	13	UP71_LITRW	P82050 litoria ewi
12	18	22.5	8	AXH_TABAT	P14595 tabanus atr
13	18	22.5	8	PLP_BRANA	P81707 brassica na
14	18	22.5	10	GON2_CHEPR	P80678 chelyosoma
15	18	22.5	10	HTP_TABAT	P14596 tabanus atr
16	18	22.5	10	PKCK_FASHE	P80525 fasciola he
17	18	22.5	11	TKNA_SCYCA	P41333 scyllorhinu
18	18	22.5	13	E122_LITRU	P82098 litoria rub
19	18	22.5	14	ADFA_TENMO	P82965 tenebrio mo
20	17	21.2	11	MLG_THETS	P41989 theromyzon
21	17	21.2	11	TKN1_UPEIN	P82026 uperoleia i
22	17	21.2	11	TKN1_UPERU	P08612 uperoleia r
23	17	21.2	13	FIBB_RABIT	P14478 cryptolagus
24	17	21.2	13	U112_CLOPA	P81353 clostridium
25	17	21.2	14	IF2G_RAT	P81795 rattus norv
26	16	20.0	5	BPPT_BOTIN	P30425 bothrops in
27	16	20.0	7	ALL2_CARMA	P81805 carcinus ma
28	16	20.0	8	ACI_THUAL	P18691 thurnus alb
29	16	20.0	8	ANG2_BOTJA	Q10582 bothrops ja
30	16	20.0	9	NEF_HV1Z8	P12481 human immun
31	16	20.0	9	UHA2_HUMAN	P40929 homo sapien
32	16	20.0	14	ANGT_HORSE	P01016 equus cabal
33	15	18.8	4	RM01_YEAST	P36515 saccharomyc

34	15	18.8	8	1	ALL7_CARMA	P81809 carcinus ma
35	15	18.8	9	1	TKC1_CALVO	P41517 calliphora
36	15	18.8	9	1	UPA6_HUMAN	P30092 homo sapien
37	15	18.8	10	1	ANG1_BOTJA	Q10581 bothrops ja
38	15	18.8	10	1	ANGT_BOVIN	P01017 bos taurus
39	15	18.8	10	1	ANGT_CHICK	P01018 gallus gall
40	15	18.8	10	1	CAL2_LITCI	P82086 litoria cit
41	15	18.8	10	1	GON3_ONCKE	P20367 oncorhynch
42	15	18.8	10	1	GON3_PETMA	P20948 petromyzon
43	15	18.8	10	1	GONL_SQUAC	P27429 squalus aca
44	15	18.8	10	1	NO40_TOBAC	P55962 nicotiana t
45	15	18.8	10	1	RT02_BOVIN	P82923 bos taurus

ALIGNMENTS

RESULT 1
GON1_CHEPR
ID GON1_CHEPR STANDARD; PRT; 10 AA.
AC P80677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
DE (Luliberin I).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
RN [1]
RP SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
and the evolutionary implications."
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: GnRH neurons lie within blood sinuses close to
the gonopods and gonads in both juveniles and adults, implying
that the neuropeptide is released into the bloodstream.
CC -!- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A5A3 CRC64;

Query Match 35.0%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 WEAYITPG 10
Db 3 WSDYFKPG 10

RESULT 2
MCR2_METTM
ID MCR2_METTM STANDARD; PRT; 14 AA.
AC P58816;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
gamma) (Fragment).

GN MRTG.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 CC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91099370; PubMed=2269306;
 RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
 RT "Two genetically distinct methyl-coenzyme M reductases in
 MT Methanobacterium thermoautotrophicum strain Marburg and delta H.";
 RL Eur. J. Biochem. 194;871-877(1990).
 CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
 CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonyl phosphate
 CC to methane and an heterodisulfide.
 CC -!- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
 CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
 CC Coenzyme F430 is a yellow nickel porphyrinoid.
 CC -!- PATHWAY: Methanogenesis; last step.
 CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains
 CC -!- DEVELOPMENTAL STAGE: THESE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
 CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
 CC CONTAINS MOSTLY MCR I.
 DR PIR; E69017; E69017.
 KW Methanogenesis; Oxidoreductase; Multigene family.
 FT INIT MET 0 14
 FT NON TER 14 14
 FT SEQUENCE 14 AA; 1557 MW; 97B9439C4223B871 CRC64;
 SQ

Query Match 28.7%; Score 23; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITPG 10
 Db :|||
 2 YKAQYTPG 9

RESULT 3
 GON1_CLUPEA STANDARD; PRT; 10 AA.
 ID GON1_CLUPEA
 AC P81749;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH)
 DE (luliberin I).
 GN GNRH1.
 OS Clupea pallasii (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea
 OX NCBI_TaxID=30724;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 RT hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GNRH family.
 DR InterPro; IPR020212; GNRH.
 DR Pfam; PF00446; GNRH; 1.
 DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 1105 MW; 284B20B72871F5A3 CRC64;
 SQ

Query Match 27.5%; Score 22; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 8.3e+02;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 WEAYITPG 10
 Db :|||
 3 WSHGLSPG 10

RESULT 4

UP01_CABEL STANDARD; PRT; 12 AA.
 ID UP01_CABEL
 AC P55954;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Unknown protein from 2D-page (Spot 1) (Fragment).
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Bristol N2;
 RX MEDLINE=97295299; PubMed=9150941;
 RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
 RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
 RT homogenates and identification of protein spots by microsequencing.";
 RL Electrophoresis 18:557-562(1997).
 DR Siena-2DPAGE; P55954; -.
 FT NON TER 12 12
 FT SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;
 SQ

Query Match 26.2%; Score 21; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKWEA 5
 Db :|||
 8 EKWPA 12

RESULT 5

EI21_LITRU STANDARD; PRT; 13 AA.
 ID EI21_LITRU
 AC P82037;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Electrin 2.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 FT SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;
 SQ

Query Match 26.2%; Score 21; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RP SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=22394055; PubMed=12506352;
 RA El Amri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
 RA Moko H.B., Beckers J.-F.M.P.;
 RT "Isolation and partial characterization of three pregnancy-associated
 RT glycoproteins from the ewe placenta.";
 RL Mol. Reprod. Dev. 64:199-206(2003).
 CC -!- FUNCTION: Thiol protease which is believed to participate in
 CC intracellular degradation and turnover of proteins. Has also been
 CC implicated in tumor invasion and metastasis.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
 CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
 CC small molecule substrates (thus differing from cathepsin L). In
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase
 CC activity, liberating C-terminal dipeptides.
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
 CC by a disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 DR InterPro: IPR000169; SHprot.acsite.
 DR PROSITE; PS00640; THIOL_PROTEASE ASN; PARTIAL.
 DR PROSITE; PS00139; THIOL_PROTEASE CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL_PROTEASE HIS; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;
 Query Match 23.8%; Score 19; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 9 PGAFD 13
 Db 2 PDSFD 6
 RESULT 10
 ESTA_SCHGA STANDARD; PRT; 10 AA.
 ID _ESTA_SCHGA
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
 OX NCBI_TaxID=13262;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97468499; PubMed=9327586;
 RX Siegfried B.D., Ono M., Swanson J.J.;
 RA "Purification and characterization of a carboxylesterase associated
 RT with organophosphate resistance in the greenbug, Schizaphis graminum
 RT (Homoptera: Aphididae).";
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro: IPR002018; CarbesteraseB
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KW Hydrolase; Serine esterase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;
 Query Match 23.8%; Score 19; DB 1; Length 10;
 Best Local Similarity 44.4%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 AYTPGAFD 13
 Db 1 APIVSGGYD 9
 RESULT 11
 UP71_LITEW STANDARD; PRT; 13 AA.
 ID _UP71_LITEW
 AC P82050;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 7.1 (Contains: Uperin 7.1.1).
 OC Litoria ewingi (Brown tree frog) (Ewing's tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylcoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104896;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinbörner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "An unusual combination of peptides from the skin glands of Ewing's
 RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
 RT activity.";
 RL Aust. J. Chem. 50:889-894(1997).
 CC -!- FUNCTION: Uperin 7.1 shows antibacterial activity against L.lactis
 CC and S.uberis. Uperin 7.1.1 is inactive.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1427; METHOD=MS; RANGE=1-13.
 CC -!- MASS SPECTROMETRY: MW=1184; METHOD=MS; RANGE=3-13.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT PEPTIDE 1 13 UPERIN 7.1.
 FT PEPTIDE 3 13 UPERIN 7.1.1.
 FT MOD RES 13 13 AMIDATION
 SQ SEQUENCE 13 AA; 1429 MW; DE17C7204CCAE322 CRC64;
 Query Match 23.8%; Score 19; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GAFDV 14
 Db 1 GWFVDV 5
 RESULT 12
 AKH_TABAT STANDARD; PRT; 8 AA.
 ID _AKH_TABAT
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 OC Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel W.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora

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CC cardiaea after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
CC PIR; A33995; A33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 22.5%; Score 18; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TPG 10
DB 5 TPG 7

RESULT 13
PLP BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=CV, TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -1- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -1- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8 8
FT SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 22.5%; Score 18; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKW 3
DB 6 DEW 8

RESULT 14
GON2 CHEPR STANDARD; PRT; 10 AA.
AC P80678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
DE (Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
RN [1]

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RP SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.P., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.R., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC THE GONODUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC -1- MASS SPECTROMETRY: MW=1117.52; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 6 INTERCHAIN.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1135 MW; 284B38D1EBE735A3 CRC64;

Query Match 22.5%; Score 18; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 WEAVITPG 10
DB 3 WSLCHAPG 10

RESULT 15
HTF TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrihaloaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehaloaemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera)."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: Hypertrihaloaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 22.5%; Score 18; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TPG 10

|||

Db 5 TPG 7

Search completed: June 8, 2004, 19:13:37
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:08:15 ; Search time 39 seconds
(without alignments)
113.263 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3421

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	29	36.2	12	2	Q53183 rhodococcus
2	26	32.5	12	8	Q9GI96 sargassum p
3	23	28.7	13	5	Q9U5J3 trypanosoma
4	23	28.7	13	10	Q8LPV3 deschampsia
5	23	28.7	14	2	Q7X461 gamma-prote
6	22	27.5	8	8	Q94PX5 felis silve
7	22	27.5	8	8	Q94PX7 felis silve
8	22	27.5	8	8	Q94PX6 felis libyc
9	22	27.5	13	8	Q9MQX0 cervus elap
10	22	27.5	13	8	Q9MQK6 rupicapra r
11	22	27.5	13	8	Q9MQK3 capra ibex
12	22	27.5	14	6	Q77538 bos taurus
13	20	25.0	12	2	Q9S550 streptococ
14	20	25.0	13	5	Q9TWM3 locusta mig
15	20	25.0	14	11	Q9QVF3 rattus sp.
16	19	23.8	11	2	Q56972 yersinia pe

17	19	23.8	11	6	Q9TRR7
18	19	23.8	11	15	Q8ADI8
19	19	23.8	12	2	Q46012
20	19	23.8	12	6	Q8MJQ0
21	19	23.8	12	6	Q8MJP8
22	19	23.8	12	6	Q8MJP7
23	19	23.8	12	6	Q8MJP9
24	19	23.8	12	6	Q8MJE3
25	19	23.8	12	6	Q8MJQ1
26	19	23.8	12	6	Q8MJE2
27	19	23.8	12	6	Q8MJE4
28	19	23.8	12	12	Q7T862
29	19	23.8	12	15	Q8QDY5
30	19	23.8	12	15	Q8QE47
31	19	23.8	12	15	Q8QDY4
32	19	23.8	12	15	Q8QE41
33	19	23.8	12	15	Q8OE45
34	19	23.8	12	15	Q8QE43
35	19	23.8	12	15	Q8QDY6
36	19	23.8	13	2	Q9RSU4
37	19	23.8	14	6	Q8MIB1
38	18	22.5	9	5	Q9TVF1
39	18	22.5	9	8	Q9TLM7
40	18	22.5	12	10	Q9ZNT6
41	18	22.5	13	2	Q55234
42	18	22.5	13	8	Q8WEK0
43	18	22.5	13	8	Q9THR8
44	18	22.5	13	12	Q67604
45	18	22.5	13	12	Q9IBN1

ALIGNMENTS

RESULT 1

Q53183	PRELIMINARY;	PRT;	12 AA.
ID	Q53183		
AC	Q53183;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DB	Beta-subunit of nitrile hydratase (Fragment).		
OS	Rhodococcus sp.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Corynebacterineae; Nocardiaceae; Rhodococcus.		
OX	NCBI_TaxID=1831;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=N-774;		
RX	MEDLINE=95072315; PubMed=7765511;		
RA	Hashimoto Y., Nishiyama M., Horinouchi S., Beppu T.;		
RT	"The nitrile hydratase gene from Rhodococcus sp. N-774 requires its		
RT	downstream region for efficient expression."		
RL	Biosci. Biotechnol. Biochem. 58:1859-1865(1994).		
DR	EMBL; D30033; BAA06273.1; -		
DR	InterPro; IPR003168; NHase_beta.		
DR	Pfam; PF02211; NHase_beta; 1.		
FT	NON TER		
SQ	SEQUENCE 12 AA; 1323 MW; 7A5DEF7D993B587B CRC64;		

Query Match 36.2%; Score 29; DB 2; Length 12;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGA 11
| : | : | : |
Db 2 DLFFEGYLEPAA 12

RESULT 2

Q9GI96	PRELIMINARY;	PRT;	12 AA.
ID	Q9GI96		
AC	Q9GI96;		

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (fragment).
GN RBCS.
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=nep127;
RA Phillips N.E.;
RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (fucales, Phaeophyceae).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;

Query Match 32.5%; Score 26; DB 8; Length 12;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ITPGAF 12
Db 3 LTPGCF 8

RESULT 3
Q9U5J3 PRELIMINARY; PRT; 13 AA.
AC Q9U5J3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heat shock protein 100 (fragment).
GN HSP100.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILTaki;
RA Webb H.D.; Gaud A.F.; Carrington M.;
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally
RT related genes or to genes showing the same developmentally regulated
RT expression.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY250727; CAB60092.1; -.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1524 MW; 37C19EC3787FA728 CRC64;

Query Match 28.7%; Score 23; DB 5; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWE 4
Db 10 DEWE 13

RESULT 4
Q8LPV3 PRELIMINARY; PRT; 13 AA.
AC Q8LPV3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Arginine decarboxylase (fragment).
OS Deschampsia antarctica (Antarctic hairgrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Deschampsia.
OX NCBI_TaxID=159298;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RA Gidekel M.; Destefano-Beltran L.; Garcia P.; Fuentes L.; Alberdi M.;
RA Bravo L.; Corcuera L.; Gutierrez A.;
RT "Deschampsia antarctica a unique source of genes during cold
RT acclimation.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090543; AAM22750.1; -.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1613 MW; 704FE228645299CB CRC64;

Query Match 28.7%; Score 23; DB 10; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWE 4
Db 3 DEWE 6

RESULT 5
Q7X461 PRELIMINARY; PRT; 14 AA.
AC Q7X461;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pduc (fragment).
GN PDUC.
OS Gamma-proteobacterium Hot 75m4.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22670503; PubMed=12788698;
RA Knietzsch A.; Bowien S.; Whited G.; Gottschalk G.; Daniel R.;
RT "Identification and characterization of coenzyme B12-dependent
RT glycerol dehydratase- and diol dehydratase-encoding genes from
RT metagenomic DNA libraries derived from enrichment cultures.";
RL Appl. Environ. Microbiol. 69:3048-3060 (2003).
DR EMBL; AY205335; AAP48660.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1451 MW; CAA96165F9978A2D CRC64;

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGAFD 13
Db 5 PGALD 9

RESULT 6
Q94PX5 PRELIMINARY; PRT; 8 AA.
AC Q94PX5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN COII.
OS Felis silvestris (Wild cat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9683;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=66, 71, 75, 90, 1, and 2;
RA Randi E., Pierpaoli M., Beaumont M., Ragni B., Sforzi A.;
RT "Genetic identification of wild and domestic cats (Felis silvestris),
RT and their hybrids using Bayesian clustering methods.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ409136; CAC41051.1; -
DR EMBL; AJ409137; CAC41054.1; -
DR EMBL; AJ409138; CAC41057.1; -
DR EMBL; AJ409139; CAC41060.1; -
DR EMBL; AJ409141; CAC41066.1; -
DR EMBL; AJ409143; CAC41072.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 951 MW; 262685BDC5A3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKWEA 5
Db 1 EKWSA 5

RESULT 7
Q94PX7 PRELIMINARY; PRT; 8 AA.
ID Q94PX7
AC Q94PX7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN COII.
OS Felis silvestris catus (Cat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=1, 2, 7, 12, 16, 17, and 110;
RA Randi E., Pierpaoli M., Beaumont M., Ragni B., Sforzi A.;
RT "Genetic identification of wild and domestic cats (Felis silvestris),
RT and their hybrids using Bayesian clustering methods.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ409128; CAC41027.1; -
DR EMBL; AJ409129; CAC41030.1; -
DR EMBL; AJ409130; CAC41033.1; -
DR EMBL; AJ409131; CAC41036.1; -
DR EMBL; AJ409132; CAC41039.1; -
DR EMBL; AJ409133; CAC41042.1; -
DR EMBL; AJ409134; CAC41045.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 951 MW; 262685BDC5A3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKWEA 5

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Db 1 EKWSA 5

RESULT 8
Q94PX6 PRELIMINARY; PRT; 8 AA.
ID Q94PX6
AC Q94PX6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN COII.
OS Felis libyca.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=61377;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=40, 1, 2, and 7;
RA Randi E., Pierpaoli M., Beaumont M., Ragni B., Sforzi A.;
RT "Genetic identification of wild and domestic cats (Felis silvestris),
RT and their hybrids using Bayesian clustering methods.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ409135; CAC41048.1; -
DR EMBL; AJ409140; CAC41063.1; -
DR EMBL; AJ409142; CAC41069.1; -
DR EMBL; AJ409144; CAC41075.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 951 MW; 262685BDC5A3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKWEA 5
Db 1 EKWSA 5

RESULT 9
Q9MQKO PRELIMINARY; PRT; 13 AA.
ID Q9MQKO
AC Q9MQKO;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COII.
OS Cervus elaphus hippelaphus (European red deer).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=46360;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=20104876; PubMed=10641890;
RA Saulle E., Di Pasquale S., Tartaglia M.;
RT "Rapid communication: nucleotide sequence of chamois, alpine ibex, and
RT red deer tRNA(Lys) and ATPase8 mitochondrial genss.";
RL J. Anim. Sci. 77:3398-3399(1999).
DR EMBL; AF104683; AAF43483.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 13 AA; 1586 MW; 70B6A415FCB3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 13;

```

Best Local Similarity 60.0%; Pred. No. 5e+03; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative

QY 1 DKWEA 5
Db 6 EKWSA 10

RESULT 10

ID Q9MQK6 PRELIMINARY; PRT; 13 AA.
AC Q9MQK6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COII.
OS Rupicapra rupicapra (Chamois).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Rupicapra.
OX NCBI_TaxID=34869;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=20104876; PubMed=10641890;
RA Saulle E., Di Pasquale S., Tartaglia M.;
RT "Rapid communication: nucleotide sequence of chamois, alpine ibex, and
red deer tRNA(Iys) and ATPase8 mitochondrial genes.";
RL J. Anim. Sci. 77:3398-3399(1999).
DR EMBL; AF104681; AAF43477.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1574 MW; 6226A044FCB3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 13;
Best Local Similarity 60.0%; Pred. No. 5e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative

QY 1 DKWEA 5
Db 6 EKWSA 10

RESULT 11

ID Q9MQK3 PRELIMINARY; PRT; 13 AA.
AC Q9MQK3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COII.
OS Capra ibex ibex (Alpine ibex).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=80420;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=20104876; PubMed=10641890;
RA Saulle E., Di Pasquale S., Tartaglia M.;
RT "Rapid communication: nucleotide sequence of chamois, alpine ibex, and
red deer tRNA(Iys) and ATPase8 mitochondrial genes.";
RL J. Anim. Sci. 77:3398-3399(1999).
DR EMBL; AF104682; AAF43480.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1

SQ SEQUENCE 13 AA; 1574 MW; 70A3B544FCB3733B CRC64;

Query Match 27.5%; Score 22; DB 8; Length 13;
Best Local Similarity 60.0%; Pred. No. 5e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative

QY 1 DKWEA 5
Db 6 EKWSA 10

RESULT 12

ID O77538 PRELIMINARY; PRT; 14 AA.
AC O77538; Q9TQV9;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
receptor mRNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRED HOLSTEIN;
RX MEDLINE=99175163; PubMed=10075683;
RA Jiang H., Okamura C.S., Lucy M.C.;
RT "Isolation and characterization of a novel promoter for the bovine
growth hormone receptor gene.";
RL J. Biol. Chem. 274:7893-7900(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
receptor mRNA.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Bovine GH receptor 5' UTR variants.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036297; AAC33315.2; -;
DR EMBL; AF085281; AAD22521.1; -;
DR EMBL; AF036290; AAC33308.1; -;
DR EMBL; AF036291; AAC33309.1; -;
DR EMBL; AF036292; AAC33310.1; -;
DR EMBL; AF036293; AAC33311.1; -;
DR EMBL; AF036294; AAC33312.1; -;
DR EMBL; AF036295; AAC33313.1; -;
DR EMBL; AF036296; AAC33314.1; -;
DR EMBL; AF326349; AAK97345.1; -;
DR GO; GO:0004872; P:receptor activity; IEA.
KW Receptor.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 5A45D458FF3A9E27 CRC64;

Query Match 27.5%; Score 22; DB 6; Length 14;
Best Local Similarity 37.5%; Pred. No. 5.4e+03; 2; Mismatches 3; Indels 0; Gaps 0;
Matches 3; Conservative

QY 1 DKWEAYIT 8
Db 2 DLWQLLLT 9


```
RESULT 13
Q9S550 PRELIMINARY; PRT; 12 AA.
AC Q9S550;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE DEXB (Fragment).
GN DEXB.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RX MEDLINE=9214122; PubMed=10198036;
RA Iannelli F., Pearce B.J., Porzi G.;
RT "The type 2 capsule locus of Streptococcus pneumoniae.";
RL J. Bacteriol. 181:2652-2654(1999).
DR EMBL; AF026471; AAD10169.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 25.0%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WEAY 6
Db 4 WDAF 7

RESULT 14
Q9TWM3 PRELIMINARY; PRT; 13 AA.
AC Q9TWM3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE LOCUSTAMYOINHIBIN, LOM-MIH=MYOINHIBITING neuropeptide.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=95063174; PubMed=7972937;
RA Schoofs L., Veelaert D., Holman G.M., Hayes T.K., De Loof A.;
RT "Partial identification, synthesis and immunolocalization of
RT locustamyoinhibin, the third myoinhibiting neuropeptide isolated from
RT Locusta migratoria.";
RL Regul. Pept. 52:139-156(1994).
SQ SEQUENCE 13 AA; 1464 MW; D84ABBB624DCC5A6 CRC64;

Query Match 25.0%; Score 20; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 EAYITPGAFD 13
Db 1 EXYXKQSAFN 10

RESULT 15
Q9QVF3 PRELIMINARY; PRT; 14 AA.
AC Q9QVF3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
```

```
DE TRANSFERRIN=PEPTIDE 35 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1499 MW; 01AE8289554E1224 CRC64;

Query Match 25.0%; Score 20; DB 11; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AYITP 9
Db 1 AYLAP 5

Search completed: June 8, 2004, 19:14:31
Job time : 42 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:07:09 ; Search time 52 Seconds
(without alignments)
76.070 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80
Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 401842

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	14	AAB61295	Aab61295 Anti-TANG
2	80	100.0	14	ABU11261	Abu11261 Human TAN
3	34	42.5	14	ABP47117	Abp47117 Human Bly
4	32	40.0	10	ADA88938	Ada88938 Murrel go
5	31	38.8	10	AAP50175	Aap50175 Gonadotro
6	31	38.8	10	AAU98286	AAu98286 M. tuberc
7	31	38.8	10	AAE23875	Aae23875 Gonadotro
8	31	38.8	14	AAW16713	Aaw16713 p185 bind
9	31	38.8	14	AAW16776	Aaw16776 p185 bind
10	31	38.8	14	AAQ98155	Aaq98155 Human SNP
11	30	37.5	10	AAW16102	Aaw16102 Peptide c
12	30	37.5	10	AAW68740	Aaw68740 Peptide b
13	30	37.5	10	AAW58219	Aaw58219 IL-1RL1 b
14	30	37.5	10	AAW09869	Aay09869 Interleuk
15	30	37.5	10	AAW17654	Aab17654 IL-1 anta
16	30	37.5	10	ABB72550	Abb72550 Interleuk
17	30	37.5	10	ABP47106	Abp47106 Human Bly
18	30	37.5	11	AAW17829	Aaw17829 Nitrite h
19	30	37.5	12	AAW88110	Aay88110 Fluoresce
20	30	37.5	12	AAW88162	Aay88162 Fluoresce
21	30	37.5	14	AAW16774	Aaw16774 p185 bind
22	30	37.5	14	AAW16711	Aaw16711 p185 bind
23	29	36.2	9	AAU94632	AAu94632 Human nov
24	29	36.2	9	AAU94454	AAu94454 Human nov
25	29	36.2	9	AAU94025	AAu94025 Human nov

26	29	36.2	10	5	ABB06179	Abb06179 Gonadotro
27	29	36.2	10	5	AAU94518	Aau94518 Human nov
28	29	36.2	10	5	AAU94729	Aau94729 Human nov
29	29	36.2	10	6	ADA88932	Ada88932 Tunicate
30	29	36.2	10	6	AAO31046	Aao31046 Tunicate
31	29	36.2	11	4	AAU02728	Aau02728 CDR regio
32	29	36.2	11	6	AAE32290	Aae32290 Arabidops
33	29	36.2	12	2	AAW11838	Aaw11838 Peptide s
34	29	36.2	12	7	ABR81735	Abr81735 Antimicro
35	29	36.2	13	5	AAU98162	Aau98162 Prostate
36	29	36.2	13	5	ABB97660	Abb97660 Human pro
37	29	36.2	13	5	ABB97658	Abb97658 Human pro
38	29	36.2	13	5	ABB97662	Abb97662 Human pro
39	28.5	35.6	10	5	ABP47167	Abp47167 Human Bly
40	28	35.0	7	3	AAW29404	Aaw29404 HIV-1 env
41	28	35.0	9	5	ABG67546	Abg67546 Human ADP
42	28	35.0	9	6	ADA23661	Ada23661 Alzheimer
43	28	35.0	10	6	ABJ57741	Abj57741 184P1E2-x
44	28	35.0	10	6	ABJ66086	Abj66086 184P1E2-x
45	28	35.0	10	6	ABJ67947	Abj67947 184P1E2-x

ALIGNMENTS

RESULT 1
AAB61295
ID AAB61295 standard; peptide; 14 AA.
XX
AC AAB61295;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 63.
XX

Human; antibody; scFv; CDR; complementarity determining region;
TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
platelet membrane glycoprotein receptor; bleeding disorder;
blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
ischaemia; cardiovascular disease; immunological disease; liver disorder;
cancer.

XX Homo sapiens.

XX OS

XX WC0200100810-A1.

XX PD 04-JAN-2001.

XX PF 30-JUN-2000; 2000WO-US018152.

XX PR 30-JUN-1999; 99US-00345468.

XX PR 06-DEC-1999; 99US-00454824.

XX PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelail J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian MD, Kingsbury G;

XX WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor,
glycoprotein VI, and its modulators, useful for preventing, treating and
diagnosing hemorrhagic disorders, thrombotic diseases and immunological
disorders.

XX Claim 31; Page 102; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
nucleic acid molecule encoding a platelet membrane glycoprotein receptor
glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 XX Sequence 14 AA;

Query Match 100.0%; Score 80; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGADV 14
 |||||
 Db 1 DKWEAYITPGADV 14

RESULT 2

ID ABU11261 standard; peptide; 14 AA.

XX AC ABU11261;

XX 06-FEB-2003 (first entry)

XX Human TANGO 268 VHCDR3 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary stenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

OS WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 8; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 XX heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 XX or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 XX binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 XX The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 XX Sequence 14 AA;

Query Match 100.0%; Score 80; DB 6; Length 14;

Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGADV 14
 |||||
 Db 1 DKWEAYITPGADV 14

RESULT 3

ABP47117

ID ABP47117 standard; peptide; 14 AA.

XX AC ABP47117;

XX 19-AUG-2002 (first entry)

XX Human BlyS binding scFv VH CDR3 SEQ ID 3128.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; anti-rheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 diagnosis and treatment of cancers and immune disorders.

PS Claim 2; Page 3120; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 14 AA;

Query Match 42.5%; Score 34; DB 5; Length 14;
 Best Local Similarity 38.5%; Pred. No. 64;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 KWEAYITPGAFDV 14

DB :||| : |||:

2 EWEDIVVGSADF 14

RESULT 4

ADA88938

ID ADA88938 standard; peptide; 10 AA.

XX AC ADA88938;

XX DT 20-NOV-2003 (first entry)

XX DE Murrel gonadotropin releasing hormone.

XX KW gonadotropin releasing hormone; GnRH; muGnRH I; muGnRH II; Indian Murrel;
 fish; fish breeding; gonadotropin.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "pyroglutamic acid"

FT Modified-site 10 /note= "amidated"

FT WO2003064460-A2.

XX PD 07-AUG-2003.

XX PF 10-JAN-2003; 2003WO-IN000015.

XX PR 30-JAN-2002; 2002US-0353041P.

XX PA (COUL) COUNCIL SCI & IND RES.

XX PI Chatterjee A, Ray P, Dasgupta S, Bhattacharaya S, Pasha S;

XX DR WPI; 2003-663464/62.

XX PT New gonadotropin releasing hormones muGnRH I and muGnRH II useful for
 induced breeding in fishes.
 XX PS Disclosure; Fig 7; 23pp; English.

XX The present invention describes gonadotropin releasing hormones (GnRH)
 CC muGnRH I (ADA88923) and muGnRH II (ADA88924), isolated from Indian Murrel
 CC fish. They can be used for inducing breeding in fishes both in
 CC combination and alone by activating production of gonadotropin. The GnRH
 CC peptide muGnRH I and muGnRH II have the amino acid sequences Gln-His-Trp-
 CC Ser-Ala-Trp-Arg-Leu-Pro-Gly (I) and Gln-His-Trp-Ser-Trp-Gly-Ile-Leu-Pro-
 CC Gly (II), respectively. Also described: (1) isolating and sequencing
 CC muGnRH I and muGnRH II; and (2) inducing breeding in fishes using GnRH
 CC comprising exposing fishes to GnRH to help release gonadotropin, and
 CC inducing breeding in fishes using the gonadotropin. The present sequence
 CC represents a GnRH amino acid sequence given in the exemplification of the
 CC present invention.

XX SQ Sequence 10 AA;

Query Match 40.0%; Score 32; DB 6; Length 10;

Best Local Similarity 50.0%; Pred. No. 98;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPG 10

DB : ||| |||

1 EHWSAYRLPG 10

RESULT 5

AAP50175

ID AAP50175 standard; protein; 10 AA.

XX AC AAP50175;

XX DT 25-MAR-2003 (revised)

XX DT 20-JAN-1992 (first entry)

XX DE Gonadotropin release hormone antagonist peptide.

XX KW GnRH; gonadotrophins; steroids; contraceptive.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT Modified-site 2 /note= "Beta-D-2NAL"

FT Modified-site 2 /label= OTHER

FT Modified-site 3 /note= "C-alpha-Me-Cl-D-Phe"

FT Modified-site 6 /label= D-Trp

FT Modified-site 6 /label= D-Tyr

XX PN EPI43573-A.

XX PD 05-JUN-1985.

XX PF 05-NOV-1984; 84EP-00307625.

XX PR 29-NOV-1983; 83US-00556148.

XX PR 30-AUG-1985; 85US-00771517.

XX PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX PI Roeske RW, Rivier JE, Vale WW;

XX DR WPI; 1985-136434/23.

XX PT New GnRH antagonist peptide(s) - useful as inhibitors of gonadotropin(s)
 and/or steroid(s) for contraceptive use.
 XX PS Example; Page 8; 20pp; English.

XX CC The claimed peptides inhibit the release of gonadotrophins and/or

CC steroids. They are antagonistic to GnRH, inhibit ovulation, and may cause
 CC resorption of a fertilised egg if administered shortly after absorption.
 CC The peptides also have utility in male contraception, and in treatment of
 CC precocious puberty, hormone dependent neoplasia, dysmenorrhoea and
 CC endometriosis. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 10 AA;

Query Match 38.8%; Score 31; DB 1; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 WRAYITPP 10
 | | : |
 Db 3 WSYLPPG 10

RESULT 6
 AAU98286
 ID AAU98286 standard; peptide; 10 AA.

XX AAU98286;

DT 15-AUG-2002 (first entry)

XX M. tuberculosis Ag85 derived immunodominant T cell epitope #13.

XX Ag85; epitope; vaccine; tuberculosis; mycolyltransferase; HLA-A*02001;
 KW Mycobacterium tuberculosis; Mycobacterium leprae; Mycobacterium bovis;
 *KW Mycobacterium ulcerans; Mycobacterium avium; antibacterial;
 KW MHC class I-restricted CD8⁺ T cell; human leukocyte antigen.
 XX

OS Mycobacterium tuberculosis.

XX Key Location/Qualifiers
 FH Region 2
 FT /note= "Amino acid contributing to the HLA-A*02001
 binding motif"
 FT Region 5
 FT /note= "Amino acid contributing to the HLA-A*02001
 binding motif"
 FT Region 7
 FT /note= "Amino acid contributing to the HLA-A*02001
 binding motif"
 FT Region 10
 FT /note= "Amino acid contributing to the HLA-A*02001
 binding motif"

XX EP1211260-A1.

PN 05-JUN-2002.

XX 30-NOV-2000; 2000EP-00204268.

XX 30-NOV-2000; 2000EP-00204268.

XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX Ottenhof THM, Geluk A;

XX WPI; 2002-464923/50.

XX Peptide of 8-11 amino acids derived from the Ag85 protein of
 PT mycobacterium induce proliferation of MHC class I-restricted CD8⁺ T cells
 PT and are useful to vaccinate against infection by mycobacterium.
 XX

XX Claim 1; Page 7; 20pp; English.

XX The invention relates to peptide (P1) derived from an Ag85 protein of
 CC mycobacterium (which is associated with mycolyltransferase activity and
 CC is involved in cell wall synthesis), comprising 8-11 amino acids, and
 CC capable of inducing proliferation of MHC class I-restricted CD8⁺ T cells
 CC in vivo. Also included are (i) a peptide comprising P1 flanked by amino

CC acids representing antigen processing sites; (2) a polypeptide comprising
 CC at least two of the peptides in (1); (3) a nucleic acid encoding one of
 CC the claimed peptides or polypeptides; (4) a vector comprising the above
 CC nucleic acid; (5) a host cell comprising the above nucleic acid or vector
 CC ; and (6) detecting and/or enumerating CD8⁺ T cells against
 CC mycobacterium, comprising tetrameric complexes of MHC (major
 CC histocompatibility group) class I and one of the claimed peptides or
 CC polypeptides. The molecules of the invention are used to prepare a
 CC vaccine against mycobacterium (e.g. Mycobacterium tuberculosis,
 CC Mycobacterium leprae, Mycobacterium bovis, Mycobacterium ulcerans,
 CC Mycobacterium avium) and thus protect against diseases such as
 CC tuberculosis. The present sequence is an M. tuberculosis Ag85 derived
 CC immunogenic peptide of the invention binding to HLA-A*02001 (human
 CC leukocyte antigen)
 XX

SQ Sequence 10 AA;

Query Match 38.8%; Score 31; DB 5; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.5e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KWEAYIT 8

Db 4 KWETFLT 10

RESULT 7

AAE29875

ID AAE29875 standard; peptide; 10 AA.

XX AAE29875;

XX 24-FEB-2003 (first entry)

DE Gonadotrophin releasing hormone analogue (GnRH-A) #38.

XX Gonadotrophin releasing hormone analogue; neurotoxin; prostate cancer;
 KW endocrine disorder; gonadotrophin related illness; endometrial cancer;
 KW pancreatic cancer; breast cancer; endometriosis; precocious puberty;
 KW GnRH-A; therapy.
 XX

OS Unidentified.

XX Key Location/Qualifiers

FH Modified-site 1 /note= "Pyroglutamic acid"

FT Misc-difference 6 /note= "D-form residue"

FT Modified-site 10 /note= "C-terminal amide"

XX WO200274327-A2.

XX 26-SEP-2002.

XX 11-MAR-2002; 2002WO-US007379.

XX 15-MAR-2001; 2001US-00810601.

XX (ALLR) ALLERGAN SALES INC.

XX Donovan S;

XX WPI; 2003-018772/01.

XX New agent comprising a light chain and a (modified) heavy chain of a
 PT botulinum, butyricum, or tetani toxin, useful for treating a
 PT gonadotrophin related illness, e.g. breast, prostate pancreatic or
 PT endometrial cancer, or endometriosis.
 XX

PS Disclosure; Page 30; 97pp; English.

XX The invention relates to an agent comprising a neurotoxin preferably

CC botulinum toxin for treating endocrine disorders for e.g. gonadotrophin
 CC related illness. The agent is useful for treating gonadotrophin related
 CC illness e.g. prostate cancer, endometrial cancer, pancreatic cancer,
 CC breast cancer, endometriosis or precocious puberty. It is also useful for
 CC decreasing gonadotrophin secretion in a mammal. The present sequence is
 CC gonadotrophin releasing hormone analogue (GnRH-A)
 XX

SQ Sequence 10 AA;

Query Match 38.8%; Score 31; DB 6; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPG 10
 : ||| :
 Db 1 EHWSYLRPG 10

RESULT 8

AAW16713
 ID AAW16713 standard; peptide; 14 AA.

AC AAW16713;

DT 23-JUL-1997 (first entry)

XX p185 binding and erbB-2 receptor modulating peptide.

XX Modulation; erbB-2; receptor; binding; p185; prevention; transformation;
 KW normal; tumour; cell; human; breast; ovary; lung; pancreas;
 KW salivary gland; kidney; adenocarcinoma; prostate; cancer; neuroblastoma;
 KW detection; treatment.

XX Synthetic.

XX WO9634617-A1.

XX 07-NOV-1996.

XX 03-MAY-1996; 96WO-US006270.

XX 03-MAY-1995; 95US-00433318.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Greene MI, Zhang X;

XX WPI; 1996-505894/50.

XX New p185-binding peptide(s) - used for the detection, treatment or
 PT prophylaxis of erbB-2-associated tumours.

XX Claim 13; Page 53; 73pp; English.

XX The present peptide, which modulates erbB-2 receptors by binding p185,
 CC can be used to prevent the transformation of normal cells into tumour
 CC cells in individuals at risk of developing p185 associated tumours, e.g.
 CC human breast, ovary, lung, pancreas, salivary gland and kidney
 CC adenocarcinomas and prostate neuroblastoma. It can also be used to detect
 CC and treat p185 associated tumours, and is given in a dose of, e.g. 0.001-
 CC 1 g, preferably 1-10 mg/kg/day by, e.g. parenteral or oral routes
 XX

SQ Sequence 14 AA;

Query Match 38.8%; Score 31; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
 : ||| :
 Db 3 DQEWYCYP 11

RESULT 9

AAW16776

ID AAW16776 standard; peptide; 14 AA.

AC AAW16776;

DT 23-JUL-1997 (first entry)

XX p185 binding and erbB-2 receptor modulating peptide.

XX Modulation; erbB-2; receptor; binding; p185; prevention; transformation;
 KW normal; tumour; cell; human; breast; ovary; lung; pancreas;
 KW salivary gland; kidney; adenocarcinoma; prostate; cancer; neuroblastoma;
 KW detection; treatment.

XX Synthetic.

XX WO9634617-A1.

XX 07-NOV-1996.

XX 03-MAY-1996; 96WO-US006270.

XX 03-MAY-1995; 95US-00433318.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Greene MI, Zhang X;

XX WPI; 1996-505894/50.

XX New p185-binding peptide(s) - used for the detection, treatment or
 PT prophylaxis of erbB-2-associated tumours.

XX Claim 13; Page 64; 73pp; English.

XX The present peptide, which modulates erbB-2 receptors by binding p185,
 CC can be used to prevent the transformation of normal cells into tumour
 CC cells in individuals at risk of developing p185 associated tumours, e.g.
 CC human breast, ovary, lung, pancreas, salivary gland and kidney
 CC adenocarcinomas and prostate neuroblastoma. It can also be used to detect
 CC and treat p185 associated tumours, and is given in a dose of, e.g. 0.001-
 CC 1 g, preferably 1-10 mg/kg/day by, e.g. parenteral or oral routes
 XX

SQ Sequence 14 AA;

Query Match 38.8%; Score 31; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
 : ||| :
 Db 3 DQEWYCYP 11

RESULT 10

AAG98155

ID AAG98155 standard; peptide; 14 AA.

AC AAG98155;

DT 19-SEP-2001 (first entry)

XX Human SNP associated peptide SEQ ID NO. 797.

XX Human; single nucleotide polymorphism; SNP; angiotensin;
 KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
 KW adenosine triphosphate-dependent RNA helicase;
 KW major histocompatibility complex Class I histocompatibility antigen; MHC;
 KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
 KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
 KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.

XX

OS Homo sapiens.
 XX WO200148245-A2.
 XX
 XX
 PD 05-JUL-2001.
 XX
 XX 27-DEC-2000; 2000WO-US035346.
 XX
 XX 27-DEC-1999; 99US-00472688.
 PR
 PA (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 PI
 XX
 XX
 DR WPI; 2001-418297/44.
 XX
 XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
 PT diseases and infections.
 XX
 XX Disclosure; Page 466; 484pp; English.
 XX
 CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
 CC polymorphic variants of proteins (AAG98010-AAG98238) related to
 CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
 CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
 CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
 CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
 CC proteins have potential immunosuppressive, immunostimulatory,
 CC antitumoric, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
 CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
 CC nervous system, an infection of pathogenic organisms. They may also be
 CC used to alter phenotypic traits such as longevity, appearance, strength,
 CC speed and endurance
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 38.8%; Score 31; DB 4; Length 14;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 YITPGAP 12
 |||||
 DB 5 YITPEAF 11
 RESULT 11
 AAH16102
 ID AAW16102 standard; peptide; 10 AA.
 XX
 XX AAW16102;
 AC
 XX
 DT 19-AUG-1997 (first entry)
 XX
 DE Peptide containing QPY or QPY-like motif.
 XX
 XX Interleukin-1; type I receptor; IL-1rI; agonist; antagonist.
 KW
 XX Synthetic.
 OS
 XX WO9639165-A1.
 PN
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US009835.
 XX
 PR 05-JUN-1995; 95US-00464538.
 XX
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 XX Barrett RW, Yanofsky SD, Baldwin D, Jacobs JW, Bovy PR, Leahy EM;
 PI Pottorf RS, Dharanipragada R, Tomlinson RC;
 XX
 XX WPI; 1997-042846/04.
 DR
 XX
 XX Interleukin-1 type I receptor inhibitor peptide(s) and compounds - used
 PT to antagonise the activity of IL-1, for treatment of e.g. AIDS,
 PT rheumatoid arthritis, chronic hepatitis B, etc.
 XX
 XX Disclosure; Page 25; 74pp; English.
 XX
 CC The invention relates to peptides which bind to the IL-1 type I receptor
 CC and which comprise the motif WXXYG-ZI-W or the motif XXQ-Z5-Y-Z6-XX, in
 CC which X can be any one of the 20 genetically coded L-amino acids or the
 CC stereoisomeric D-amino acids or unnatural amino acids; Z1 is L, I, A or Q
 CC ; Z5 is P or azetidine (presumably intended to be azetidine carboxylic
 CC acid); and Z6 is S, A, V or L. The present sequence is that of a random
 CC peptide from a library of peptides containing the "XXQ-Z5-Y-Z6-XX" motif,
 CC the library being constructed to screen the peptides for activity. IL-1
 CC type I receptor-binding peptides may be useful in the treatment of a
 CC variety of IL-1 related disorders including atherosclerosis, rheumatoid
 CC arthritis, osteoporosis, HIV infection and AIDS, bacterial infection,
 CC respiratory distress syndrome, acute myelogenous leukaemia, graft versus
 CC host disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
 CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B, tuberculosis,
 CC obstructive jaundice, Paget's disease and osteomalacia, IDDM, Kawasaki's
 CC disease, inflammatory bowel disease, sepsis, toxic shock and luteal phase
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 37.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 WEAYITP 9
 |||||
 DB 3 WQPYATP 9
 RESULT 12
 AAW68740
 ID AAW68740 standard; peptide; 10 AA.
 XX
 XX AAW68740;
 AC
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Peptide binding interleukin-1 type I receptor.
 XX
 XX Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1rI;
 KW treatment; IL-1 disorder.
 XX
 XX Synthetic.
 OS
 XX US5786331-A.
 PN
 XX 28-JUL-1998.
 PD
 XX
 XX 05-JUN-1995; 95US-00465391.
 PF
 XX 02-FEB-1994; 94US-00190788.
 PR
 PR 01-FEB-1995; 95US-00383474.
 XX
 XX (HMRI) HOECHST MARION ROUSSEL INC.
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PI Yanofsky SD, Jacobs JW, Bovy PR, Leahy EM, Barrett RW;
 XX PI Pottorf RS, Baldwin D;
 XX XX
 XX DR WPI; 1998-436582/37.
 XX PT Antagonisation of action of interleukin-1 on type I receptor - by
 XX PT contacting receptor with selected peptides.
 XX XX
 XX PS Disclosure; Col 14; 118pp; English.
 XX CC AAW68739-44 represent peptide sequences, identified from a peptide
 XX CC library based on the peptide AAW68906. The peptides antagonise the action
 XX CC of interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1RTI).
 XX CC The peptides are used in the treatment of disorders mediated by IL-1,
 XX CC e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
 XX CC infections, respiratory distress syndrome, acute myelogenous leukaemia,
 XX CC graft-versus-host disease, pneumoconiosis, cirrhosis, cuprophane
 XX CC haemodialysis, cardiopulmonary bypass, hepatitis B, thermal injury,
 XX CC reticulohistocytosis, sarcoidosis, tuberculosis, obstructive jaundice,
 XX CC Paget's disease, osteomalacia, diabetes, Kawasaki's disease, inflammatory
 XX CC bowel disease, sepsis, toxic shock and luteal phase
 XX XX
 XX SQ Sequence 10 AA;
 Query Match 37.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 WEAYITP 9
 Db | : | | |
 3 WQPYATP 9
 RESULT 13
 AAW58219
 ID AAW58219 standard; peptide; 10 AA.
 XX AC AAW58219;
 XX XX
 XX DT 14-AUG-1998 (first entry)
 XX DE IL-1RTI binding peptide SEQ ID NO:145 based in SEQ ID NO:259.
 XX XX
 XX KW Interleukin-1 type I receptor; binding peptide; IL-1R; IL-1RTI;
 XX KW competitive inhibition; cytokine; blocker; IL-1 related disorder;
 XX KW diagnosis; atherosclerosis; rheumatoid arthritis; osteoporosis.
 XX XX
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX XX
 XX PN US5767234-A.
 XX XX
 XX PD 16-JUN-1998.
 XX XX
 XX PF 01-FEB-1995; 95US-00383474.
 XX XX
 XX PR 02-FEB-1994; 94US-00190788.
 XX XX
 XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX XX
 XX PI Baldwin D, Jacobs JW, Yanofsky SD, Barrett RW;
 XX XX
 XX DR WPI; 1998-361782/31.
 XX XX
 XX PT Peptide(s) that bind to interleukin-1 type I receptor - useful in
 XX PT screening assays for interleukin receptors blockers, diagnosis and
 XX PT therapy.
 XX XX
 XX PS Disclosure; Col 13; 89pp; English.
 XX XX
 XX CC A compound has been developed that binds to an interleukin-1 (IL-1) type
 XX CC I receptor with an IC50 of 2.5 mM or less and has a molecular weight of

CC <3 kD, where the binding of the compound to the receptor is competitively
 CC inhibited by a peptide of 8-25 amino acids comprising the core sequence:
 CC Z7-Z8-Q-Z5-Y-Z6-Z9-Z10, where Z5 = Pro or azetidine; Z6 = Ser, Ala, Val
 CC or Leu; Z7 = Tyr, Trp or Phe; Z8 = Glu, Phe, Val, Trp or Tyr; Z9 = Met,
 CC Phe, Val, Arg, Gln, Lys, Thr, Ser, Asp, Leu, Ile or Glu; and Z10 = Glu,
 CC Leu, Trp, Val, His, Ile, Gly, Ala, Asp, Tyr, Asn, Gln or Pro. Peptides of
 CC the invention are used in screening assays for IL-1 receptor blockers.
 CC They are also used as probes for detecting IL-1 type I receptor
 CC expression on the surface of cells. The peptides are useful in treating
 CC IL-1-related disorders, e.g. atherosclerosis, rheumatoid arthritis,
 CC osteoporosis, HIV infection, AIDS, bacterial infection, respiratory
 CC distress syndrome, acute myelogenous leukaemia (AML), graft versus host
 CC disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
 CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B, thermal
 CC injury, reticulohistocytosis, sarcoidosis, tuberculosis, obstructive
 CC jaundice, Paget's disease and osteomalacia, Kawasaki's disease,
 CC inflammatory bowel disease, sepsis, toxic shock, and luteal phase. The
 CC present sequence represents a peptide from the present invention
 XX XX
 XX SQ Sequence 10 AA;
 Query Match 37.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 WEAYITP 9
 Db | : | | |
 3 WQPYATP 9
 RESULT 14
 AAY09869
 ID AAY09869 standard; peptide; 10 AA.
 XX AC AAY09869;
 XX XX
 XX DT 07-MAY-1999 (first entry)
 XX DE Interleukin-1 type I receptor binding peptide #190.
 XX XX
 XX KW Interleukin-1 type I receptor; IL-1RTI; inflammatory bowel disease;
 XX KW rheumatoid arthritis; osteoarthritis; psoriasis; encephalitis;
 XX KW glomerulonephritis; respiratory distress syndrome.
 XX XX
 XX OS Synthetic.
 XX XX
 XX PN US5880096-A.
 XX XX
 XX PD 09-MAR-1999.
 XX XX
 XX PF 05-JUN-1995; 95US-00463076.
 XX XX
 XX PR 02-FEB-1994; 94US-00190788.
 XX PR 01-FEB-1995; 95US-00383474.
 XX XX
 XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX XX
 XX PI Yanofsky SD, Barrett RW;
 XX XX
 XX DR WPI; 1999-204004/17.
 XX XX
 XX PT New peptides which bind to the interleukin-1 type I receptor (IL-1RTI) -
 XX PT useful for the study of IL-1RTI mediated activities and the
 XX PT treatment/prevention of diseases with an inappropriate production or
 XX PT response to interleukin-1.
 XX XX
 XX PS Disclosure; Col 14; 120pp; English.
 XX XX
 XX CC The invention relates to new peptides which bind to the interleukin
 XX CC -1 type I receptor (IL-1RTI). These include 'lead' peptides identified
 XX CC using random peptide diversity generating systems (e.g. 'peptides on
 XX CC phage' and 'peptides on plasmids' systems) and derivatives of the 'lead'
 XX CC peptides which have a similar structure or shape as the lead compounds

CC but which differ with respect to susceptibility to hydrolysis or
 CC proteolysis and/or with respect to biological properties. These peptides
 CC are useful as agonists/antagonists for the study of IL-1RII mediated
 CC activities (e.g. as labels and probes), for the identification of new IL-
 CC 1 receptor blockers, and for the identification, diagnosis and
 CC treatment/prevention of diseases with an inappropriate production or
 CC response to IL-1, e.g. rheumatoid arthritis, osteoarthritis, psoriasis,
 CC inflammatory bowel disease, encephalitis, glomerulonephritis, and
 CC respiratory distress syndrome
 XX
 SQ Sequence 10 AA;

Query Match 37.5%; Score 30; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
 | : | | |
 Db 3 WQFYATP 9

RESULT 15

AAB17654
 ID AAB17654 standard; peptide; 10 AA.

XX
 AC AAB17654;

DT 31-OCT-2000 (first entry)

XX DE IL-1 antagonist peptide sequence SEQ ID NO:758.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

XX PD 04-MAY-2000.

XX PF 25-OCT-1999; 99WO-US025044.

XX PR 23-OCT-1998; 98US-0105371P.

XX PR 22-OCT-1999; 99US-00428082.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 10; Page 457; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,

CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 10 AA;

Query Match 37.5%; Score 30; DB 3; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WEAYITP 9
 | : | | |
 Db 3 WQFYATP 9

Search completed: June 8, 2004, 19:13:14
 Job time : 54 secs


```
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-16
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Query Match 71.9%; Score 64; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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QY 2 IKODGSEKYYADSVRG 17
| ||| |||||:|
Db 2 ISYDGSNKYYADSVKG 17
```

```
RESULT 3
US-09-383-667-18
; Sequence 18, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-18
```

```
Query Match 71.9%; Score 64; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 2 IKODGSEKYYADSVRG 17
| ||| |||||:|
Db 2 ISYDGSNKYYADSVKG 17
```

```
RESULT 4
US-09-560-198A-12
; Sequence 12, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peta SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
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; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-198A-12
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Query Match 68.5%; Score 61; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00036;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 2 IKODGSEKYYADSVRG 17
| ||| |||||:|
Db 2 ISYDGSIKYYADSVKG 17
```

```
RESULT 5
US-09-383-667-20
; Sequence 20, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-20
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Query Match 66.3%; Score 59; DB 4; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0008;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 2 IKODGSEKYYADSVR 16
| ||| |||||:|
Db 2 ISYDGSKYYADSVK 16
```

```
RESULT 6
US-09-383-667-22
; Sequence 22, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
```

EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 22
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-22

Query Match 62.9%; Score 56; DB 4; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0026;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IKODGSEKYYADSVRG 17
| : : : : :
Db 2 ISHGGKKEYADSVRG 17

RESULT 7
US-08-264-093-22
Sequence 22, Application US/08264093

Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear

Query Match 56.2%; Score 50; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 0.029;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IKODGSEKYYADSVRG 17
| : : : : :
Db 2 ISSNGSGTYADSVRG 17

RESULT 8

US-08-650-262-14
Sequence 14, Application US/08650262
Patent No. 5866124
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5866124man
APPLICANT: Pluschke, Gerd
APPLICANT: Murray, Brendan
TITLE OF INVENTION: Genetically engineered antibodies
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866124artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: NJ
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,262
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 92810188.0
FILING DATE: 17-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Henry P. No. 5866124ak
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-18995/A
TELECOMMUNICATION INFORMATION:
STREET: 908-277-5110
TELEFAX: 908-277-4306
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-650-262-14

Query Match 53.9%; Score 48; DB 2; Length 17;
Best Local Similarity 56.2%; Pred. No. 0.065;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IKODGSEKYYADSVRG 17
| : : : : :
Db 2 ISSDSNYYADTVKG 17

RESULT 9
US-08-208-886C-81
Sequence 81, Application US/08208886C
Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298 2987
; TELEFAX: 908 298 5388
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-208-886C-81

Query Match 49.4%; Score 44; DB 1; Length 16;
Best Local Similarity 58.3%; Pred. No. 0.3;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDSEKYYADSV 15
Db 4 ENGDKHYADSV 15

RESULT 10
US-08-704-744-83
; Sequence 83, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388

; TELEX:
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-744-83

Query Match 49.4%; Score 44; DB 1; Length 16;
Best Local Similarity 58.3%; Pred. No. 0.3;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDSEKYYADSV 15
Db 4 ENGDKHYADSV 15

RESULT 11
US-08-469-557-62
; Sequence 62, Application US/08469557
; Patent No. 5770403
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,557
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,793
; FILING DATE: August 16, 1994
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-469-557-62

Query Match 49.4%; Score 44; DB 1; Length 16;
Best Local Similarity 58.3%; Pred. No. 0.3;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDGSEKXYADSV 15
Db 4 ENGNDKHYADSV 15

RESULT 12
US-08-290-793B-62
; Sequence 62, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindali, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,793B
; FILING DATE: August 16, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
```

```
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-290-793B-62

Query Match 49.4%; Score 44; DB 2; Length 16;
Best Local Similarity 58.3%; Pred. No. 0.3;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDGSEKXYADSV 15
Db 4 ENGNDKHYADSV 15

RESULT 13
US-07-988-925-2
; Sequence 2, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L.
; APPLICANT: Clark, Michael R.
; APPLICANT: Gorman, Scott D.
; APPLICANT: Routledge, Edward G.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye PC
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,925
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206422.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB92/01933
; FILING DATE: 21-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C.
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
US-07-988-925-2

Query Match 48.3%; Score 43; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.48;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
Db 2 ISTSGGRTYYRDSVKG 17

RESULT 14

US-08-362-780-2
; Sequence 2, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726

; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-2

Query Match 48.3%; Score 43; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.48;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
Db 2 ISTSGGRTYYRDSVKG 17

RESULT 15

US-09-497-997C-32
; Sequence 32, Application US/09497997C

; Patent No. 6635248
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
; APPLICANT: AVRAMEAS, ALEXANDRE
; APPLICANT: BUTTIN, GERARD
; APPLICANT: AVRAMEAS, STRAITIS
; APPLICANT: SARON, MARIE-FRANCOISE
; APPLICANT: BLONDEL, BRUNO
; APPLICANT: COUDERC, THERESA
; APPLICANT: MICHELSON, SUSAN
; APPLICANT: ZIPETO, DONATO
; TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
; FILE REFERENCE: 0660-0166-0XCONT
; CURRENT APPLICATION NUMBER: US/09/497,997C
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01740
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-32

Query Match 48.3%; Score 43; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.48;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
Db 2 ISRGGGYSYLDVSKG 17

Search completed: June 8, 2004, 19:08:12
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:59:43 ; Search time 42 Seconds
(without alignments)
113.875 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89
Sequence: 1 NIKQSGSEKYYADSVRG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 segs, 281338677 residues

Total number of hits satisfying chosen parameters: 213306

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	17	9	US-09-832-312-62
2	89	100.0	17	11	US-09-829-495-62
3	82	92.1	17	15	US-10-173-551-16
4	75	84.3	17	10	US-09-977-797A-98
5	73	82.0	17	10	US-09-977-797A-110
6	70	78.7	17	15	US-10-338-366-16
7	64	71.9	17	10	US-09-972-656-48
8	64	71.9	17	12	US-10-384-060-46
9	64	71.9	17	16	US-10-399-701-6
10	62	69.7	17	9	US-09-828-708-23
11	61	68.5	17	9	US-09-828-708-23
12	61	68.5	17	10	US-09-791-153A-17
13	61	68.5	17	12	US-09-948-939-32
14	61	68.5	17	12	US-09-948-939-34
15	61	68.5	17	12	US-10-243-308-12

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61 68.5 17 14 US-10-243-265-12 Sequence 12, Appl
59 66.3 17 12 US-09-948-939-33 Sequence 33, Appl
18 58 17 14 US-10-031-874A-109 Sequence 109, App
19 58 17 12 US-09-920-267C-2 Sequence 2, Appli
20 56 17 9 US-09-798-058-6 Sequence 6, Appli
21 56 17 14 US-10-320-094-6 Sequence 6, Appli
22 56 17 15 US-10-320-418-6 Sequence 6, Appli
23 54 17 14 US-10-031-874A-105 Sequence 105, App
24 53 17 14 US-10-031-874A-30 Sequence 30, Appl
25 52 17 14 US-10-031-874A-103 Sequence 103, App
26 52 17 14 US-10-031-874A-110 Sequence 110, App
27 52 17 14 US-10-031-874A-111 Sequence 111, App
28 50 17 9 US-09-828-708-22 Sequence 22, Appl
29 50 17 14 US-10-031-874A-39 Sequence 39, Appl
30 50 17 14 US-10-031-874A-174 Sequence 174, App
31 49 17 9 US-09-192-854-139 Sequence 139, App
32 49 17 9 US-09-968-561A-248 Sequence 248, App
33 49 17 10 US-09-968-744A-248 Sequence 248, App
34 49 17 17 12 US-09-968-561A-38 Sequence 248, App
35 49 17 14 US-10-031-874A-116 Sequence 116, App
36 48 17 10 US-09-977-797A-106 Sequence 106, App
37 47 16 15 US-10-443-466A-38 Sequence 38, Appl
38 47 17 9 US-09-192-854-10 Sequence 10, Appl
39 47 17 9 US-09-968-561A-14 Sequence 14, Appl
40 47 17 9 US-09-968-561A-68 Sequence 38, Appl
41 47 17 9 US-09-968-561A-68 Sequence 38, Appl
42 47 17 9 US-09-968-561A-74 Sequence 74, Appl
43 47 17 9 US-09-968-561A-80 Sequence 80, Appl
44 47 17 9 US-09-968-561A-86 Sequence 86, Appl
45 47 17 9 US-09-968-561A-92 Sequence 92, Appl

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ALIGNMENTS

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RESULT 1
US-09-832-312-62
; Sequence 62, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-62

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Query Match 100.0%; Score 89; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKQSGSEKYYADSVRG 17

Db 1 NIKQSGSEKYYADSVRG 17

RESULT 2

US-09-829-495-62
; Sequence 62, Application US/09829495

; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Susfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Petrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-62

Query Match 100.0%; Score 89; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYYADSVRG 17
Db 1 NIKQDGESEKYYADSVRG 17

RESULT 3
US-10-173-551-16
; Sequence 16, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855-2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-16

Query Match 92.1%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYYADSVRG 17
Db 1 NIKQDGESEKYYADSVRG 17

RESULT 4
US-09-977-797A-98
; Sequence 98, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-98

Query Match 84.3%; Score 75; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYYADSVRG 17
Db 1 NIKQDGESEKYYADSVRG 17

RESULT 5
US-09-977-797A-110
; Sequence 110, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-110

Query Match 82.0%; Score 73; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYYADSVRG 17
Db 1 NIKPDGSDKYYVDSVKG 17

RESULT 6
US-10-338-366-16
; Sequence 16, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Trembl, John
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19

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; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-16
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Query Match      78.7%; Score 70; DB 15; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.00015;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 NIKDGSSEKYVDSVRG 17
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Db 1 NINEDGSEKYVDSVKG 17
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RESULT 7

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US-09-972-656-48
; Sequence 48, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: Tsai, Mei-Mei
; CURRENT APPLICATION NUMBER: A-799
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-48
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Query Match      71.9%; Score 64; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0014;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 2 IKQDGSSEKYVDSVRG 17
    ||| ||||| |||||
Db 2 ISYDGSNKYVDSVKG 17
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RESULT 8

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US-10-384-060-46
; Sequence 46, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 17
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 33 CDR2 sequence
US-10-384-060-46
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Query Match      71.9%; Score 64; DB 12; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0014;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 2 IKQDGSSEKYVDSVRG 17
    ||| ||||| |||||
Db 2 ISYDGSNKYVDSVKG 17
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RESULT 9

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US-10-399-701-6
; Sequence 6, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAT AG
; TITLE OF INVENTION: Rekombinant anti-GPIIb/IIIa-antibodies as agents for
; FILE REFERENCE: 23600PMO DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 100 57 443.2
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
; OTHER INFORMATION: an optimized antibody against GPIIb/IIIa
US-10-399-701-6
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Query Match      71.9%; Score 64; DB 16; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0014;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 2 IKQDGSSEKYVDSVRG 17
    ||| ||||| |||||
Db 2 ISYDGSNKYVDSVKG 17
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RESULT 10

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US-09-828-708-24
; Sequence 24, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-24
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Query Match      69.7%; Score 62; DB 9; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0029;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 2 IKQDGEKYYADSVRG 17
Db 2 ISYDGNKKYYADSVKG 17

RESULT 11
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; Sequence 23, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-23

Query Match 68.5%; Score 61; DB 9; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.0042;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DGSEKYYADSVRG 17
Db 5 DGSNKKYYADSVKG 17

RESULT 12
US-09-791-153A-17
; Sequence 17, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-17

Query Match 68.5%; Score 61; DB 10; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0042;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
Db 2 ISYDGNKKYYADSVKG 17

RESULT 13
US-09-948-939-32
; Sequence 32, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
```

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; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATUERE:
; OTHER INFORMATION: heavy chain CDR2 (HuMab 10D1)
US-09-948-939-32

Query Match 68.5%; Score 61; DB 12; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0042;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
Db 2 ISYDGNKKYYADSVKG 17

RESULT 14
US-09-948-939-34
; Sequence 34, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATUERE:
; OTHER INFORMATION: heavy chain CDR2 (HuMab 1E2)
US-09-948-939-34

Query Match 68.5%; Score 61; DB 12; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.0042;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DGSEKYYADSVRG 17
Db 5 DGSNKKYYADSVKG 17

RESULT 15
US-10-243-308-12
; Sequence 12, Application US/10243308
; Publication No. US20030064069A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
```

; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peta SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/10/243,308
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US/09/560,198
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-308-12

Query Match 68.5%; Score 61; DB 12; Length 17;
Best Local Similarity 75.0%; Pred. No: 0.0042;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKODGSEKYYADSVRG 17
| | | | | | | | | |
Db 2 ISYDGSIKYYADSVKG 17

Search completed: June 8, 2004, 19:06:08
Job time : 43 secs

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OM protein ~ protein search, using sw model

Run on: June 8, 2004, 18:59:13 ; Search time 53 Seconds
(without alignments)
90.628 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDSEKIYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 470470

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	17	4 AAB61294	Aab61294 Anti-TANG
2	89	100.0	17	6 ABU11260	Abu11260 Human TAN
3	82	92.1	17	5 AAO17611	Aao17611 Human FAP
4	78	87.6	17	5 AAU75740	Aau75740 Anti-(MCP
5	75	84.3	17	2 AAY05049	Aay05049 Tumour an
6	75	84.3	17	7 ADC82816	Adc82816 CDR regio
7	73	82.0	17	2 AAY05055	Aay05055 Tumour an
8	73	82.0	17	7 ADC82828	Adc82828 CDR regio
9	72	80.9	17	3 AAB39824	Aab39824 Anti-hiL1
10	71	79.8	17	2 AAW24547	Aaw24547 CDR #2 of
11	70	78.7	17	6 AAE38065	Aae38065 Human 17G
12	69	77.5	17	3 AAB39833	Aab39833 Anti-hiL1
13	67	75.3	17	3 AAB39822	Aab39822 Anti-hiL1
14	66	74.2	17	3 AAB39487	Aab39487 Anti-hiL1
15	66	74.2	17	3 AAB39819	Aab39819 Anti-hiL1
16	66	74.2	17	3 AAB39825	Aab39825 Anti-hiL1
17	66	74.2	17	3 AAB39820	Aab39820 Anti-hiL1
18	66	74.2	17	3 AAB39511	Aab39511 Anti-hiL1
19	66	74.2	17	3 AAB39823	Aab39823 Anti-hiL1
20	66	74.2	17	3 AAB39871	Aab39871 Anti-hiL1
21	66	74.2	17	3 AAB39881	Aab39881 Anti-hiL1
22	66	74.2	17	3 AAB39834	Aab39834 Anti-hiL1
23	66	74.2	17	3 AAB39865	Aab39865 Anti-hiL1
24	66	74.2	17	3 AAB39503	Aab39503 Anti-hiL1
25	66	74.2	17	3 AAB39870	Aab39870 Anti-hiL1

26	66	74.2	17	3 AAB39826	Aab39826 Anti-hiL1
27	66	74.2	17	3 AAB39828	Aab39828 Anti-hiL1
28	66	74.2	17	3 AAB39827	Aab39827 Anti-hiL1
29	66	74.2	17	3 AAB39821	Aab39821 Anti-hiL1
30	66	74.2	17	3 AAB39842	Aab39842 Anti-hiL1
31	66	74.2	17	3 AAB39868	Aab39868 Anti-hiL1
32	66	74.2	17	6 ABR63608	Abr63608 Human gly
33	65	73.0	17	3 AAY79069	Aay79069 Anti-fact
34	65	73.0	17	3 AAB39877	Aab39877 Anti-hiL1
35	65	73.0	17	3 AAB39872	Aab39872 Anti-hiL1
36	65	73.0	17	3 AAB39829	Aab39829 Anti-hiL1
37	65	73.0	17	3 AAB39835	Aab39835 Anti-hiL1
38	64	71.9	17	2 AAW90298	Aaw90298 Human ant
39	64	71.9	17	2 AAW90324	Aaw90324 Human ant
40	64	71.9	17	2 AAW90328	Aaw90328 Human ant
41	64	71.9	17	3 AAY79074	Aay79074 Anti-fact
42	64	71.9	17	3 AAY79076	Aay79076 Anti-fact
43	64	71.9	17	3 AAB39873	Aab39873 Anti-hiL1
44	64	71.9	17	3 AAB39869	Aab39869 Anti-hiL1
45	64	71.9	17	3 AAB39830	Aab39830 Anti-hiL1

ALIGNMENTS

RESULT 1

AAB61294

ID AAB61294 standard; peptide; 17 AA.

XX AAB61294;

XX 04-APR-2001 (first entry)

DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 62.

Human; antibody; scFv; CDR; complementarity determining region;
TANGO 268; cardiac; cerebroprotective; cytostatic; anticoagulant;
thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
platelet membrane glycoprotein receptor; bleeding disorder;
blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
ischaemia; cardiovascular disease; immunological disease; liver disorder;
cancer.

XX Homo sapiens.

XX WO200100810-A1.

XX 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US018152.

XX 30-JUN-1999; 99US-00345468.

XX 06-DEC-1999; 99US-00454824.

XX 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelail J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian MD, Kingsbury G;

XX WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor.

XX glycoprotein VI, and its modulators, useful for preventing, treating and

XX diagnosing hemorrhagic disorders, thrombotic diseases and immunological

XX disorders.

XX Claim 31; Page 102; 227pp; English.

XX The present sequence is given in a specification relating to an isolated

XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor

XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

XX and polypeptides and their modulators, e.g. antisense nucleic acids,

XX

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NIKQDSEKYYADSVRG 17

RESULT 2
 ABU11260
 ID ABU11260 standard; peptide; 17 AA.
 AC ABU11260;

DT 06-FEB-2003 (first entry)

DE Human TANGO 268 VHCDR2 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WC200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 7; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NIKQDSEKYYADSVRG 17

RESULT 3
 AA017611

ID AA017611 standard; peptide; 17 AA.

XX AA017611;

XX 08-AUG-2002 (first entry)

XX Human PAPalpha specific VL region from VH50 CDR2 peptide.

XX Human; PAPalpha; fibroblast activating protein alpha; antibody; Ab;
 KW gene therapy; cancer; wound healing; inflammation; cytostatic.

XX Homo sapiens.

XX WC200168708-A2.

XX 20-SEP-2001.

XX 16-MAR-2001; 2001WO-EP004716.

XX 17-MAR-2000; 2000DE-01013286.

XX 11-SEP-2000; 2000GB-00022216.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;

XX Schmidt A;

XX WPI; 2002-041180/05.

XX N-PSDB; AAL46556.

XX New human humanized antibody that specifically binds to fibroblasts
 PT activating protein alpha, useful for treating cancer or tumor, and for
 PT imaging tumors associated with activated stromal fibroblasts, e.g. lung
 PT or breast cancer.

XX Disclosure; Fig 6C; 109pp; English.

XX The present invention relates to a human or humanised antibody (Ab) which
CC specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC antibodies are useful for preparing a composition for the treatment of
CC cancer, and for imaging tumours associated with activated stromal
CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC cancer, pancreatic cancer and metastatic brain cancer, and diseases
CC associated with the same, such as inflammation and wound healing. The
CC present sequence is a peptide described in the exemplification of the
CC invention
XX Sequence 17 AA;
SQ

light chain variable domain (Vh, Vl). The antibody of the invention inhibits binding of MCP-1 (and also eotaxin) to specific receptors, so preventing migration of monocytes and T cells. These are human antibodies with very high affinity for MCP-1, but no significant reaction with other human CC-type chemokines or MCP-1 from other species. The MCP-1 binding molecules, specifically antibodies that cross-react with eotaxin, are used to prevent or treat MCP-1 or eotaxin-mediated disorders, particularly those that involve migration or activation of monocytes and T cells, e.g. allergic (allergic rhinitis, hypersensitivity responses, allergic contact dermatitis), inflammatory diseases (asthma, psoriasis, COPD, inflammatory bowel disease, multiple sclerosis) autoimmune disease (rheumatoid arthritis; diabetes, systemic lupus erythematosus), diseases of bone and cartilage (osteoporosis, osteoarthritis, periodontal disease) haematological disorders (haemolytic anaemia, idiopathic thrombocytopenia) graft rejection, cancers that include leucocyte infiltration, (re)stenosis, arteriosclerosis, osteoporosis and many other diseases listed in the specification. The present sequence represents the human anti-(MCP) antibody heavy chain sequence hypervariable domain peptide CDR2 of the invention

Sequence 17 AA:

CC diverse population immobilised on the solid support with 2 or more
 CC ligands; and (c) determining at least one binding molecule which
 CC selectively binds to one or more of the ligands. The method allows for
 CC the rapid and efficient methods for the identification of binding
 CC molecules which exhibit selective affinity for one or more ligands of
 CC interest. They are used particularly for identifying tumour-specific
 CC binding polypeptides which can be used as targeting agents for cancer
 CC therapy that minimises impact on non-tumour tissues

XX
 SQ Sequence 17 AA;

Query Match 84.3%; Score 75; DB 2; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1e-05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NINQDSEKYYVDSVEG 17
 |||||

RESULT 6
 ADC82816
 ID ADC82816 standard; peptide; 17 AA.
 AC
 AC ADC82816;
 XX
 DT 01-JAN-2004 (first entry)
 DE CDR region #14 in heavy chain of human Fab fragment.
 XX
 KW Binding molecule; selective affinity; ligand;
 KW anti-immunoglobulin reagent; phage expressed antibody library;
 KW tumour antigen; complementarity determining region; CDR; human disease;
 KW cellular pathology; human; Fab; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX US2003044772-A1.
 XX
 XX 06-MAR-2003.
 XX
 XX 15-OCT-2001; 2001US-00977797.
 XX
 XX 04-AUG-1997; 97US-0113667P.
 XX
 XX 04-AUG-1998; 98US-00129026.
 XX
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 XX Watkins JD, Huse WD, Wu H;
 XX
 XX WPI; 2003-625402/59.
 XX
 XX N-PSDB; ADC82815.
 XX
 XX Identifying binding molecules having selective affinity for ligands for
 XX discovering reagents for treating diseases, by contacting solid support
 XX coated with anti-immunoglobulin reagent to a phage expressed antibody
 XX library.
 XX
 XX Example 5; Page 17; 26pp; English.

CC The present invention relates to a method for identifying a binding
 CC molecule having selective affinity for a ligand. The method involves
 CC providing a solid support coated with an anti-immunoglobulin reagent, and
 CC a phage expressed antibody library, and contacting the solid support to
 CC the phage expressed antibody library. The invention also discloses a
 CC method for identifying an antibody having selective affinity for a
 CC tumour, and a complementarity determining region (CDR) of an antibody
 CC selective for a tumour antigen. The methods of the invention are useful
 CC for identifying a binding molecule having selective affinity for a
 CC ligand, for the discovery of specific reagents for diagnosis and
 CC treatment of human diseases, for identifying binding molecules to, for
 CC example tumour cells or other cellular pathologies for the selective
 CC targeting of therapeutic agents, or for the identification of binding

CC molecules to normal or diseased tissues for the selective targeting of,
 CC for example diagnostic agents such as imaging reagents. The methods are
 CC rapid and efficient for the identification of binding molecules which
 CC exhibit selective affinity for one or more ligands of interest. The
 CC methods allow the simultaneous screening of multiple binding molecules
 CC against multiple ligands of interest. Moreover, very little information
 CC is required regarding the identity or function of either the binding
 CC molecule or the ligand. For example diverse populations of binding
 CC molecules can be simultaneously screened against diverse populations of
 CC ligands to rapidly identify numerous molecules exhibiting a desired
 CC binding specificity. The methods provide improved sensitivity and
 CC specificity of detection through the selective immobilisation of the
 CC binding molecule population on a solid support. The present sequence
 CC represents a CDR region in the heavy chain of human Fab fragment.

XX
 SQ Sequence 17 AA;

Query Match 84.3%; Score 75; DB 7; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1e-05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NINQDSEKYYVDSVEG 17
 |||||

RESULT 7
 AAY05055
 ID AAY05055 standard; peptide; 17 AA.
 XX
 AC AAY05055;
 XX
 DT 16-JUN-1999 (first entry)
 XX
 DE Tumour antigen antibody heavy chain CDR2 clone F133.
 XX
 KW Tumour antigen; antibody; CDR; complementarity determining region;
 KW binding molecule identification; tumour-specific binding polypeptide;
 KW cancer therapy; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX WO9906834-A2.
 XX
 XX 11-FEB-1999.
 XX
 XX 04-AUG-1998; 98WO-US016280.
 XX
 XX 04-AUG-1997; 97US-00905825.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 XX Watkins JD, Huse WD, Wu H;
 XX
 XX WPI; 1999-153951/13.
 XX
 XX N-PSDB; AAX28232.
 XX
 XX Identifying binding molecules for ligands, particularly tumour antigens -
 XX by selectively immobilising a population of binding molecules to a solid
 XX support and screening for binding to two or more ligands.
 XX
 XX Claim 15; Page 60; 80pp; English.

CC This sequence represents a heavy chain complementarity determining region
 CC (CDR) from a tumour antigen specific antibody. The invention relates to a
 CC method for identifying a binding molecule having selective affinity for a
 CC ligand comprising: (a) selectively immobilising a diverse population of
 CC binding molecules to a solid support; (b) simultaneously contacting the
 CC diverse population immobilised on the solid support with 2 or more
 CC ligands; and (c) determining at least one binding molecule which
 CC selectively binds to one or more of the ligands. The method allows for
 CC the rapid and efficient methods for the identification of binding
 CC molecules which exhibit selective affinity for one or more ligands of

CC interest. They are used particularly for identifying tumour-specific
 CC binding polypeptides which can be used as targeting agents for cancer
 CC therapy that minimises impact on non-tumour tissues

XX SQ Sequence 17 AA;

Query Match 82.0%; Score 73; DB 2; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.2e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||:|||||:
 Db 1 NIKPDGSDKYVDVSKG 17

RESULT 8

ADC82828
 ID ADC82828 standard; peptide; 17 AA.

XX AC ADC82828;

XX DT 01-JAN-2004 (first entry)

XX DE CDR region #20 in heavy chain of human Fab fragment.

XX KW Binding molecule; selective affinity; ligand;
 KW anti-immunoglobulin reagent; phage expressed antibody library;
 KW tumour antigen; complementarity determining region; CDR; human disease;
 KW cellular pathology; human; Fab; heavy chain.

XX OS Homo sapiens.

XX FN U5203044772-A1.

XX PD 06-MAR-2003.

XX PF 15-OCT-2001; 2001US-00977797.

XX PR 04-AUG-1997; 97US-0113667P.

XX PR 04-AUG-1998; 98US-00129026.

XX PA (MOLB-) APPLIED MOLECULAR EVOLUTION.

XX PI Watkins JD, Huse WD, Wu H;

XX DR WPI; 2003-625402/59.

XX DR N-PSDB; ADC82827.

XX PT Identifying binding molecules having selective affinity for ligands for
 PT discovering reagents for treating diseases, by contacting solid support
 PT coated with anti-immunoglobulin reagent to a phage expressed antibody
 PT library.

XX PS Example 5; Page 17; 26pp; English.

XX CC The present invention relates to a method for identifying a binding
 CC molecule having selective affinity for a ligand. The method involves
 CC providing a solid support coated with an anti-immunoglobulin reagent, and
 CC a phage expressed antibody library, and contacting the solid support to
 CC the phage expressed antibody library. The invention also discloses a
 CC method for identifying an antibody having selective affinity for a
 CC tumour, and a complementarity determining region (CDR) of an antibody
 CC selective for a tumour antigen. The methods of the invention are useful
 CC for identifying a binding molecule having selective affinity for a
 CC ligand, for the discovery of specific reagents for diagnosis and
 CC treatment of human diseases, for identifying binding molecules to, for
 CC example tumour cells or other cellular pathologies for the selective
 CC targeting of therapeutic agents, or for the identification of binding
 CC molecules to normal or diseased tissues for the selective targeting of,
 CC for example diagnostic agents such as imaging reagents. The methods are
 CC rapid and efficient for the identification of binding molecules which
 CC exhibit selective affinity for one or more ligands of interest. The
 CC methods allow the simultaneous screening of multiple binding molecules

CC against multiple ligands of interest. Moreover, very little information
 CC is required regarding the identity or function of either the binding
 CC molecule or the ligand. For example diverse populations of binding
 CC molecules can be simultaneously screened against diverse populations of
 CC ligands to rapidly identify numerous molecules exhibiting a desired
 CC binding specificity. The methods provide improved sensitivity and
 CC specificity of detection through the selective immobilisation of the
 CC binding molecule population on a solid support. The present sequence
 CC represents a CDR region in the heavy chain of human Fab fragment.

XX SQ Sequence 17 AA;

Query Match 82.0%; Score 73; DB 7; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.2e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
 |||||:|||||:
 Db 1 NIKPDGSDKYVDVSKG 17

RESULT 9

AAB39824
 ID AAB39824 standard; peptide; 17 AA.

XX AC AAB39824;

XX DT 05-FEB-2001 (first entry)

XX DE Anti-hLL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 340.

XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antisthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX OS Homo sapiens.

XX PN WO200056772-A1.

XX PD 28-SEP-2000.

XX PF 24-MAR-2000; 2000WO-US007946.

XX PR 25-MAR-1999; 99US-0126603P.

XX PX (BADI) BASF AG.

XX PA (GEMY) GENETICS INST INC.

XX PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A, R;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.

XX PS Claim 33; Fig 2B; 377pp; English.

XX CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and

CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antiparasitic; antidiabetic; cardiac; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 CC Sequence 17 AA;

Query Match 80.9%; Score 72; DB 3; Length 17;
 Best Local Similarity 76.5%; Pred. No. 3.3e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDGSSEKYYADSVRG 17

Db 1 NIKQDGSSEKYYADSVRG 17

RESULT 10

AAW24547

ID AAW24547 standard; peptide; 17 AA.

XX AC AAW24547;

XX DT 09-OCT-1997 (first entry)

XX DE CDR #2 of r101-2 heavy chain variable region.

XX KW Immunoglobulin; variable region; heavy chain; thyrotropin receptor;

XX KW thyroid stimulating activity; light chain; Basedow's disease; antibody;

XX KW peripheral blood lymphocyte; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PI JF09140386-A.

XX PN 03-JUN-1997.

XX PF 22-NOV-1995; 95JP-00328235.

XX PR 22-NOV-1995; 95JP-00328235.

XX PA (EIKE) EIKEN KAGAKU KK.

XX PS WPI; 1997-344899/32.

XX PT Antibody containing immunoglobulin heavy chain mutation - with thyroid

XX PT function stimulating activity.

XX PS Claim 12; Page 14; 18pp; Japanese.

XX CC AAW24540-W24551 represent the complementarity determining regions (CDRs)
 CC of immunoglobulin heavy and light chain variable regions isolated from
 CC peripheral blood lymphocyte strains (see AAW24536-W24539 for full length
 CC immunoglobulin chains). These sequences were isolated from the B6B7 and
 CC 101-2 strains of peripheral blood lymphocytes of a Basedow's disease
 CC patient. These sequences are replaced, deleted or inserted into an
 CC antibody, to create the antibodies of the invention. The antibodies of
 CC the invention have thyroid function stimulating activity, and act by
 CC combining with thyrotropin receptor. The antibody can be used in a method
 CC to detect autoantibodies which have thyroid function stimulating activity

XX SQ Sequence 17 AA;

Query Match 79.8%; Score 71; DB 2; Length 17;

Best Local Similarity 76.5%; Pred. No. 4.8e-05;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDGSSEKYYADSVRG 17

Db 1 DIKPDGSEKYYVDSVKG 17

RESULT 11

AAE38065

ID AAE38065 standard; peptide; 17 AA.

XX AC AAE38065;

XX DT 06-NOV-2003 (first entry)

XX DE Human 17G1 CD30 antibody VH CDR2 peptide.

XX KW Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; systemic sclerosis; Grave's disease; ALCL;
 KW atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
 KW acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
 KW Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
 KW adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
 KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
 KW heavy chain variable domain; VH; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO2003059282-A2.

XX PD 24-JUL-2003.

XX PF 07-JAN-2003; 2003WO-US000440.

XX PR 09-JAN-2002; 2002US-0347649P.

XX PR 19-AUG-2002; 2002US-0404427P.

XX PR 06-DEC-2002; 2002US-0431684P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Graziano R, Trembl J;

XX DR WPI; 2003-598476/56.

XX DR N-PSDB; AAD57377.

XX PT New human monoclonal antibody that binds to human CD30, useful for
 PT treating or preventing tumor or autoimmune disease, e.g., rheumatoid
 PT arthritis.

XX PS Claim 13; Page 116; 122pp; English.

XX CC The invention relates to human monoclonal antibody that binds to human
 CC CD30. The antibody is useful for treating or preventing tumour or
 CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
 CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome, HIV
 CC chronic renal failure, acute infectious mononucleosis, herpes or HIV
 CC (human immunodeficiency virus) virus-associated diseases. The antibody is
 CC also useful for treating Hodgkin's disease, anaplastic large cell
 CC lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic
 CC lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity
 CC based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the
 CC rhino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Kaposi's
 CC sarcoma and other T-cell or B-cell lymphomas. The present sequence is
 CC human CD30 antibody VH (heavy chain variable domain) CDR (complementarity
 CC determining region) peptide

XX SQ Sequence 17 AA;

Query Match 78.7%; Score 70; DB 6; Length 17;

Best Local Similarity 70.6%; Pred. No. 7.1e-05;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDGSSEKYYADSVRG 17

Db 1 NIKQDGSSEKYYADSVRG 17

```

RESULT 12
AAB39833
ID AAB39833 standard; peptide; 17 AA.
AC AAB39833;
XX
XX 05-FEB-2001 (first entry)
XX
XX Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 349.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neuoprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO200056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US007946.
XX
XX 25-MAR-1999; 99US-0126603P.
XX
XX (BADI ) BASF AG.
XX (GEMY ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire BJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
XX WPI; 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis.
XX
XX Claim 33; Fig 2B; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX represent other CDR sequences. Light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in AAC61062-
XX C61071. The antibody of the invention is a neutralising antibody and has
XX antirheumatic; antiarthritic; antisclerotic; antinflammatory;
XX neuoprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
XX antibacterial and immunosuppressive activity. The antibodies or antigen-
XX binding fragments are useful in the treatment of disorders associated
XX with detrimental release of human IL-12, especially Crohn's disease,
XX multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX manufacture of a pharmaceutical composition to treat human IL-12
XX disorders
XX
XX Sequence 17 AA;
XX
XX Query Match 77.5%; Score 69; DB 3; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 0.00011;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 IKDGSSEKYADSVRG 17
XX || ||| ||||| |||
QY

```

```

Db
2 IKYDGSNKYADSVKG 17

RESULT 13
AAB39822
ID AAB39822 standard; peptide; 17 AA.
XX
XX AAB39822;
XX
XX 05-FEB-2001 (first entry)
XX
XX Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 338.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neuoprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX WO200056772-A1.
XX
XX 28-SEP-2000.
XX
XX 24-MAR-2000; 2000WO-US007946.
XX
XX 25-MAR-1999; 99US-0126603P.
XX
XX (BADI ) BASF AG.
XX (GEMY ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire BJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
XX WPI; 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX disease and multiple sclerosis.
XX
XX Claim 33; Fig 2B; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
XX interleukin-12 (IL-12). The invention also includes antigen binding
XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX anti-IL-12 antibody heavy and light chain complementarity determining
XX region (CDR) amino acid sequences, and also includes variable region
XX amino acid sequences. Other variable region amino acid sequences are
XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX represent other CDR sequences. Light chain CDR3 consensus sequences are
XX given in AAB40064-B40067. Primers used in the identification and
XX construction of the antibodies of the invention are given in AAC61062-
XX C61071. The antibody of the invention is a neutralising antibody and has
XX antirheumatic; antiarthritic; antisclerotic; antinflammatory;
XX neuoprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
XX antibacterial and immunosuppressive activity. The antibodies or antigen-
XX binding fragments are useful in the treatment of disorders associated
XX with detrimental release of human IL-12, especially Crohn's disease,
XX multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX manufacture of a pharmaceutical composition to treat human IL-12
XX disorders
XX
XX Sequence 17 AA;
XX
XX Query Match 75.3%; Score 67; DB 3; Length 17;
XX Best Local Similarity 70.6%; Pred. No. 0.00023;
XX Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 NTKQDGSSEKYADSVRG 17
XX

```

Db 1 HIRYDGSNKYYADSVKG 17
 :|: ||| ||| ||| ||| ||| :|

RESULT 14
 AAB39487
 ID AAB39487 standard; protein; 17 AA.
 XX
 AC AAB39487;
 DT
 XX 05-FEB-2001 (first entry)
 DE Anti-hIL-12 antibody heavy chain CDR2 amino acid sequence SEQ ID 3.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 16; Page 225; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX
 SQ Sequence 17 AA;

Query Match 74.2%; Score 66; DB 3; Length 17;
 Best Local Similarity 75.0%; Pred. NO. 0.00034;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
 :|: ||| ||| ||| ||| :|
 Db 2 HIRYDGSNKYYADSVKG 17
 :|: ||| ||| ||| ||| :|

RESULT 15
 AAB39819
 ID AAB39819 standard; peptide; 17 AA.
 XX
 AC AAB39819;
 DT
 XX 05-FEB-2001 (first entry)
 DE Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 335.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.

XX Claim 33; Fig 2B; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX
 SQ Sequence 17 AA;

Query Match 74.2%; Score 66; DB 3; Length 17;
 Best Local Similarity 75.0%; Pred. NO. 0.00034;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKODGSEKYYADSVRG 17
| : ||| ||| ||| :
Db 2 IRYDGSNKYYADSVKG 17

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Job time : 54 secs

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OM protein - protein search, using sw model

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(without alignments)
11.223 Million cell updates/sec

Title: US-09-610-118-61
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Sequence: 1 SYWMS 5

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 24558

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	90.3	5	2	US-08-318-157B-23
2	28	90.3	5	4	US-09-253-794-23
3	27	87.1	5	1	US-08-244-626-12
4	27	87.1	5	1	US-08-318-970B-1
5	27	87.1	5	2	US-08-480-434-32
6	27	87.1	5	2	US-08-053-451B-32
7	27	87.1	5	4	US-09-406-532-5
8	27	87.1	5	4	US-09-091-071-6
9	25	80.6	5	4	US-09-508-413A-2
10	24	77.4	5	1	US-08-318-970B-3
11	23	74.2	5	2	US-08-480-434-22
12	23	74.2	5	2	US-08-480-434-31
13	23	74.2	5	2	US-08-053-451B-22
14	23	74.2	5	2	US-08-053-451B-31
15	23	74.2	5	4	US-08-479-089A-7
16	23	74.2	5	4	US-07-669-545B-7
17	22	71.0	5	1	US-07-946-421-4
18	20	64.5	4	1	US-07-869-933-21
19	20	64.5	4	3	US-09-103-663-21
20	20	64.5	5	1	US-07-789-184-158
21	20	64.5	5	1	US-08-475-263-158
22	20	64.5	5	1	US-08-485-886-158
23	20	64.5	5	2	US-08-477-362-158
24	20	64.5	5	2	US-08-477-134-158
25	20	64.5	5	2	US-08-476-176B-50
26	20	64.5	5	3	US-08-473-489A-158
27	20	64.5	5	3	US-08-127-721A-50

28	20	64.5	5	3	US-08-485-246A-50	Sequence 50, Appl
29	20	64.5	5	3	US-08-485-695-158	Sequence 158, App
30	20	64.5	5	3	US-08-018-760-158	Sequence 158, App
31	20	64.5	5	3	US-07-987-264-1	Sequence 1, Appli
32	20	64.5	5	4	US-09-688-188B-40	Sequence 40, Appl
33	20	64.5	5	4	US-09-628-665-8	Sequence 8, Appli
34	20	64.5	5	4	US-09-291-417D-40	Sequence 40, Appl
35	19	61.3	5	1	US-08-068-947-1	Sequence 1, Appli
36	19	61.3	5	1	US-08-353-400-27	Sequence 27, Appl
37	19	61.3	5	4	US-09-382-689A-4	Sequence 4, Appli
38	19	61.3	5	4	US-08-877-605-9	Sequence 9, Appli
39	19	61.3	5	4	US-08-877-605-14	Sequence 14, Appl
40	18	58.1	3	1	US-08-440-504A-1	Sequence 1, Appli
41	18	58.1	3	3	US-08-433-613-1	Sequence 1, Appli
42	18	58.1	4	1	US-08-321-625-14	Sequence 14, Appl
43	18	58.1	4	1	US-08-222-851-19	Sequence 19, Appl
44	18	58.1	4	1	US-08-469-486-39	Sequence 39, Appl
45	18	58.1	4	1	US-08-440-504A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-318-157B-23
; Sequence 23, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CREA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-157B-23

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

Db 1 TYWMS 5

RESULT 2

US-09-253-794-23
; Sequence 23, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; ; MOUSE MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/253,794

FILING DATE: 22-Feb-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,157

FILING DATE: 05-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 18733/464

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-253-794-23

Query Match 90.3%; Score 28; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

Db 1 TYWMS 5

RESULT 3

US-08-244-626-12
; Sequence 12, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Walsh, Louise
; APPLICANT: Crowe, James Scott
; APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

ADDRESSER: Rothwell, Pigg, Ernst & Kurz, p.c.

STREET: 555 Thirteenth Street, N. W.

CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,626

FILING DATE: July 15, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/02251

FILING DATE: December 4, 1992

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Ernst, Barbara G.

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-153A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-244-626-12

Query Match 87.1%; Score 27; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5

Db 2 YWMS 5

RESULT 4

US-08-318-970B-1

; Sequence 1, Application US/08318970B

; Patent No. 5589573

; GENERAL INFORMATION:

; APPLICANT: Hideaki HAGIWARA, et al.

; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC

; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY

; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Office of Sherman and Shalloway

; STREET: 413 N. Washington Street

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: Dell System 210; Intel 80 285 Microprocessor

OPERATING SYSTEM: MS DOS 3.3

SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,970B

FILING DATE: October 6, 1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Richard A. Steinberg

REGISTRATION NUMBER: 26,588

REFERENCE/DOCKET NUMBER: S-2371

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 549-2282

```

; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDRI-1
; OTHER INFORMATION: hypervariable region
US-08-318-970B-1

Query Match      87.1%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWM 4
Db      1 SYWM 4

RESULT 5
US-08-480-434-32
; Sequence 32, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-480-434-32

Query Match      87.1%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
Db      2 YWMS 5
```

```

RESULT 6
US-08-053-451B-32
; Sequence 32, Application US/08053451B
; Patent No. 595584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-32

Query Match      87.1%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
Db      2 YWMS 5

RESULT 7
US-09-406-532-5
; Sequence 5, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
```

```
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: 15B8 heavy chain CDR 1
US-09-406-532-5

Query Match      87.1%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWM 4
      ||||
Db      1 SYWM 4

RESULT 8
US-09-091-071-6
; Sequence 6, Application US/09091071
; Patent No. 6610500
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DESIGN OF HORMONE-LIKE ANTIBODIES WITH
; TITLE OF INVENTION: AGONISTIC AND ANTAGONISTIC FUNCTIONS
; NUMBER OF SEQUENCES: 9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,071
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA96/00815
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525180.7
; FILING DATE: 08-DEC-1995
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-071-6

Query Match      87.1%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWM 4
      ||||
Db      1 SYWM 4

RESULT 9
US-09-508-413A-2
; Sequence 2, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
; APPLICANT: von Eichel-Streiber, Christoph
; APPLICANT: Moos, Michael
; TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
; TITLE OF INVENTION: PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
; TITLE OF INVENTION: DIFFICILE TOXINS
; FILE REFERENCE: 415142000200
; CURRENT APPLICATION NUMBER: US/09/508,413A
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: PCT/EP98/05759
```

```
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-508-413A-2

Query Match      80.6%; Score 25; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWMS 5
      :|||:
Db      1 NYWMN 5

RESULT 10
US-08-318-970B-3
; Sequence 3, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR1-3
; OTHER INFORMATION: hypervariable region
US-08-318-970B-3

Query Match      77.4%; Score 24; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWM 4
      :|||:
Db      1 NYWM 4

RESULT 11
US-08-480-434-22
```


APPLICANT: Amlot, Peter L.
APPLICANT: Akbar, Arne N.
APPLICANT: Heinrich, Gunther
APPLICANT: Cammisuli, Salvatore
TITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6383487artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,089A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/669,545
FILING DATE:
APPLICATION NUMBER: GB 9019323
FILING DATE: 05-SRP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-479-089A-7

Query Match 74.2%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWM 4
Db 2 YWM 4

Search completed: June 8, 2004, 18:59:07
Job time : 24 secs

APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-31

Query Match 74.2%; Score 23; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWMS 5
Db 2 FWMS 5

RESULT 15
US-08-479-089A-7
Sequence 7, Application US/08479089A
Patent No. 6383487
GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 19:04:14 ; Search time 21 Seconds
(without alignments)
77.869 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDGEKYYADSVRG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2990

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	29.2	9	A37027	macrophage chemota
2	26	29.2	15	PH1610	Ig H chain V-D-J r
3	25	28.1	12	A54315	entactin/nidogen -
4	25	28.1	16	E28027	protein p8 - curie
5	24	27.0	9	PD0443	3-oxoacid CoA-tran
6	24	27.0	10	PT0291	Ig heavy chain CRD
7	24	27.0	13	A57789	gallbladder stone
8	24	27.0	14	PH1597	Ig H chain V-D-J r
9	24	27.0	16	PH1589	Ig H chain V-D-J r
10	24	27.0	17	B49404	T-cell receptor be
11	23	25.8	13	PH1479	T-cell receptor be
12	23	25.8	14	PH1608	Ig H chain V-D-J r
13	23	25.8	16	G24304	ribosomal protein
14	22	24.7	10	S33844	alpha-2-macroglobu
15	22	24.7	12	A39233	myosin heavy chain
16	22	24.7	13	S47389	T-cell antigen rec
17	22	24.7	14	PT0232	Ig heavy chain CRD
18	22	24.7	14	PT0252	Ig heavy chain CRD
19	22	24.7	14	PD0762	T-cell receptor be
20	22	24.7	15	PD0444	coupling factor 6
21	21	23.6	10	B49581	sialokin II - ye
22	21	23.6	11	D61033	ranatactykinin D -
23	21	23.6	12	PH1481	T-cell receptor be
24	21	23.6	14	PH1615	Ig H chain V-D-J r
25	21	23.6	14	PH1601	Ig H chain V-D-J r
26	21	23.6	14	C39170	acyl-[acyl-carrier
27	21	23.6	15	T46625	hypothetical prote
28	21	23.6	15	A56970	GLYMA1 - soybean
29	21	23.6	17	A61334	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

A37027
macrophage chemotactic factor - human (fragment)
N/Alternate names: T-cell hybridoma D6-18 protein
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 23-Feb-1997
C/Accession: A37027
R.Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
Cell. Immunol. 123, 212-225, 1989
A/Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.
A/Reference number: A37027; MUID:89376581; PMID:2505934
A/Accession: A37027
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <YOS>

Query Match 29.2%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KQDQSE 8
:::|::|
DB 4 RZDQSE 9

RESULT 2

PH1610
Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1610
R.Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1610
A/Molecule type: DNA
A/Residues: 1-15 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 29.2%; Score 26; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGSEKYYA 12
:|::|
DB 5 NGSPYYA 12

RESULT 3
A54315

Ig heavy chain J r
cytochrome c553 -
T-cell receptor be
hypothetical 1.6K
hypothetical 1.6K
alpha-conotoxin Cn
2S albumin small c
Ig heavy chain CRD
T-cell receptor V-
Ig H chain V-D-J r
T-cell receptor al
ubiquinol-cytochro
nucleoside-diphosp
fibrinogen alpha c
Ig heavy chain DJ
T-cell receptor be

entactin/nidogen - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C;Accession: A54315
 R;Katz, A.; Fish, A.J.; Kleppel, M.M.; Hagen, S.G.; Michael, A.F.; Butkowski, R.J.
 Kidney Int. 40, 643-652, 1991
 A;Title: Renal entactin (nidogen): isolation, characterization and tissue distribution.
 A;Reference number: A54315; MUID:92079440; PMID:1745013
 A;Accession: A54315
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <KAT>
 A;Experimental source: renal tubular basement membrane
 A;Note: sequence extracted from NCBI backbone (NCBIP:71053)
 C;Superfamily: nidogen; BGF homolog; LDL receptor YWTP-containing repeat homology; thy2

Query Match 28.1%; Score 25; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 DSVRG 17
 |||||
 Db 5 DSVRG 9

RESULT 4
 E28027
 Protein p8 - curled-leaved tobacco (fragment)
 C;Species: Nicotiana glauca (tobacco)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
 C;Accession: E28027
 R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
 A;Reference number: A94167
 A;Accession: E28027
 A;Molecule type: protein
 A;Residues: 1-16 <BAU>
 A;Note: 10-Lys was also found

Query Match 28.1%; Score 25; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 8.4e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKODGSEKY 10
 : |||||
 Db 8 VANDGSKTY 16

RESULT 5
 PD0443
 3-Oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
 C;Accession: PD0443
 R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
 submitted to JIPID, August 1998
 A;Description: Proteome analysis of mouse brain.
 A;Reference number: PD0441
 A;Contents: Striatum
 A;Accession: PD0443
 A;Molecule type: protein
 A;Residues: 1-9 <KAW>
 C;Keywords: CoA-transferase

Query Match 27.0%; Score 24; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 KYVADSV 15
 |||||
 Db 2 KEVTDPV 8

RESULT 6

PT0291
 Ig heavy chain CRD3 region (clone 4-115B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0291
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0291
 A;Molecule type: DNA
 A;Residues: 1-10 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotrimer; immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 SEKYIADS 14
 |||||
 Db 3 SPTYIYDS 10

RESULT 7
 A57789
 gallbladder stone matrix protein 1, 41K - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
 C;Accession: A57789
 R;Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, February 1996
 A;Description: The proteins of gallbladder stones.
 A;Reference number: A57789
 A;Accession: A57789
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <BIN>
 A;Experimental source: two gallbladder, one bladder, one kidney stone of different pati
 A;Note: 9-Leu and 12-Lys were also found

Query Match 27.0%; Score 24; DB 2; Length 13;
 Best Local Similarity 45.5%; Pred. No. 9.9e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 QDGSSEKYADS 14
 |||||
 Db 3 QDSDSGFVEDS 13

RESULT 8
 PH1597
 IG H chain V-D-J region (wild-type clone 304) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1597
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1597
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSEKYIA 12

Db 5 GSGYYA 11
|| |||

RESULT 9

PH1589
Ig H chain V-D-J region (wild-type clone 140) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1589
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1589
A:Molecule type: DNA
A:Residues: 1-16 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 DGSSEKYAD 13
||| |||
Db 7 DGSPPHYAMD 15

RESULT 10

B49404
T-cell receptor beta chain VDJ region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: B49404
R;Brooke, E.G.; Balk, S.P.; Aupeix, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.
Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993
A:Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells express oligoclonal T
A:Reference number: A49404; MUID:94089717; PMID:7505446
A:Accession: B49404
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <BRO>
A:Cross-references: GB:S67400; NID:g455868; PIDN:AAB29275.1; PID:g455869
A:Experimental source: alpha/beta + CD4-CD8- T cells
A:Note: sequence extracted from NCBI backbone (NCBIN:141024, NCBIIP:141025)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 27.0%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QDGSSEKY 11
||| |||
Db 7 QGGYEQYF 14

RESULT 11

PH1479
T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1479
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1479
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology

C;Keywords: receptor; T-cell

Query Match 25.8%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QDGSSEKY 11
||| |||
Db 5 QAGYEQYF 12

RESULT 12

PH1608
Ig H chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1608; PH1603
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1608
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 335
A:Accession: PH1603
A:Molecule type: DNA
A:Residues: 1-14 <LEV2>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 324
C:Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GSEXYA 12
||| |||
Db 5 GNSYYA 11

RESULT 13

G24304
ribosomal protein H [validated] - Haloarcula marismortui (fragment)
C:Species: Haloarcula marismortui
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C:Accession: G24304
R;Shoham, M.; Dijk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit of
A:Reference number: A24304
A:Accession: G24304
A:Molecule type: protein
A:Residues: 1-16 <SHO>
C:Keywords: protein biosynthesis; ribosome

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KYAD 13
||| |||
Db 4 KYND 8

RESULT 14

S33844
alpha-2-macroglobulin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: S33844
R;Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J.
Eur. J. Biochem. 214, 803-809, 1993
A:Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mammary m

A;Reference number: S33843; MUID:93307297; PMID:7686489

A;Accession: S33844

A;Molecule type: protein

A;Residues: 1-10 <WAR>

C;Superfamily: alpha-2-macroglobulin

C;Keywords: Glycoprotein; plasma; proteinase inhibitor; thiolester bond

Query Match 24.7%; Score 22; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 DGSEKYY 11

Db 3 DGKEPQY 9

RESULT 15

A39233

myosin heavy chain 1, smooth muscle - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 13-Feb-1998

C;Accession: A39233

R;Kelley, C.A.; Adelstein, R.S.

J. Biol. Chem. 265, 17876-17882, 1990

A;Title: The 204-kDa smooth muscle myosin heavy chain is phosphorylated in intact cells

A;Reference number: A39233; MUID:91009254; PMID:2170399

A;Accession: A39233

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KEL>

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: smooth muscle

Query Match 24.7%; Score 22; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DGSEK 9

Db 6 DGSEE 10

Search completed: June 8, 2004, 19:07:36

Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:02:48 ; Search time 11 Seconds
(without alignments)
80.472 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDSEKYYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 943

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	31.5	10	1 SPI_HALRO	Q10997 halocynthia
2	25	28.1	15	1 FIBA_SYNCA	P14463 syncerus ca
3	23	25.8	16	1 AF2S_MALPA	P83142 malva parvi
4	22	24.7	10	1 UXA6_CHLPR	P38007 chlamydia t
5	22	24.7	17	1 B29K_PORGI	P81784 porphyromon
6	21	23.6	10	1 TKS2_AEDAE	P42635 aedes aegypt
7	21	23.6	11	1 TKND_RANCA	P22691 rana catesb
8	21	23.6	14	1 TKNM_RANWA	P40951 rana margar
9	20	22.5	14	1 CXAL_CONCN	P56973 conus conso
10	20	22.5	15	1 FIBA_ANAPL	P12801 anas platyr
11	20	22.5	15	1 PGTS_PELAC	P80564 pelobacter
12	19	21.3	10	1 TKNB_RANCA	P22689 rana catesb
13	19	21.3	11	1 NXSN_PSETE	P59072 pseudonaja
14	19	21.3	13	1 ADFB_TENMO	P83109 tenebrio mo
15	18.5	20.8	16	1 BRB_BASAL	P83187 basella alb
16	18.5	20.8	16	1 FIBA_MUSVI	P14458 mustela vis
17	18	20.2	9	1 FARD_CALVO	P41868 calliphora
18	18	20.2	13	1 ITB5_BOVIN	P80747 bos taurus
19	18	20.2	15	1 NXSO_PSETE	P59073 pseudonaja
20	18	20.2	16	1 CERB_RAT	P23436 rattus norv
21	17	19.1	10	1 TKN1_SCYCA	P08608 scyllorhinu
22	17	19.1	10	1 TKS1_AEDAE	P42634 aedes aegypt
23	17	19.1	11	1 TKNA_RANRI	P29207 rana ridibu
24	17	19.1	14	1 GLGS_SPIOL	P55235 spinacia ol
25	17	19.1	14	1 MV14_PHEVI	P46980 pheretima v
26	17	19.1	15	1 APF3_MALPA	P83137 malva parvi
27	17	19.1	16	1 RU6_VIBPR	Q56715 vibrio prot
28	16	18.0	8	1 TKS1_AEDAE	P42634 aedes aegypt
29	16	18.0	11	1 ASL2_BACSE	P83147 bacteroides
30	16	18.0	11	1 FAR9_CALVO	P41864 calliphora
31	16	18.0	11	1 TKN_PHYFU	P08615 physalaemus
32	16	18.0	14	1 FIBB_MANLE	P14474 mandrillus
33	16	18.0	14	1 RS19_PFWBP	Q52093 pigeon pea

34 16 18.0 15 1 ACBA_ACICA P28467 acinetobact
35 16 18.0 15 1 MILT_ONCKE P81037 oncornynchu
36 16 18.0 15 1 TRPA_LEUMA P81753 leucophaea
37 16 18.0 15 1 UC14_MAIZE P80620 zea mays (m
38 16 18.0 17 1 RM35_YEAST P36530 saccharomyc
39 15 16.9 4 1 E0S1_HUMAN P02731 homo sapien
40 15 16.9 7 1 LANC_CARUI P36960 carnobacter
41 15 16.9 9 1 FAR6_MACRS P83279 macrobrachi
42 15 16.9 9 1 LFCA_STAAT P36884 staphylococ
43 15 16.9 10 1 COXO_THUOB P80982 thunnus obe
44 15 16.9 10 1 PPCK_FASHE P80525 fasciola he
45 15 16.9 10 1 SP34_DICMU P81545 dictyosteli

ALIGNMENTS

RESULT 1
SPI_HALRO
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TSSUB=Hemolymph;
RC MEDLINE=96321313; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000-Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halocynthia
roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- SUBUNIT: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- FUNCTION: Monomer.
CC -!- SIMILARITY: Belongs to the serpin family.
DR INTERPRO: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NON TER 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 31.5%; Score 28; DB 1; Length 10;
Best Local Similarity 71.4%; Pred.No.59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KQDGEK 9
|:|:|
Db 2 KQDGEK 8

RESULT 2
FIBA_SYNCA
ID FIBA_SYNCA STANDARD; PRT; 15 AA.
AC P14463;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Syncerus caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Syncerus.
OX NCBI_TaxID=9970;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;

RA Doolittle R.F., Schubert D., Schwartz S.A.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 RT Dromedary camel, mule deer, and cape buffalo.";
 RL Arch. Biochem. Biophys. 118:456-467(1967).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;
 Query Match 28.1%; Score 25; DB 1; Length 15;
 Best Local Similarity 40.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 4 QDQSEKYAD 13
 :||| :| :|
 Db 1 EDGSGEFLAE 10
 RESULT 3
 AF2S_MALPA
 ID AF2S_MALPA STANDARD; PRT; 16 AA.
 AC P83142;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).
 OS Malva parviflora (little mallow) (Cheeseweed).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
 CC NCBI_TaxID=145753;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RX MEDLINE=20568734; PubMed=11118343;
 RA Wang X., Bunkers G.J.;
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva
 RT parviflora).";
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
 CC -1- FUNCTION: Possesses antifungal activity against P.infestans but
 CC not F.graminearum.
 CC -1- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9E8FB7EE65 CRC64;
 Query Match 25.8%; Score 23; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 KQDSEKY 10
 :| :| :|
 Db 6 KRDPQKY 13
 RESULT 4
 UXA6_CHLTR
 ID UXA6_CHLTR STANDARD; PRT; 10 AA.
 AC P38007;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 CC NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=L2/434/Bu;
 RA Bini D., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christensen G., Birkelund S., Vreton E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to Swiss-Prot.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
 DR Siena-2DPAGE; P38007; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;
 Query Match 24.7%; Score 22; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IKQDG 6
 :| :| :|
 Db 6 IKKDG 10
 RESULT 5
 B29K_PORGI
 ID B29K_PORGI STANDARD; PRT; 17 AA.
 AC P81784;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 29 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 CC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 CC Porphyromonadaceae; Porphyromonas.
 CC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VPB 3547;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 KW Antigen.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1756 MW; 383DE6AA14331AE0 CRC64;
 Query Match 24.7%; Score 22; DB 1; Length 17;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 12 ADSVRG 17
 :| :| :|
 Db 10 ADNVQG 15
 RESULT 6
 TKS2_AEDAE
 ID TKS2_AEDAE STANDARD; PRT; 10 AA.
 AC P42635;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sialokinin II.
 OS Aedes aegypti (Yellowfever mosquito).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 CC NCBI_TaxID=7159;
 RN [1]

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RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RL mosquito Aedes aegypti.";
CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC site of feeding.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B49581; B49581.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 9.6e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DGSEKYY 11
Db 1 DTGDKFY 7

RESULT 7
TKND_RANCA STANDARD; PRT; 11 AA.
ID TKND_RANCA
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RL brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595 (1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RL intestine.";
RL Regul. Pept. 46:81-88 (1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D61033; D61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKYIA 12

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Db 5 ERFYA 9

RESULT 8
TKNM_RANMA STANDARD; PRT; 14 AA.
ID TKNM_RANMA
AC P40951;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranamargarin.
OS Rana margaratae (Chinese frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=121156;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90026852; PubMed=2803524;
RA Tang Y.Q., Tian S.H., Wu S.X., Hua J.C., Wu G.F., Zhao E.M., Lu Y.A.,
RA Zhu Y.Q., Zou G., Tsou K.;
RT "Isolation and structure of ranamargarin, a new tachykinin from the
RL skin of Chinese frog Rana margaratae";
RL Sci. China, Ser. B, Chem. Life Sci. 32:570-579 (1989).
RN [2]
RP SYNTHESIS.
RX MEDLINE=90253600; PubMed=2340087;
RA Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Zou G.;
RT "Synthesis and biological activity of a new frog skin peptide,
RT ranamargarin.";
RL Sci. China, Ser. B, Chem. Life Sci. 33:170-177 (1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR02040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1617 MW; D4593AB408C3673D CRC64;

Query Match 23.6%; Score 21; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DGSEKYY 11
Db 5 DRAKKFY 11

RESULT 9
CXAL_CONCN STANDARD; PRT; 14 AA.
ID CXAL_CONCN
AC P56973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Cn1A [Contains: Alpha-conotoxin Cn1B].
OS Conus consors (Singed cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101297;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=99255390; PubMed=10320362;
RA Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,
RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,

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RA Lancelin J.-M.;
RT "Biochemical characterization and nuclear magnetic resonance
RT structure of novel alpha-conotoxins isolated from the venom of Conus
RT consors.";
RL Biochemistry 38:6317-6326(1999).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide seems to be a potent and selective
CC blocker of muscular subtype of nAChR.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A58963; A58963.
DR PDB; 1B45; 09-JUL-99.
RW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.
FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD RES 14 14 AMIDATION.
FT HELIX 6 8
FT TURN 9 10
SQ SEQUENCE 14 AA; 1548 MW; DEBE91969BF5E5BD CRC64;
Query Match 22.5%; Score 20; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 KYIA 12
Db |||:
10 KYIS 13
RESULT 10
FIBA ANAPL
ID FIBA ANAPL STANDARD; PRT; 15 AA.
AC P12801;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE.
RX MEDLINE=85168193; PubMed=3983613;
RA Min Y., Ping Z., Yaoshi Z.;
RT "Purification and primary structures of duck fibrinopeptides A and
RT B.";
RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; JP0101; JP0101.
RW Blood coagulation; Plasma; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1580 MW; D78A51FF88B40373 CRC64;
Query Match 22.5%; Score 20; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.2e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 QDGSEKY 10
Db |||:
1 QDGKSSF 7
RESULT 11
PGTS PELAC
ID PGTS PELAC STANDARD; PRT; 15 AA.
AC P80564;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase small subunit (EC 1.97.1.2)
DE (transhydroxylase) (fragment).
OS Pelobacter acidigallici.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
RT "One molecule of molybdopterine guanine dinucleotide is associated
RT with each subunit of the heterodimeric Mo-Fe-S protein
RT transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
RT and mass spectrometry.";
RL Eur. J. Biochem. 237:406-413(1996).
CC -1- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-
CC trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
CC tetrahydroxybenzene.
CC -1- COFACTOR: Molybdenum (molybdopterine).
CC -1- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR; S65429; S65429.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1843 MW; 0567BDD004C28499 CRC64;
Query Match 22.5%; Score 20; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 EKYY 11
Db |||:
2 EQYY 5
RESULT 12
TKNB RANCA
ID TKNB RANCA STANDARD; PRT; 10 AA.
AC P22689;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin B (RTK B).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N.; Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;

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RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RL intestine."
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B61033; B61033.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1210 MW; 9175556B59D5BAB5 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 YYADSVRG 17
Db 1 YKDSFYG 8

RESULT 13
NXSN PSFTE
ID NXSN PSFTE STANDARD; PRT; 11 AA.
AC P59072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
OS Pseudonaja textilis (Eastern brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=8673;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=venom;
RX MEDLINE=99449602; PubMed=10518793;
RA Gong N.L., Armugam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
RT cloning, expression and protein characterization."
RL Eur. J. Biochem. 265:982-989(1999).
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
CC acetylcholine receptors (nAChR).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake toxin.
DR PROSITE; PS00272; SNAKE TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE 3 3
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 21.3%; Score 19; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KYYADSV 15
Db 5 KGYRDTV 11

RESULT 14
ADFB_TENMO
ID ADFB_TENMO STANDARD; PRT; 13 AA.
AC P83109;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor B (ADFB).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
RA Hull J.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
RT antidiuretic peptide."
RL Peptides 24:27-34(2003).
CC -!- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC CGMP as second messenger. May function as an antidiuretic
CC hormone.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC pairs of bilaterally symmetrical cells in the protocerebrum.
CC -!- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
KW Neuropeptide; Hormone.
SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;

Query Match 21.3%; Score 19; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DGSEK 9
Db 3 DGSYK 7

RESULT 15
BRB_BASAL
ID BRB_BASAL STANDARD; PRT; 16 AA.
AC P83187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-asarubin (Fragment).
OS Basella alba (Malabar spinach) (Ceylon spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Basellaceae; Basella.
OX NCBI_TaxID=3589;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21547763; PubMed=11688973;
RA Wang H., Ng T.B.;
RT "Novel antifungal peptides from ceylon spinach seeds."
RL Biochem. Biophys. Res. Commun. 288:765-770(2001).
CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,
CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.
CC Inhibits HIV-1 reverse transcriptase and cell-free translation.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.
KW Fungicide.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1952 MW; 28F9FE4FC181682C CRC64;

Query Match 20.8%; Score 18.5; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 4.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

```

QY 9 KYYADSVRG 17
|:| : :||
Db 8 KFY-EQLRG 15

Search completed: June 8, 2004, 19:06:33
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 19:06:39 ; Search time 39 Seconds
(without alignments)
137.534 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDGESEKYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5061

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_kvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	16	2	P82597
2	25	28.1	12	6	Q9TRU9
3	25	28.1	14	4	Q16118
4	25	28.1	16	6	Q9TR18
5	24	27.0	15	4	Q9UC11
6	24	27.0	17	11	Q9QVA2
7	23	25.8	11	13	Q90WA2
8	23	25.8	13	6	Q7YR14
9	23	25.8	13	6	Q7YRD1
10	22	24.7	15	10	Q9S8V6
11	21	23.6	11	5	Q9UAR8
12	21	23.6	13	10	Q7X955
13	21	23.6	13	11	Q8CIW3
14	21	23.6	15	13	P83012
15	21	23.6	16	3	Q9UR86
16	21	23.6	16	10	Q9S8D6

17	21	23.6	16	15	Q8J699	Q8J699 human t-lym
18	21	23.6	16	15	Q8J6A6	Q8J6A6 human t-lym
19	21	23.6	16	15	Q8J6I4	Q8J6I4 human t-lym
20	21	23.6	16	15	Q8J6A1	Q8J6A1 human t-lym
21	21	23.6	16	15	Q8J6A3	Q8J6A3 human t-lym
22	21	23.6	16	15	Q8J697	Q8J697 human t-lym
23	21	23.6	16	15	Q8J6A0	Q8J6A0 human t-lym
24	21	23.6	16	15	Q8J6A5	Q8J6A5 human t-lym
25	21	23.6	16	15	Q8J6A2	Q8J6A2 human t-lym
26	21	23.6	16	15	Q8J696	Q8J696 human t-lym
27	21	23.6	16	15	Q8J698	Q8J698 human t-lym
28	21	23.6	16	15	Q8J6A4	Q8J6A4 human t-lym
29	21	23.6	17	10	P83182	P83182 hordeum vul
30	21	23.6	17	11	Q9QV51	Q9QV51 mus sp. 60
31	20	22.5	9	4	Q8IUJ5	Q8IUJ5 homo sapien
32	20	22.5	10	8	Q37103	Q37103 saccharomyc
33	20	22.5	10	12	Q83978	Q83978 influenzavi
34	20	22.5	10	12	Q86580	Q86580 simian para
35	20	22.5	14	2	Q54394	Q54394 streptomyce
36	20	22.5	15	4	Q9UBK0	Q9UBK0 homo sapien
37	20	22.5	15	10	Q9S8V7	Q9S8V7 triticum ae
38	20	22.5	15	10	Q9S8M9	Q9S8M9 raphanus sa
39	20	22.5	15	10	P82439	P82439 nicotiana t
40	20	22.5	17	2	Q46093	Q46093 campylobact
41	20	22.5	17	6	Q18774	Q18774 oryctolagus
42	20	22.5	17	7	Q9TNQ2	Q9TNQ2 homo sapien
43	20	22.5	17	11	Q80WD2	Q80WD2 mus sp. ha-
44	20	22.5	17	13	Q9PS50	Q9PS50 carassius a
45	19	21.3	11	15	Q85620	Q85620 moloney mur

ALIGNMENTS

RESULT 1

P82597	PRELIMINARY;	PRT;	16 AA.
ID	P82597		
AC	P82597;		
DT	01-OCT-2000 (TReMBLrel. 15, Created)		
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Thermotable monoacylglycerol lipase (MSLP) (24 kDa) (EC 3.1.1.23) (Fragment).		
DE	(Fragment).		
OS	Bacillus sp.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1409;		
RN	[1]		
RP	SEQUENCE.		
RC	STRAIN=H-257;		
RX	MEDLINE=20198254; PubMed=10731713;		
RA	Imamura S., Kitaura S.;		
RT	"Purification and characterization of a monoacylglycerol lipase from the moderately thermophilic Bacillus sp. H-257.";		
RL	J. Biochem. 127:419-425(2000).		
CC	FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY OCCURRING WITH 1-MONOLAURYLGLYCEROL.		
CC	ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.		
CC	SUBUNIT: MONOMER.		
CC	MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.		
CC	MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS OTHER BACTERIAL LIPASES.		
DR	GO: GO:0047372; F:acylglycerol lipase activity; IEA.		
DR	GO: GO:0016787; F:hydrolase activity; IEA.		
KW	Hydrolase.		
FT	NON TER		
SQ	SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;		

Query Match 30.3%; Score 27; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSEKYVAD 13
 : : : : :
 Db 9 GAFFVYAE 16

RESULT 2
 Q9TRU9 ID Q9TRU9 PRELIMINARY; PRT; 12 AA.
 AC Q9TRU9; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ENACTIN/NIDOGN, E/N (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92079440; PubMed=1745013;
 RA Katz A., Fish A.J., Kleppel M.M., Hagen S.G., Michael A.F.,
 RA Butkowski R.J.;
 RT "Renal extractin (nidogen): isolation, characterization and tissue
 RT distribution.";
 RL Kidney Int. 40:643-652(1991).
 DR PIR; A54315; A54315. 1
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1293 MW; 8F11F032FF12D5BA CRC64;

Query Match 28.1%; Score 25; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 DSVRG 17
 : : : : :
 Db 5 DSVRG 9

RESULT 3
 Q16118 ID Q16118 PRELIMINARY; PRT; 14 AA.
 AC Q16118;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Cyclic adenosine 3',5'-monophosphate response element binding protein
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94158910; PubMed=8114764;
 RA Waeber G., Meyer T.E., LeSieur M., Hermann H.L., Gerard N.,
 RA Habener J.H.;
 RT "Developmental stage-specific expression of cyclic adenosine 3',5'-
 RT monophosphate response element binding protein CREB during
 RT spermatogenesis involves alternative exon splicing.";
 RL Mol. Endocrinol. 7:1501-1501(1993).
 DR EMBL; S68577; AAB29985.2; --
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1698 MW; C42ECDBEE6B7CEB6 CRC64;

Query Match 28.1%; Score 25; DB 4; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKQDGE 8
 : : : : :
 Db 5 KQDVSE 11

RESULT 4
 Q9TR18 ID Q9TR18 PRELIMINARY; PRT; 16 AA.

AC Q9TR18; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HISTIOCYTE-secreted-factor (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96179491; PubMed=8603813;
 RA Satomi N., Haranaka R., Haranaka K.;
 RT "Purification, characterization and anti-tumor activity of a new
 RT cytokine, histiocyte-secreted-factor (HSF).";
 RL Int. J. Cancer 66:209-213(1996).
 SQ SEQUENCE 16 AA; 1905 MW; 35516B99C09B9436 CRC64;

Query Match 28.1%; Score 25; DB 6; Length 16;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 DGSEKYVA 12
 : : : : :
 Db 7 NGMEQHYA 14

RESULT 5
 Q9UCI1 ID Q9UCI1 PRELIMINARY; PRT; 15 AA.

AC Q9UCI1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Tropomyosin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93195352; PubMed=8450225;
 RA Das K.M., Dasgupta A., Mandal A., Geng X.;
 RT "Autoimmunity to cytoskeletal protein tropomyosin. A clue to the
 RT pathogenetic mechanism for ulcerative colitis.";
 RL J. Immunol. 150:2487-2493(1993).
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF00261; Tropomyosin; 1.
 SQ SEQUENCE 15 AA; 1802 MW; 7A0993CA5A54254C CRC64;

Query Match 27.0%; Score 24; DB 4; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NTKQDGSERY 10
 : : : : :
 Db 1 HIAEDADRV 10

RESULT 6
 Q9QVA2 ID Q9QVA2 PRELIMINARY; PRT; 17 AA.

AC Q9QVA2; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Protein kinase C substrate PF80 (Fragment).
 OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=93099617; PubMed=1464108;
RA Komatsu S., Hirano H.;
RT "80 kDa mouse sperm protein as a substrate of protein kinase C.";
RL Chem. Pharm. Bull. 40:2780-2782(1992).
SQ SEQUENCE 17 AA; 2025 MW; B8272D8940BD0B41 CRC64;

Query Match 27.0%; Score 24; DB 11; Length 17;
Best Local Similarity 45.5%; Pred. No. 4.7e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 SEKYYADSVRG 17
Db |||||
5 SEKVFXKLEG 15

RESULT 7
Q90WA2 PRELIMINARY; PRT; 11 AA.
AC Q90WA2

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Extracellular fatty acid binding protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Blood;
RA Wang Q., Li N., Deng X., Li H.;
RT "Single Nucleotide Polymorphism Analysis on Encoding Region of
RT Extracellular Fatty Acid Binding Protein Genes and Their Associations
RT With the Fatness Trait in Chicken.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF402001; AAK34062.1; -.
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1277 MW; 873417F02B187AAA CRC64;

Query Match 25.8%; Score 23; DB 13; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DGSEKYA 12
Db |||||
4 DDGELYYS 11

RESULT 8
Q7YR14 PRELIMINARY; PRT; 13 AA.
AC Q7YR14

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Estrogen receptor alpha (Fragment).
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

RA Szedler T., Zwierzchowski L.;
RT "5' region of bovine estrogen receptor alpha.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY332655; AAP92821.1; -.
KW Receptor.
FT NON TER 13
SQ SEQUENCE 13 AA; 1493 MW; 83F58EC3EB88E735 CRC64;

Query Match 25.8%; Score 23; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 SEKYYADSVR 16
Db ::::|
4 TKSLHSDSVR 13

RESULT 9
Q7YRD1 PRELIMINARY; PRT; 13 AA.
AC Q7YRD1

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Estrogen receptor alpha (Fragment).
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE FROM N.A.

RA Szedler T., Zwierzchowski L.;
RT "5' region of Bison bonasus estrogen receptor alpha.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY340597; AAQ15294.1; -.

FT NON TER 13
SQ SEQUENCE 13 AA; 1493 MW; 83F58EC3EB88E735 CRC64;

Query Match 25.8%; Score 23; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 SEKYYADSVR 16
Db ::::|
4 TKSLHSDSVR 13

RESULT 10
Q988V6 PRELIMINARY; PRT; 15 AA.
AC Q988V6

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE High-molecular-weight glutenin subunit (Fragment).
OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE.

RX MEDLINE=93003354; PubMed=1390908;
RA Tao H.P., Adalsteins A.E., Kasarda D.D.;
RT "Intermolecular disulfide bonds link specific high-molecular-weight
RT glutenin subunits in wheat endosperm.";
RL Biochim. Biophys. Acta 1159:13-21(1992).
SQ SEQUENCE 15 AA; 1649 MW; 29DBF77EBSA51F0D CRC64;

Query Match 24.7%; Score 22; DB 10; Length 15;
Best Local Similarity 44.4%; Pred. No. 8.8e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSEKYYADS 14

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Db          5 GQQGYPTS 13
| : || |
| : || |

RESULT 11
Q9UAR8
ID QUAR8 PRELIMINARY; PRT; 11 AA.
AC QUAR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sialokinin I preproprotein (Fragment).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX MEDLINE=2009025; PubMed=10620041;
RA Beertsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
RT "Characterization of the Sialokinin I gene encoding the salivary
RT vasodilator of the yellow fever mosquito, Aedes aegypti.";
RL Insect Mol. Biol. 8:459-467(1999).
DR EMBL; AF1081100; AAD16884.1; -.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
FT NON_TER 1
FT SEQUENCE 11 AA; 1203 MW; 8BADCF77C6B59C33A CRC64;

Query Match 23.6%; Score 21; DB 5; Length 11;
Best Local Similarity 42.9%; Pred. No. 9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGSEKY 11
| : || |
| : || |
Db 1 DTGDFY 7

RESULT 12
Q7X955
ID Q7X955 PRELIMINARY; PRT; 13 AA.
AC Q7X955;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Agamous-like protein (Fragment).
GN AGAMOUS.
OS Capsella bursa-pastoris (Shepherd's purse).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Capsella.
OX NCBI_TaxID=3719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22667639; PubMed=12782724;
RA Hong R.L., Hamaguchi L., Busch M.A., Weigel D.;
RT "Regulatory Elements of the Floral Homeotic Gene AGAMOUS Identified by
RT Phylogenetic Footprinting and Shadowing.";
RL Plant Cell 15:1296-1309(2003).
DR EMBL; AY254701; AAP35235.1; -.
FT NON_TER 1
FT NON_TER 13
FT SEQUENCE 13 AA; 1498 MW; 10D0802C01A9B444 CRC64;

Query Match 23.6%; Score 21; DB 10; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 KYADSVRG 17
| : || |
| : || |

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Db          3 EYSNNSVKG 11
| : || |
| : || |

RESULT 13
Q8CIW3
ID Q8CIW3 PRELIMINARY; PRT; 13 AA.
AC Q8CIW3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MORF4-related protein (Fragment).
GN MORF411 OR TEXI89.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RX MEDLINE=22220132; PubMed=12234683;
RA Tominaga K., Pereira-Smith O.;
RT "The genomic organization, promoter position and expression profile of
RT the mouse MRG15 gene.";
RL Gene 294:215-215(2002).
DR EMBL; AY072694; AAL67900.1; -.
DR MGD; MGI:1096551; Morf411.
FT NON_TER 13
FT NON_TER 13
FT SEQUENCE 13 AA; 1544 MW; 9B0B3B837D5A276A CRC64;

Query Match 23.6%; Score 21; DB 11; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KQDGSKY 10
| : || |
| : || |
Db 4 KQDPKPKF 11

RESULT 14
P83012
ID P83012 PRELIMINARY; PRT; 15 AA.
AC P83012;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome C oxidase polypeptide VA, mitochondrial (EC 1.9.3.1)
DE (Fragment).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Rectal gland;
RC Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.;
RT "Phospholipase in the rectal gland of sharks.";
RL Submitted (JUN-2001) to Swiss-Prot.
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC -1- FERRECYTOCHROME C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0009481; F:a3-type cytochrome c oxidase; IEA.
DR GO; GO:0009482; F:b3-type cytochrome c oxidase; IEA.
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
DR GO; GO:0009485; F:cb3-type cytochrome c oxidase; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.

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DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1720 MW; 937518D7590B35C5 CRC64;

Query Match 23.6%; Score 21; DB 13; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 QDQSEKYYAD 13
Db 4 KQETDEEFDAN 14

RESULT 15
Q9UR86 PRELIMINARY; PRT; 16 AA.
AC Q9UR86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Class I cytochrome C isoform A (Fragment).
OS Candida parapsilosis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5480;
RN [1]
RP SEQUENCE.
RX MEDLINE=93305688; PubMed=8391313;
RA Camougrand N.; Velours J.; Denis M.; Guerin M.;
RT "Isolation, characterization and function of the two cytochromes c of
RT the yeast Candida parapsilosis.";
RL Biochim. Biophys. Acta 1143:135-141(1993).
SQ SEQUENCE 16 AA; 1646 MW; 762F64F875F237B CRC64;

Query Match 23.6%; Score 21; DB 3; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QDQSEK 9
Db 5 EKGSEK 10

Search completed: June 8, 2004, 19:12:09
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:56:22 ; Search time 20 Seconds
(without alignments)
24.048 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	51.6	5	A32516	cholecystokinin-5
2	14	45.2	5	JH0253	gut pentapeptide -
3	13	41.9	5	PT0308	Ig heavy chain CRD
4	13	41.9	5	PT0580	T-cell receptor be
5	12	38.7	5	PT0729	T-cell receptor be
6	11	35.5	3	F37196	bradykinin-potenti
7	11	35.5	4	A37832	phenol 2-monooxyge
8	11	35.5	4	A34626	RPCH-related neuro
9	11	35.5	4	B53284	T-cell receptor be
10	11	35.5	4	PT0661	T-cell receptor be
11	11	35.5	5	I40469	dnaxX-like protein
12	11	35.5	5	A60803	neuropeptide - sea
13	11	35.5	5	G37196	bradykinin-potenti
14	11	35.5	5	PT0281	Ig heavy chain CRD
15	9	29.0	3	I50412	gene p20K protein
16	9	29.0	5	S70154	URF2 protein - kan
17	9	29.0	5	B37325	pap fibroblast regul
18	9	29.0	5	A37114	hypoxanthine phosph
19	8	25.8	5	E60274	major protein anti
20	8	25.8	5	PT0278	Ig heavy chain CRD
21	8	25.8	5	S68326	blood cell protein
22	7	22.6	3	A22565	R-phycoerythrin al
23	7	22.6	3	A33391	TRH-like tripeptid
24	7	22.6	3	S68328	blood cell protein
25	7	22.6	4	A32039	tyrosine-melanocyt
26	7	22.6	4	I61883	protamine p1 - ora
27	7	22.6	4	PT0240	Ig heavy chain CRD
28	7	22.6	4	S43959	Ig mu chain v regi
29	7	22.6	4	I37013	protamine p1 - Cer

ALIGNMENTS

RESULT 1

A32516

cholecystokinin-5 - dog

N:Alternate names: CCK-5

C:Species: Canis lupus familiaris (dog)

C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C:Accession: A32516

R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.

Am. J. Physiol. 252, G272-G275, 1987

A>Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest

A:Reference number: A32516; MUID:87153871; PMID:3826354

A:Accession: A32516

A:Molecule type: protein

A:Residues: 1-5 <SH1>

C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystol

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; neuropeptide

F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 51.6%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WM 4

DB 2 WM 3

RESULT 2

JH0253

gut pentapeptide - Japanese eel

C:Species: Anguilla japonica (Japanese eel)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995

C:Accession: JH0253

R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 828-832, 1991

A>Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A:Reference number: JH0253; MUID:92062113; PMID:1953755

A:Accession: JH0253

A:Molecule type: protein

A:Residues: 1-5 <UES>

A:Experimental source: gut

C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric

, and of the circular muscle of the gastro-intestinal junction.

Query Match 45.2%; Score 14; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3

DB 2 FW 3

```
RESULT 3
PT0308
IG heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match      41.9%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 WMS 5
Db      2 WES 4

RESULT 4
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      41.9%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SYW 3
Db      2 SSW 4

RESULT 5
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0640; PT0685; PT0729
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0640
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Accession: PT0685
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
```

```
A;Accession: PT0729
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor

Query Match      38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SYW 3
Db      3 SDW 5

RESULT 6
F37196
bradykinin-potentiating peptide 6 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: F37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: F37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      35.5%; Score 11; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 W 3
Db      3 W 3

RESULT 7
A37832
Phenol 2-monoxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
C;Species: Pseudomonas sp.
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
C;Accession: A37832
R;Powlowski, J.; Shingler, V.
J. Bacteriol. 172, 6834-6840, 1990
A;Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase
A;Reference number: A37832; MUID:91072231; PMID:2254259
A;Accession: A37832
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <POW>
C;Keywords: oxidoreductase

Query Match      35.5%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SY 2
Db      1 SY 2

RESULT 8
A34626
RPGH-related neuropeptide - ferruginous spindle
C;Species: Fuscus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
```


R.Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
 Biochem. Biophys. Res. Commun. 167, 273-279, 1990
 A>Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
 A;Reference number: A34626; MUID:90179762; PMID:2310394
 A;Accession: A34626
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <KUR>
 C;Keywords: neuropeptide

Query Match 35.5%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0;

QY 3 W 3
 |
 Db 4 W 4

RESULT 9
 B53284
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C;Accession: B53284
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
 Mol. Immunol. 28, 881-888, 1991

A>Title: Evolutionarily conserved organization and sequences of germline diversity and J
 A;Reference number: A53284; MUID:91342695; PMID:1678859
 A;Accession: B53284
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-4 <HAR>
 A;Cross-references: GB:S60737; NID:g233916; PIDN:AA819518.1; PID:g233918
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
 C;Keywords: T-cell receptor

Query Match 35.5%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0;

QY 3 W 3
 |
 Db 2 W 2

RESULT 10
 PT0661
 T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0661
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0661
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 4 postnatal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 35.5%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0;

QY 3 W 3
 |
 Db 3 W 3

RESULT 11

I40469
 dnazx-like protein - Bacillus subtilis (fragment)
 C;Species: Bacillus subtilis
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
 C;Accession: I40469
 R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
 Mol. Gen. Genet. 215, 478-482, 1989
 A>Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
 A;Reference number: I40469; MUID:89218958; PMID:2468993
 A;Accession: I40469
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-5 <RES>
 A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204
 C;Genetics:
 A;Start codon: GTG

Query Match 35.5%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0;

QY 1 SY 2
 ||
 Db 2 SY 3

RESULT 12
 A60803
 neuropeptide - sea anemone (Anthopleura elegantissima)
 C;Species: Anthopleura elegantissima
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: A60803
 R;Graff, D.; Grimmelikhuijzen, C.J.P.
 Brain Res. 442, 354-358, 1988
 A>Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.
 A;Reference number: A60803; MUID:88222764; PMID:2897223
 A;Accession: A60803
 A;Molecule type: protein
 A;Residues: 1-5 <GRA>
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 35.5%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0;

QY 3 W 3
 |
 Db 5 W 5

RESULT 13
 G37196
 bradykinin-potentiating peptide 7 - island jararaca
 C;Species: Bothrops insularis (island jararaca)
 C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
 C;Accession: G37196
 R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
 J. Protein Chem. 9, 221-227, 1990
 A>Title: Primary structure and biological activity of bradykinin potentiating peptides fr
 A;Reference number: A37196; MUID:90351557; PMID:2386615
 A;Accession: G37196
 A;Status: preliminary
 A;Molecule type: Protein
 A;Residues: 1-5 <GIN>
 C;Keywords: pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 35.5%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0;

QY 3 W 3
Db 3 W 3

RESULT 14

PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
Db 4 W 4

RESULT 15

I50412
Gene p20K protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: I50412
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
J. Biol. Chem. 268, 8131-8139, 1993
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
A;Reference number: A46643; MUID:93216790; PMID:8463325
A;Accession: I50412
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3 <MAO>
A;Cross-references: GB:I02537; NID:g212616; PID:g212617
C;Genetics:
A;Gene: p20K

Query Match 29.0%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MS 5
Db 1 MS 2

Search completed: June 8, 2004, 18:59:40
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:53:05 ; Search time 11 Seconds
(without alignments)
23.668 Million cell updates/sec

Title: US-09-610-118-61
Perfect score: 31
Sequence: 1 SYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	38.7	5	1 UF01_MOUSE	P38639 mus musculus
2	11	35.5	4	1 OCP3_OCTMI	P58649 octopus min
3	11	35.5	5	1 BPF7_BOTIN	P30425 bothrops in
4	7	22.6	4	1 FAR3_HIRME	P42562 hirudo medi
5	7	22.6	4	1 FAR4_HIRME	P42563 hirudo medi
6	7	22.6	4	1 FYRI_ATEL	P58706 anthopleura
7	7	22.6	5	1 AL14_CARNA	P81817 carcinus ma
8	7	22.6	5	1 FARP_ARTTR	P41853 artiopesthi
9	7	22.6	5	1 PRCT_PERRAM	P01373 periphaneta
10	7	22.6	5	1 PSK_DAUCA	P58261 daucus caro
11	6	19.4	4	1 DCM5_PSECH	P19918 pseudomonas
12	6	19.4	4	1 FNRF_MACNI	P01162 macrocallis
13	6	19.4	5	1 B10A_CITR	P13071 citrobacter
14	6	19.4	5	1 B10B_CITR	P12997 citrobacter
15	5	16.1	4	1 DCM1_PSECH	P19916 pseudomonas
16	5	16.1	5	1 E103_LITRU	P82099 litorea rub
17	4	12.9	4	1 E051_HUMAN	P02731 homo sapien
18	4	12.9	4	1 FKKA_ATEL	P58705 anthopleura
19	4	12.9	4	1 RM01_YEAST	P36515 saccharomyc
20	4	12.9	5	1 PAP2_PARMA	P81864 pardachirus
21	4	12.9	5	1 RE11_LITRU	P82070 litorea rub
22	4	12.9	5	1 RE21_LITRU	P82071 litorea rub
23	4	12.9	5	1 RE31_LITRU	P82072 litorea rub
24	4	12.9	5	1 RE32_LITRU	P82073 litorea rub
25	4	12.9	5	1 UC22_MAI2E	P80628 zea mays (m
26	4	12.9	5	1 UXA4_CHLFR	P38005 chlamydia t
27	3	9.7	4	1 ACH1_ACHFU	P35904 achatina fu
28	3	9.7	4	1 FLRF_HIRME	P42561 hirudo medi
29	3	9.7	4	1 FLRN_ATEL	P58707 anthopleura
30	3	9.7	4	1 OCP1_OCTMI	P58648 octopus min
31	3	9.7	5	1 E104_LITRU	P82100 litorea rub
32	3	9.7	5	1 SUGA_ACHDO	P19991 acheta dome
33	3	9.7	5	1 TPIS_CANFA	P54714 canis famli

34 2 6.5 3 1 GRWM_HUMAN P01157 homo sapien
35 2 6.5 3 1 THYL_PIG P01151 sus scrofa
36 1 3.2 3 1 LUXE_VIBFI P24272 vibrio fisc
37 1 3.2 4 1 TUFT_HUMAN P01858 homo sapien
38 1 3.2 5 1 TRM3_ECOLI P13973 escherichia

ALIGNMENTS

RESULT 1
UF01_MOUSE
ID UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=9500907; Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 38.7%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 WM 4
DB 1 WI 2

RESULT 2
OCP3_OCTMI
ID OCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain.
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 35.5%; Score 11; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
 |
 Db 3 W 3

RESULT 3
 ID BP7 BOTIN STANDARD; PRT; 5 AA.
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 CC NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
 RL J Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.
 CC PIR; G37196; G37196.
 DR Hypotensive agent; Pyrrolidone carboxylic acid.
 KW MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
 SQ

Query Match 35.5%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
 |
 Db 3 W 3

RESULT 4
 ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuroptide YMRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 CC NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamidae neuroptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
 CC Neuropeptide; Amidation.
 KW MOD RES 4 4 AMIDATION.
 FT SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 SQ

Query Match 22.6%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 |
 Db 1 Y 1

RESULT 5
 ID FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuroptide YMRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 CC NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamidae neuroptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
 CC Neuropeptide; Amidation.
 KW MOD RES 4 4 AMIDATION.
 FT SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
 SQ

Query Match 22.6%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 |
 Db 1 Y 1

RESULT 6
 ID FVRI_ANTEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-Riamide I [Contains: Antho-Riamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
 CC Nynanthae; Actiniidae; Anthopleura.
 CC NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nethacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuroptides from sea anemones: the unusual, biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its des-phenylactyl fragment Tyr-Arg-Ile-NH2.";
 RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nethacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuroptides, Antho-KAamide and Antho-Riamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding

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CC CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
KW Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 Y 2
Db 2 Y 2

RESULT 7
AL14 CARMA STANDARD; PRT; 5 AA.
AC P81617;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestri J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5 AMIDATION (POTENTIAL).
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 Y 2
Db 1 Y 1

RESULT 8
FARP ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE FMRamide-like neuropeptide RYRFP-amide.
OS Artiposthia triangulata (New Zealand flatworm).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYRFPamide: a turbellarian FMRamide-related peptide (FARP).";

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RL Regul. Pept. 50:37-43(1994).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 Y 2
Db 2 Y 2

RESULT 9
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT_PERAM
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978; 6850; 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872561;
RX MEDLINE=86232789; PubMed=2356151;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility.
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons and in
CC the crab pericardial organs.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

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Query Match 22.6%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 Db 2 Y 2

RESULT 10
 PSK DAUCA
 ID PSK DAUCA STANDARD; PRT; 5 AA.
 AC P58261;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)]
 DE Daucus
 OS Daucus carota (Carrot)
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Daucinae;
 OC Daucus.
 OX NCBI_TaxID=4039;
 RN [1]
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
 RC STRAIN=cv. US-Harumakigosun;
 RX MEDLINE=20212743; PubMed=10750705;
 RA Hanai H., Matsumoto T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
 RA Kanada H., Sakagami Y.;
 RT "A secreted peptide growth factor, phytosulfokine, acting as a
 RT stimulatory factor of carrot somatic embryo formation."
 RL Plant Cell Physiol. 41:27-32(2000).
 CC -1- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
 CC cells, but does not stimulate differentiation into the somatic
 CC embryos.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Sulfation is important for activity and for the binding to a
 CC putative membrane receptor (By similarity).
 CC -1- SIMILARITY: Belongs to the phytosulfokine family.
 KW Growth factor; Sulfation.
 FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
 FT MOD RES 1 1 SULFATION.
 FT MOD RES 3 3 SULFATION.
 SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 Db 1 Y 1

RESULT 11
 DCMS PSECH
 ID DCMS PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE
 RC Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RX MEDLINE=90055678; PubMed=2818128;

Query Match 19.4%; Score 6; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MS 5
 Db 1 MA 2

RESULT 12
 FMRP MACNI
 ID FMRP MACNI STANDARD; PRT; 4 AA.
 AC P01162;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FMRamide (Peak C) (Cardioexcitatory neuropeptide).
 OS Macrocaltista nimosa (Sun-ray clam),
 OS Nereis virens (Sandworm),
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OS Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Macrocallista.
 OX NCBI_TaxID=6594, 6353, 6421, 27815;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC SPECIES=M.nimosa; TISSUE=Cerebral pedal, and Visceral ganglion;
 RX MEDLINE=77215956; PubMed=877582;
 RA Price D.A., Greenberg M.J.;
 RT "Structure of a molluscan cardioexcitatory neuropeptide."
 RL Science 197:670-671(1977).
 RN [2]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC SPECIES=M.nimosa; TISSUE=Ganglion;
 RX MEDLINE=78012038; PubMed=909875;
 RA Price D.A., Greenberg M.J.;
 RT "Purification and characterization of a cardioexcitatory neuropeptide
 RT from the central ganglia of a bivalve mollusc."
 RL Prep. Biochem. 7:261-281(1977).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=N.virens;
 RX MEDLINE=90259866; PubMed=2342992;
 RA Krajniak K.G., Price D.A.;
 RT "Authentic FMRamide is present in the polychaete Nereis virens."
 RL Peptides 11:75-77(1990).
 RN [4]
 RP SEQUENCE
 RC SPECIES=H.medicinalis;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 RN [5]
 RP SEQUENCE
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;

RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydrotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: Binds 2 2Fe-2S clusters.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; P01146; P01146.
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
 FT NON TER 4 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD3DD6F00000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MS 5
 Db 1 MA 2

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RT "FMRPamide-related peptides from the kidney of the snail, Helisoma
RL trivolvis";
CC Peptides 15:31-36(1994).
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
CC activities include augmentation, induction, and regularization of
CC cardiac contraction.
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WM 4
Db 1 FM 2

RESULT 13
BIOA CITFR
ID BIOA CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
-----
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EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; 140697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON-TER 5 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MS 5
Db 1 MA 2

RESULT 14
BIOB CITFR
ID BIOB CITFR STANDARD; PRT; 5 AA.
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN BIOB.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -!- PATHWAY: Biotin biosynthesis; last step.
CC -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC family.
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EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; 140698; I40698.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON-TER 5 5
SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MS 5
Db 1 MA 2

RESULT 15
DCML PSECH
ID DCML PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTH.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;

```

RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydophilic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR: PL0140; PL0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;

Query Match 16.1%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 M 4
|
Db 1 M 1

Search completed: June 8, 2004, 18:57:50
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:54:42 ; Search time 39 Seconds
(without alignments)
40.451 Million cell updates/sec

Title: US-09-610-118-61
Perfect score: 31
Sequence: 1 SYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	SUMMARIES		Description
		Query Match	Length DB ID	
1	11	35.5	2 5	P83570
2	6	19.4	5 10	Q99007 hordeum vul
3	5	16.1	4 5	P83568 sepia offic
4	5	16.1	5 2	P83073 bacillus ce
5	3	9.7	5 13	P83308 gallus gall
6	2	6.5	4 11	Q08433 rattus sp.

ALIGNMENTS

RESULT 1
P83570
ID P83570 PRELIMINARY; PRT; 2 AA.
AC P83570;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX PubMed=9437704;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trip-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis.";
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -1- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY
CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT
CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 2
FT MOD_RES 2
SQ SEQUENCE 2 AA; 261 MW; 73781000000000000000 CRC64;

Query Match 35.5%; Score 11; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 W 3
Db 2 W 2

RESULT 2
Q99007
ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN AMY1 GENE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91329704; PubMed=1831055;
RX Jacobsen J.V., Close T.J.;
RA "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers.";
RT Plant Mol. Biol. 16:713-721(1991).
RL EMBL; X54643; CAA38455.1; -.
FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F000000 CRC64;

Query Match 19.4%; Score 6; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MS 5
Db 1 MA 2

RESULT 3
P83568
ID P83568 PRELIMINARY; PRT; 4 AA.
AC P83568;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Phormone peptide ILMB.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Egg;
 RX PubMed=10944467;
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "ILMB: a waterborne pheromonal peptide released by the eggs of Sepia
 RT officinalis.";
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RN [2]
 RN SEQUENCE.
 RC TISSUE=Egg;
 RX PubMed=12207899;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 RT attracting peptide.";
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: FOLLICULAR, FULLY GROWN OOCYTE AND EGG(EC2).
 CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
 DR GO; GO:0005186; F:pheromone activity; IEA.
 KW Pheromone.
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

 Query Match 16.1%; Score 5; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 M 4
 Db 3 M 3

 RESULT 4
 P83073
 ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RN SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to Swiss-Prot.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

 Query Match 16.1%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0;

 QY 4 M 4
 Db 1 M 1

 RESULT 5
 P83308
 ID P83308 PRELIMINARY; PRT; 5 AA.

AC P83308;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PMRFamide-like neuropeptide (LFLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to PMRFamide.";
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 5
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

 Query Match 9.7%; Score 3; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 2 Y 2
 Db 5 F 5

 RESULT 6
 Q08433
 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Gunn.
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
 RT "Genetic defect of Bilirubin UDP-glucuronosyltransferase in the
 RT hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL; S38636; AAB19259.1; .
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

 Query Match 6.5%; Score 2; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 4 M 4
 Db 3 L 3

 Search completed: June 8, 2004, 18:58:31
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:49:26 ; Search time 53 Seconds
(without alignments)
26.655 Million cell updates/sec

Title: US-09-610-118-61
Perfect score: 31
Sequence: 1 SYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 34717

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	4 AAB61293	Aab61293 Anti-TANG
2	31	100.0	5	6 ABU11259	Abu11259 Human TAN
3	28	90.3	5	2 AAR85499	Aar85499 ScFv(FWP5
4	28	90.3	5	2 AAR97316	Aar97316 Humanised
5	28	90.3	5	2 AAY05038	Aay05038 Tumour an
6	28	90.3	5	5 ABB07357	Abb07357 22A5 IgM
7	28	90.3	5	5 AAO17609	Aao17609 Human FAP
8	28	90.3	5	7 ADC82794	Adc82794 CDR regio
9	27	87.1	5	2 AAR74929	Aar74929 H-CDR-1 o
10	27	87.1	5	2 AAW83024	Aaw83024 Anti-Fas
11	27	87.1	5	2 AAY05045	Aay05045 Tumour an
12	27	87.1	5	3 AAB14741	Aab14741 Mouse ant
13	27	87.1	5	3 AAW90891	Aaw90891 Murine an
14	27	87.1	5	3 AAY32257	Aay32257 Light cha
15	27	87.1	5	3 AAY92158	Aay92158 Murine 15
16	27	87.1	5	3 AAB19754	Aab19754 Erythrope
17	27	87.1	5	4 AAB61281	Aab61281 Anti-TANG
18	27	87.1	5	5 ABB74906	Abb74906 Humanised
19	27	87.1	5	5 AAU11183	Aau11183 Mouse ant
20	27	87.1	5	5 AAU75739	Aau75739 Anti-(MCP
21	27	87.1	5	5 ABB74860	Abb74860 Humanised
22	27	87.1	5	6 ABU11247	Abu11247 Human TAN
23	27	87.1	5	7 ADC82808	Adc82808 CDR regio
24	25	80.6	5	2 AAW23429	Aaw23429 CDR-1 of
25	25	80.6	5	2 AAW93474	Aaw93474 mAK TTC8

26	24	77.4	4	5	AAE22200	Aae22200 Murine MC
27	24	77.4	5	2	AAR74931	Aar74931 H-CDR-1 o
28	24	77.4	5	2	AAR75482	Aar75482 Mouse ant
29	24	77.4	5	2	AAW24546	Aaw24546 CDR #1 of
30	24	77.4	5	2	AAW44181	Aaw44181 Monoclonal
31	24	77.4	5	4	AAB62861	Aab62861 Anti-SAF-
32	24	77.4	5	6	ABR63615	Abr63615 Human gly
33	24	77.4	5	7	ADC17604	Adc17604 Type IV c
34	24	77.4	5	7	ADC17609	Adc17609 Type IV c
35	24	77.4	5	7	ADC17612	Adc17612 Type IV c
36	24	77.4	5	7	ADC97705	Adc97705 Mouse mon
37	23	74.2	5	2	AAR62882	Aar62882 Murine an
38	23	74.2	5	2	AAW70923	Aaw70923 CDR1 of t
39	23	74.2	5	2	AAW62192	Aaw62192 Mouse ant
40	23	74.2	5	2	AAW57588	Aaw57588 Chimeric
41	23	74.2	5	2	AAV02550	Aav02550 Artificia
42	23	74.2	5	2	AAW89632	Aaw89632 Mouse hum
43	23	74.2	5	3	AAV77518	Aav77518 Antibody
44	23	74.2	5	3	AAV80139	Aav80139 Chimeric
45	23	74.2	5	3	AAB12174	Aab12174 Human CDR

ALIGNMENTS

RESULT 1
AAB61293
ID AAB61293 standard; peptide; 5 AA.

XX AAB61293;

XX AC AAB61293;

XX DT 04-APR-2001 (first entry)

XX DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 61.

XX KW Human; antibody; scFv; CDR; complementarity determining region;
XX TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
XX thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX platelet membrane glycoprotein receptor; bleeding disorder;
XX blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX cancer.

XX OS Homo sapiens.

XX PN WO200100810-A1.

XX PD 04-JAN-2001.

XX PF 30-JUN-2000; 2000WO-US018152.

XX PR 30-JUN-1999; 99US-00345468.

XX PR 06-DEC-1999; 99US-00454824.

XX PR 14-FEB-2000; 2000US-00503387.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ, Villedel J, Jandrot-Perrus M, Vainchenker W;

XX PL Gill DS, Qian MD, Kingsbury G;

XX DR WPI; 2001-080877/09.

XX PT New genes encoding human platelet-expressed collagen receptor,
XX glycoprotein VI, and its modulators, useful for preventing, treating and
XX diagnosing hemorrhagic disorders, thrombotic diseases and immunological
XX disorders.

XX PS Claim 31; Page 102; 227pp; English.

XX CC The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 XX Sequence 5 AA;

Query Match 100.0%; Score 31; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 1 SYWMS 5

RESULT 2

ABU11259
 ID ABU11259 standard; peptide; 5 AA.

XX AC ABU11259;

XX 06-FEB-2003 (first entry)

XX Human TANGO 268 VHCDRI Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Disclosure; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology, platelets,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 XX Sequence 5 AA;

Query Match 100.0%; Score 31; DB 6; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 1 SYWMS 5

RESULT 3

AAR85499

ID AAR85499 standard; peptide; 5 AA.

XX AC AAR85499;

XX 16-MAR-1996 (first entry)

XX ScFv(FWP51) CDR1H.

XX Single chain antibody; scFv; antibody engineering; antitumour;
 KW tumour antigen binding; cytotoxic T-lymphocyte; cell targeting;
 KW monoclonal antibody; cancer; adoptive immunotherapy;
 KW complementarity determining region; CDR.

XX Synthetic.

XX WO9530014-A1.

XX 09-NOV-1995.

XX 20-APR-1995; 95WO-EP001494.

XX 02-MAY-1994; 94EP-00810244.

XX (CIBA) CIBA GEIGY AG.

XX Groner B, Moritz D;

XX WPI; 1995-393085/50.

XX New bifunctional proteins for use in killing tumour cells - contg. a
 PT tumour antigen binding domain, a hinge region and a zeta chain derived
 PT from a T-cell antigen receptor.

XX Disclosure; Page 6; 46pp; English.

XX Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H

CC (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components of
CC the heavy chain variable region and light chain variable region,
CC respectively, of single chain antibody scFv (FWP51) (AAR85495). The CDRs
CC are derived from mouse monoclonal antibody FWP51 (ECACC 90112118)
CC directed to the human growth factor receptor HER2. The scFv is used as
CC the tumour antigen binding domain of a bifunctional protein that is
CC expressed in cytotoxic T-lymphocytes (CTLs), allowing adoptive
CC immunotherapy of cancer
XX
SQ Sequence 5 AA;

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 1 SYWMS 5

RESULT 4
AAR97316
ID AAR97316 standard; peptide; 5 AA.

XX AC AAR97316;

XX DT 15-OCT-1996 (first entry)

XX DE Humanised monoclonal antibody heavy chain CDR.

XX KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
XX complementary determining region; anti-carcinoembryonic antigen; CEA;
XX diagnosis; imaging; therapy; immune response.

XX OS Mus musculus.

XX PN WO9611013-A1.

XX PD 18-APR-1996.

XX PF 28-SEP-1995; 95WO-US011964.

XX PR 05-OCT-1994; 94US-00318157.

XX PA (IMMU-) IMMUNOMEDICS INC.

XX PI Hansen HU, Armour KL;

XX DR WPI; 1996-209653/21.

XX PT New humanised anti-CEA monoclonal antibody - having engrafted murine
XX CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

XX PS Claim 5; Page 38; 62pp; English.

XX CC New humanised monoclonal antibodies (MAbs) comprising the complementary
XX determining regions (CDRs) of a parental murine class III anti-
XX carcinoembryonic (CEA) MAb grafted to the framework regions (FRs) of a
XX heterologous antibody which can be derived from any species including
XX human, retain the anti-CEA binding specificity of the parental murine MAb
XX but are less immunogenic in a human subject than the parental MAb. The
XX humanised antibodies can be used in diagnosis, imaging and therapy of CEA
XX -producing cancers and patients receiving the humanised antibodies and
XX conjugates show improved therapeutic results, decreased immune responses
XX and decreased immune-mediated adverse effects compared to the parent
XX antibody. This sequence is a murine derived CDR region which corresponds
XX to CDR 1 in the heavy chain of the humanised MAb. See AAR97313-97333

XX SQ Sequence 5 AA;

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 1 TYWMS 5

RESULT 5
AAY05038
ID AAY05038 standard; peptide; 5 AA.

XX AC AAY05038;

XX DT 16-JUN-1999 (first entry)

XX DE Tumour antigen antibody heavy chain CDR1 clone F15.

XX KW Tumour antigen; antibody; CDR; complementarity determining region;
XX binding molecule identification; tumour-specific binding polypeptide;
XX cancer therapy; heavy chain.

XX OS Homo sapiens.

XX PN WO9906834-A2.

XX PD 11-FEB-1999.

XX PF 04-AUG-1998; 98WO-US016280.

XX PR 04-AUG-1997; 97US-00905825.

XX PA (IXSY-) IXSYS INC.

XX PI Watkins JD, Huse WD, Wu H;

XX DR WPI; 1999-153951/13.

XX DR N-PSDB; AAX28215.

XX PT Identifying binding molecules for ligands, particularly tumour antigens -
XX by selectively immobilising a population of binding molecules to a solid
XX support and screening for binding to two or more ligands.

XX PS Claim 15; Page 60; 80pp; English.

XX CC This sequence represents a heavy chain complementarity determining region
XX (CDR) from a tumour antigen specific antibody. The invention relates to a
XX method for identifying a binding molecule having selective affinity for a
XX ligand comprising: (a) selectively immobilising a diverse population of
XX binding molecules to a solid support; (b) simultaneously contacting the
XX diverse population immobilised on the solid support with 2 or more
XX ligands; and (c) determining at least one binding molecule which
XX selectively binds to one or more of the ligands. The method allows for
XX the rapid and efficient methods for the identification of binding
XX molecules which exhibit selective affinity for one or more ligands of
XX interest. They are used particularly for identifying tumour-specific
XX binding polypeptides which can be used as targeting agents for cancer
XX therapy that minimises impact on non-tumour tissues

XX SQ Sequence 5 AA;

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 1 TYWMS 5

RESULT 6

ABB07357

ID ABB07357 standard; peptide; 5 AA.

XX AC ABB07357;

XX 09-APR-2002 (first entry)
 XX DT
 XX DE 22A5 IgM heavy chain variable region CDR1 sequence.
 XX KW Immunoglobulin; Ig; reperfusion; ischemic injury; pathogenic; CDR;
 XX KW vasotropic; antibody; 22A5; IgM; complementarity determining region.
 XX OS Mus musculus.
 XX PN WO200193892-A1.
 XX PD 13-DEC-2001.
 XX PF 08-JUN-2001; 2001WO-US018510.
 XX PR 08-JUN-2000; 2000US-0210272P.
 XX PA (BLOO-) CENT BLOOD RES INC.
 XX PI Carroll MC, Moore FD, Hechtman HB;
 XX DR WPI; 2002-139643/18.
 XX DR N-PSDB; ABA94514.
 XX PT Treating or preventing immunoglobulin-mediated reperfusion or ischemic
 XX PT injury resulting from e.g. angioplasty or bypass surgery, by
 XX PT administering an inhibitor of pathogenic immunoglobulin and ischemic
 XX PT antigen interaction.
 XX PS Claim 54; Page 72; 77pp; English.
 XX CC The invention provides a method of treating or preventing immunoglobulin-
 CC mediated reperfusion or ischemic injury in a subject. The method involves
 CC administering an inhibitor of an interaction between a pathogenic
 CC immunoglobulin, and an ischemic-specific antigen or a component of the
 CC complement pathway. The method is useful for treating or preventing
 CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
 CC injury that results following a naturally occurring episode, a surgical
 CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
 CC surgery), or in an injury that occurs in a cardiovascular tissue. The
 CC method is also useful for treating or preventing, in a subject, tissue
 CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
 CC pathogenic IgMs. The present sequence represents the complementarity
 CC determining region (CDR1) of a heavy chain variable region of 22A5 IgM, a
 CC pathogenic immunoglobulin
 XX SQ Sequence 5 AA;
 Query Match 90.3%; Score 28; DB 5; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 Db :|||:
 1 SYWMN 5
 RESULT 7
 ID AAO17609
 AC AAO17609 standard; peptide; 5 AA.
 XX AC AAO17609;
 XX DT 08-AUG-2002 (first entry)
 XX DE Human FAPAlpha specific VL region from VH50 CDR1 peptide.
 XX KW Human; FAPAlpha; fibroblast activating protein alpha; antibody; Ab;
 XX KW gene therapy; cancer; wound healing; inflammation; cytostatic.
 XX OS Homo sapiens.
 XX PN

PN WO200168708-A2.
 XX 20-SEP-2001.
 XX PF 16-MAR-2001; 2001WO-EP004716.
 XX PR 17-MAR-2000; 2000DE-01013286.
 XX PR 11-SEP-2000; 2000GB-00022216.
 XX PA (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
 XX PI Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
 XX PI Schmidt A;
 XX DR WPI; 2002-041180/05.
 XX DR N-PSDB; AAL46554.
 XX PT New human humanized antibody that specifically binds to fibroblasts
 XX PT activating protein alpha, useful for treating cancer or tumor, and for
 XX PT imaging tumors associated with activated stromal fibroblasts, e.g. lung
 XX PT or breast cancer.
 XX PS Disclosure; Fig 6C; 109pp; English.
 XX CC The present invention relates to a human or humanised antibody (Ab) which
 CC specifically binds to fibroblast activating protein alpha (FAPAlpha). The
 CC antibodies are useful for preparing a composition for the treatment of
 CC cancer, and for imaging tumours associated with activated stromal
 CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer, bladder
 CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, and diseases
 CC cancer, pancreatic cancer and metastatic brain cancer, and diseases
 CC associated with the same, such as inflammation and wound healing. The
 CC present sequence is a peptide described in the exemplification of the
 CC invention
 XX SQ Sequence 5 AA;
 Query Match 90.3%; Score 28; DB 5; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 Db :|||:
 1 NYWMS 5
 RESULT 8
 ID ADC82794
 AC ADC82794 standard; peptide; 5 AA.
 XX AC ADC82794;
 XX DT 01-JAN-2004 (first entry)
 XX DE CDR region #3 in heavy chain of human Fab fragment.
 XX KW Binding molecule; selective affinity; ligand;
 XX KW anti-immunoglobulin reagent; phage expressed antibody library;
 XX KW tumour antigen; complementarity determining region; CDR; human disease;
 XX KW cellular pathology; human; Fab; heavy chain.
 XX OS Homo sapiens.
 XX PN US2003044772-A1.
 XX PD 06-MAR-2003.
 XX PF 15-OCT-2001; 2001US-00977797.
 XX PR 04-AUG-1997; 97US-0113667P.
 XX PR 04-AUG-1998; 98US-00129026.
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PT to evaluate drugs in animal models and to treat Fas-associated diseases
 PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
 PT hepatitis and AIDS.

XX PS Claim 9; Page 184; 292pp; English.

XX CC This is the amino acid of complementarity determining region 1 (CDR-H1)
 CC of the heavy chain (see AAW83041) of murine anti-human Fas monoclonal
 CC antibody HFE7A. The invention relates to antibodies, especially humanised
 CC antibodies (see AAW83031-37), recognising the Fas antigen. Such
 CC antibodies preferably comprise a heavy chain and a light chain including
 CC CDRs (see AAW83024-29) from the heavy and light chains of HFE7A.
 CC Humanised antibodies are produced by CDR grafting. The antibodies are
 CC capable of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. They are used to
 CC evaluate, in animal models, treatments of diseases that involve Fas/Fas
 CC ligand interactions, and also to treat such diseases, including
 CC autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's
 CC disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease,
 CC rheumatoid arthritis, autoimmune haemolytic anaemia, sterility,
 CC myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia
 CC purpura and insulin-dependent diabetes), allergies, atopy,
 CC arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis,
 CC hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all
 CC claimed). (Updated on 25-MAR-2003 to correct DR field.)

XX SQ Sequence 5 AA;

Query Match 87.1%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWM 4
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 Db 1 SYWM 4

RESULT 11

AAI05045
 ID AAY05045 standard; peptide; 5 AA.

AC AAY05045;

DT 16-JUN-1999 (first entry)

DE Tumour antigen antibody heavy chain CDR1 clone TA50.

XX KW Tumour antigen; antibody; CDR; complementarity determining region;
 KW binding molecule identification; tumour-specific binding polypeptide;
 KW cancer therapy; heavy chain.

XX OS Homo sapiens.

XX PN WO9906834-A2.

XX PD 11-FEB-1999.

XX PF 04-AUG-1998; 98WO-US016280.

XX PR 04-AUG-1997; 97US-00905825.

XX PA (IXSY-) IXSYS INC.

XX PI Watkins JD, Huse WD, Wu H;

XX WPI; 1999-153951/13.

DR N-PSDB; AAX28222.

XX PT Identifying binding molecules for ligands, particularly tumour antigens -
 PT by selectively immobilising a population of binding molecules to a solid
 PT support and screening for binding to two or more ligands.

XX

PS Claim 15; Page 60; 80pp; English.

XX CC This sequence represents a heavy chain complementarity determining region
 CC (CDR) from a tumour antigen specific antibody. The invention relates to a
 CC method for identifying a binding molecule having selective affinity for a
 CC ligand comprising: (a) selectively immobilising a diverse population of
 CC binding molecules to a solid support; (b) simultaneously contacting the
 CC diverse population immobilised on the solid support with 2 or more
 CC ligands; and (c) determining at least one binding molecule which
 CC selectively binds to one or more of the ligands. The method allows for
 CC the rapid and efficient methods for the identification of binding
 CC molecules which exhibit selective affinity for one or more ligands of
 CC interest. They are used particularly for identifying tumour-specific
 CC binding polypeptides which can be used as targeting agents for cancer
 CC therapy that minimises impact on non-tumour tissues

XX SQ Sequence 5 AA;

Query Match 87.1%; Score 27; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 ||||
 Db 1 SYWIS 5

RESULT 12

AAI14741

ID AAB14741 standard; peptide; 5 AA.

AC AAB14741;

DT 24-NOV-2000 (first entry)

DE Mouse anti-Fas antibody HFE7A heavy chain CDR1.

XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
 KW complementarity determining region; CDR; human Fas; Fas ligand;
 KW apoptosis modulator; programmed cell death; autoimmune disease; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
 KW aplastic anaemia; pancytopenia; hepatitis; AIDS; graft rejection;
 KW heavy chain.

XX OS Mus musculus.

XX PN JP2000169393-A.

XX PD 20-JUN-2000.

XX PF 30-SEP-1999; 99JP-00278301.

XX PR 30-SEP-1998; 98JP-00276883.

XX PA (SANY) SANKYO CO LTD.

XX WPI; 2000-485645/43.

XX PT Preventive or treating agent for the diseases caused by an abnormality in
 PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
 PT antibody.

XX PS Claim 10; Page 64; 139pp; Japanese.

XX CC The invention relates to compositions for the prevention or treatment of
 CC diseases caused by an abnormality in the Fas/Fas ligand system containing
 CC an anti-Fas antibody as the active component. The anti-Fas antibody is
 CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
 CC humanised version of HFE7A containing identical CDRs (complementarity
 CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
 CC antibody of the invention acts as a modulator of apoptosis. The
 CC compositions of the invention may therefore be used in the treatment or
 CC prevention of conditions such as autoimmune diseases, allergy, atopy,

CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
 CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
 CC rejection. Sequences AAB14741-B14743 represent CDRs 1-3 of the heavy
 CC chain of the murine anti-human Fas monoclonal antibody HFE7A, which is
 CC produced by hybridoma HFE7A (FERM-BP-5828)

SQ Sequence 5 AA;
 Query Match 87.1%; Score 27; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMM 4
 Db 1 SYMM 4
 ||||
 ||||

RESULT 13
 AAW90891
 ID AAW90891 standard; peptide; 5 AA.
 XX AC AAW90891;
 XX DT 08-AUG-2000 (first entry)
 XX DE Murine anti-Fas antibody peptide fragment #1.
 XX KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyrometric; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antirheosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX OS Mus musculus.
 XX FN EP990663-A2.
 XX PD 05-APR-2000.
 XX PF 29-SEP-1999; 99EP-00307711.
 XX PR 30-SEP-1998; 98JP-00276881.
 XX PR 30-SEP-1998; 98JP-00276882.
 XX PA (SANY) SANKYO CO LTD.
 XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 XX DR New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX PT inflammatory or autoimmune disease, induces apoptosis selectively in
 XX PT cells with abnormal Fas-Fas ligand systems.
 XX PS Disclosure; Page 97; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyrometric,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (II) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method of
 CC the invention

XX SQ Sequence 5 AA;
 Query Match 87.1%; Score 27; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMM 4
 Db 1 SYMM 4
 ||||
 ||||

RESULT 14
 AAY32257
 ID AAY32257 standard; peptide; 5 AA.
 XX AC AAY32257;
 XX DT 15-FEB-2000 (first entry)
 XX DE Light chain CDR H1 of mouse anti-CD23 Mab C11.
 XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX OS Mus musculus.
 XX FN WO9958679-A1.
 XX PD 18-NOV-1999.
 XX PF 07-MAY-1999; 99WO-GB001434.
 XX PR 09-MAY-1998; 98GB-00009839.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Bonney JMF, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX DR N-PSDB; AAZ34742.
 XX PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX PT diabetes, multiple sclerosis and psoriasis.
 XX PS Claim 1; Page 40; 81pp; English.

CC This sequence represents complementarity determining region 1 (CDR H1)
 CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

(see also AAY32263). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents

XX SQ Sequence 5 AA;

Query Match 87.1%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|||
Db 2 YWMS 5

RESULT 15

AA92158
ID AAY92158 standard; peptide; 5 AA.

XX AC AAY92158;

XX DT 01-AUG-2000 (first entry)

XX DE Murine 15B8 heavy chain variable region CDR 1.

XX KW Heavy chain; variable region; complementarity determining region; CDR 1;
anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;
XX KW vascular-general; proliferative; antiischemic; cerebroprotective;
XX KW cardiant; agonist; antibody inhibition.

XX OS Mus musculus.

XX PN WC200018804-A1.

XX PD 06-APR-2000.

XX PF 28-SEP-1999; 99WO-US022428.

XX PR 28-SEP-1998; 98US-0102098P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Holmes SD, Erickson-Miller CL, Winkler JD;

XX WPI; 2000-293114/25.

XX PT Tie2 receptor agonist antibodies useful for promoting angiogenesis in
XX PT patients suffering from strokes and myocardial infarctions.

XX PS Claim 12; Page 40; 50pp; English.

XX CC AAY92158-60 are heavy chain CDR (complementarity determining regions)
XX CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal antibody
XX CC 15B8. Tie2 is a single-transmembrane, tyrosine kinase receptor ('Tie'
XX CC stands for tyrosine kinase receptor with immunoglobulin and endothelial
XX CC growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be
XX CC administered to enhance angiogenesis in mammals suffering from ischemic
XX CC disease, myocardial infarction or cerebral stroke or other vascular
XX CC diseases such as diabetes. It may also be used to enhance endothelial
XX CC cell survival and to promote haematopoietic or megakaryocyte cell

CC proliferation (claimed)

XX

SQ Sequence 5 AA;

Query Match 87.1%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWM 4

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Db 1 SYWM 4

Search completed: June 8, 2004, 18:57:17

Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:58:38 ; Search time 41 Seconds
(without alignments)
34.310 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 16841

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	9	US-09-832-312-61
2	31	100.0	5	11	US-09-829-495-61
3	28	90.3	5	10	US-09-253-794-23
4	28	90.3	5	9	US-09-977-797A-76
5	27	87.1	5	9	US-09-748-960-12
6	27	87.1	5	9	US-09-832-312-49
7	27	87.1	5	10	US-09-977-797A-90
8	27	87.1	5	11	US-09-829-495-49
9	27	87.1	5	12	US-10-226-795-23
10	27	87.1	5	14	US-10-216-484-2
11	27	87.1	5	14	US-10-384-933-2
12	25	80.6	5	10	US-09-155-106-1
13	24	77.4	4	12	US-09-948-004-32
14	24	77.4	5	14	US-10-206-699-209
15	24	77.4	5	14	US-10-206-699-214

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16 24 77.4 5 14 US-10-206-699-217
17 24 77.4 5 15 US-10-173-551-15
18 23 74.2 5 9 US-09-770-002-1
19 23 74.2 5 9 US-09-423-800-62
20 23 74.2 5 10 US-09-269-921-6
21 23 74.2 5 10 US-09-509-098-8
22 23 74.2 5 12 US-10-344-733-62
23 23 74.2 5 12 US-10-384-060-39
24 23 74.2 5 14 US-10-182-018-62
25 23 74.2 5 14 US-10-169-003-62
26 23 74.2 5 14 US-10-218-253-6
27 23 74.2 5 14 US-10-337-981-62
28 23 74.2 5 15 US-10-173-551-5
29 21 67.7 5 10 US-09-920-262A-1
30 21 67.7 5 16 US-10-070-406A-6
31 20 64.5 5 10 US-09-291-417-40
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37 20 64.5 5 14 US-10-206-699-229
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42 19 61.3 5 10 US-09-977-797A-88
43 19 61.3 5 10 US-09-962-756-1586
44 19 61.3 5 13 US-10-029-301-4
45 19 61.3 5 15 US-10-253-471-1586
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ALIGNMENTS

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; Sequence 61, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-61
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Query Match 100.0%; Score 31; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 SYWMS 5
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Db 1 SYWMS 5
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RESULT 2
US-09-829-495-61
; Sequence 61, Application US/09829495
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match 87.1%; Score 27; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWM 4
| | | |
Db 1 SYWM 4

RESULT 6
US-09-832-312-49
; Sequence 49, Application US/09832312
; Patent No. US20010949829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-49

Query Match 87.1%; Score 27; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
| | | |
Db 1 SYWIS 5

RESULT 7
US-09-977-797A-90
; Sequence 90, Application US/09977797A
; Publication No. US2003004772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-977-797A-90

Query Match 87.1%; Score 27; DB 10; Length 5;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
| | | |
Db 1 SYWIS 5

RESULT 8
US-09-829-495-49
; Sequence 49, Application US/09829495
; Publication No. US2004001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Ferrus M
; APPLICANT: Valinchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-49

Query Match 87.1%; Score 27; DB 11; Length 5;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
| | | |
Db 1 SYWIS 5

RESULT 9
US-10-226-795-23
; Sequence 23, Application US/10226795
; Publication No. US20040053865A1
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-23

Query Match 87.1%; Score 27; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
: : : : :
Db 2 YWMS 5

RESULT 10
US-10-216-484-2
; Sequence 2, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Takahashi, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-2

Query Match 87.1%; Score 27; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWM 4
: : : : :
Db 1 SYWM 4

RESULT 11
US-10-384-933-2
; Sequence 2, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Takahashi, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-2

Query Match 87.1%; Score 27; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWM 4
: : : : :
Db 1 SYWM 4

RESULT 12
US-09-155-106-1
; Sequence 1, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /09/155,106
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-1

Query Match 80.6%; Score 25; DB 10; Length 5;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
: : : : :
Db 1 NYWMT 5

RESULT 13
US-09-948-004-32
; Sequence 32, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: Mack, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; TITLE OF INVENTION: immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-948-004-32

Query Match 77.4%; Score 24; DB 12; Length 4;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
: : : : :
Db 2 YWMS 5

Db 1 YWMN 4

Search completed: June 8, 2004, 19:04:08
Job time : 42 secs

RESULT 14

US-10-206-699-209
; Sequence 209, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MEHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 209
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-209

Query Match 77.4%; Score 24; DB 14; Length 5;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWM 4
|||:
Db 2 SYWL 5

RESULT 15

US-10-206-699-214
; Sequence 214, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MEHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-214

Query Match 77.4%; Score 24; DB 14; Length 5;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWM 4
|||:
Db 2 SYWL 5

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 10.375 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB pep.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB pep.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB pep.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB pep.*
- 5: /cgn2_6/prodata/2/iaa/6C COMB pep.*
- 6: /cgn2_6/prodata/2/iaa/6D COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	82.1	166	4	US-09-797-464A-5
2	32	82.1	174	4	US-09-797-464A-9
3	32	82.1	363	4	US-09-797-464A-11
4	32	82.1	395	4	US-09-797-464A-2
5	32	82.1	515	4	US-09-107-532A-5317
6	32	82.1	893	4	US-09-514-302-4
7	32	82.1	1938	4	US-09-514-302-2
8	31	79.5	222	1	US-07-869-933-12
9	31	79.5	222	1	US-07-869-933-28
10	31	79.5	222	3	US-09-103-663-12
11	31	79.5	222	3	US-09-103-663-28
12	31	79.5	382	4	US-08-311-731A-45
13	30	76.9	126	4	US-09-485-973-6
14	30	76.9	252	5	PCT-US96-01314-58
15	30	76.9	253	5	PCT-US96-01314-53
16	30	76.9	268	4	US-09-134-000C-4101
17	30	76.9	618	3	US-08-361-083-72
18	30	76.9	618	4	US-09-536-784-72
19	30	76.9	627	4	US-08-851-567B-28
20	30	76.9	676	3	US-08-630-172-10
21	30	76.9	676	3	US-09-375-419-10
22	30	76.9	769	2	US-08-789-078-1
23	30	76.9	769	2	US-08-752-633-1
24	30	76.9	769	2	US-08-476-062A-45
25	30	76.9	769	2	US-07-728-215-31
26	30	76.9	769	4	US-08-938-085A-31
27	30	76.9	769	4	US-10-072-844-31

28 30 76.9 769 4 US-10-072-838-31 Sequence 31, Appl
29 30 76.9 769 4 US-10-072-841A-31 Sequence 31, Appl
30 30 76.9 769 5 PCT-US95-04886-1 Sequence 1, Appli
31 30 76.9 769 5 PCT-US96-01314-45 Sequence 45, Appl
32 30 76.9 796 4 US-09-107-532A-7065 Sequence 7065, Ap
33 30 76.9 891 4 US-09-328-352-6637 Sequence 6637, Ap
34 30 76.9 1189 4 US-08-851-567B-26 Sequence 26, Appl
35 29 74.4 16 2 US-08-932-876-1 Sequence 1, Appli
36 29 74.4 25 1 US-08-378-761A-30 Sequence 30, Appl
37 29 74.4 25 1 US-08-485-286-30 Sequence 30, Appl
38 29 74.4 25 6 5248606-16 Patent No. 5248606
39 29 74.4 40 2 US-08-879-405-6 Sequence 6, Appli
40 29 74.4 40 2 US-08-842-799-6 Sequence 6, Appli
41 29 74.4 40 5 PCT-US96-11458-6 Sequence 6, Appli
42 29 74.4 93 4 US-09-543-681A-4648 Sequence 4648, Ap
43 29 74.4 109 3 US-09-157-370-5 Sequence 5, Appli
44 29 74.4 129 4 US-09-615-192A-307 Sequence 307, App
45 29 74.4 348 4 US-09-797-464A-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-797-464A-5
; Sequence 5, Application US/09797464A
; Patent No. 6630340
; GENERAL INFORMATION:
; APPLICANT: Wiltling, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-5

Query Match 82.1%; Score 32; DB 4; Length 166;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
DB 108 SYDSSNVV 115

RESULT 2
US-09-797-464A-9
; Sequence 9, Application US/09797464A
; Patent No. 6630340
; GENERAL INFORMATION:
; APPLICANT: Wiltling, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-9

Query Match 82.1%; Score 32; DB 4; Length 174;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
| | | | | | | |
Db 117 SYDSSNV 124

RESULT 3
US-09-797-464A-11
; Sequence 11, Application US/09797464A
; Patent No. 6630340
; GENERAL INFORMATION:
; APPLICANT: Wiltling, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-11

Query Match 82.1%; Score 32; DB 4; Length 363;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
| | | | | | | |
Db 299 SYDSSNV 306

RESULT 4
US-09-797-464A-2
; Sequence 2, Application US/09797464A
; Patent No. 6630340
; GENERAL INFORMATION:
; APPLICANT: Wiltling, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-2

Query Match 82.1%; Score 32; DB 4; Length 395;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
| | | | | | | |
Db 331 SYDSSNV 338

RESULT 5
US-09-107-532A-5317
; Sequence 5317, Application US/09107532A

Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5317:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...515
; SEQUENCE DESCRIPTION: SEQ ID NO: 5317:
US-09-107-532A-5317

Query Match 82.1%; Score 32; DB 4; Length 515;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
: | | | | | | | |
Db 175 AYDSSNV 181

RESULT 6
US-09-514-302-4
; Sequence 4, Application US/09514302
; Patent No. 6338959
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: OZAKI, Katsuya
; APPLICANT: ARA, Katsutoshi
; APPLICANT: KAWAI, Shuji
; APPLICANT: ITO, Susumu
; TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND
; ALKALINE ALPHA-AMYLASE ACTIVITIES
; FILE REFERENCE: 2173-105P
; CURRENT APPLICATION NUMBER: US/09/514,302
; CURRENT FILING DATE: 2000-02-28

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/ EARLIER APPLICATION NUMBER: 08/952,084
/ EARLIER FILING DATE: 1997-11-10
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 893
/ TYPE: PRT
/ ORGANISM: Bacillus sp.
US-09-514-302-4

Query Match      82.1%; Score 32; DB 4; Length 893;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYDSSNV 8
Db      624 SYDSSDII 631

RESULT 7
US-09-514-302-2
/ Sequence 2, Application US/09514302
/ Patent No. 6338959
/ GENERAL INFORMATION:
/ APPLICANT: HATADA, Yuji
/ APPLICANT: IGARASHI, Kazuaki
/ APPLICANT: OZAKI, Katsuya
/ APPLICANT: ARA, Katsutoshi
/ APPLICANT: KAWAI, Shuji
/ APPLICANT: ITO, Susumu
/ TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PHOSPHATASE AND
/ FILE REFERENCE: 2173-105P
/ CURRENT APPLICATION NUMBER: US/09/514,302
/ CURRENT FILING DATE: 2000-02-28
/ EARLIER APPLICATION NUMBER: 08/952,084
/ EARLIER FILING DATE: 1997-11-10
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 1938
/ TYPE: PRT
/ ORGANISM: Bacillus sp.
US-09-514-302-2

Query Match      82.1%; Score 32; DB 4; Length 1938;
Best Local Similarity 62.5%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYDSSNV 8
Db      1669 SYDSSDII 1676

RESULT 8
US-07-869-933-12
/ Sequence 12, Application US/07869933
/ Patent No. 5770396
/ GENERAL INFORMATION:
/ APPLICANT: KINET, Jean-Pierre
/ TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
/ TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
/ TITLE OF INVENTION: IMMUNOGLOBULIN
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/869,933
/ FILING DATE: 19920416
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 40399/154 NIHD
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)836-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 222 amino acids
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/869,933
/ FILING DATE: 19920416
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 40399/154 NIHD
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)836-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 222 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Rat
/ STRAIN: FcRI alpha subunit
US-07-869-933-12

Query Match      79.5%; Score 31; DB 1; Length 222;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYDSSNV 7
Db      130 SYDSSNI 136

RESULT 9
US-07-869-933-28
/ Sequence 28, Application US/07869933
/ Patent No. 5770396
/ GENERAL INFORMATION:
/ APPLICANT: KINET, Jean-Pierre
/ TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
/ TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
/ TITLE OF INVENTION: IMMUNOGLOBULIN
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/869,933
/ FILING DATE: 19920416
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 40399/154 NIHD
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)836-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 222 amino acids
/ MEDIUM TYPE: Floppy disk
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; STRAIN: alpha subunit
US-07-869-933-28

Query Match 79.5%; Score 31; DB 1; Length 222;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSNV 7
Db 130 SYDSNNI 136

RESULT 10
US-09-103-663-12
; Sequence 12, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-103-663-12

Query Match 79.5%; Score 31; DB 3; Length 222;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSNV 7
Db 130 SYDSNNI 136

RESULT 11
US-09-103-663-28
; Sequence 28, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-28

Query Match 79.5%; Score 31; DB 3; Length 222;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSNV 7

Db 130 SYDSNNI 136

RESULT 12
US-08-311-731A-45
; Sequence 45, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-45

Query Match 79.5%; Score 31; DB 4; Length 382;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSNV 8
Db 147 AYDSPNV 154

RESULT 13
US-09-485-973-6
; Sequence 6, Application US/09485973
; Patent No. 6488935
; GENERAL INFORMATION:
; APPLICANT: De Villiers Zur Hausen, Ethel-Micelle
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: PAPILLOMA VIRUS, AGENTS FOR THE DETECTION THEREOF AND FOR THE
; TITLE OF INVENTION: THERAPY
; TITLE OF INVENTION: OF THE DISEASES CAUSED BY SAID VIRUS
; FILE REFERENCE: 008484-0082-999
; CURRENT APPLICATION NUMBER: US/09/485,973
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/DE98/02379
; PRIOR FILING DATE: 1998-08-12

;; PRIOR APPLICATION NUMBER: 197 35 118.2
;; PRIOR FILING DATE: 1997-08-13
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 6
;; LENGTH: 126
;; TYPE: PRT
;; ORGANISM: Papillomavirus Capsid Protein
US-09-485-973-6

Query Match 76.9%; Score 30; DB 4; Length 126;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNV 7
Db 30 YDSSNI 35

RESULT 14
PCT-US96-01314-58
;; Sequence 58, Application PC/TUS9601314
;; GENERAL INFORMATION:
;; APPLICANT: M. Amin Arnaut
;; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM PS/2 Model 50Z or 55SX
;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/01314
;; FILING DATE: 30-JAN-96
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/380,167
;; FILING DATE: 30-JAN-95
;; ATTORNEY/AGENT INFORMATION:
;; NAME: John W. Freeman
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 00786/267001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 252 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US96-01314-58

Query Match 76.9%; Score 30; DB 5; Length 252;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
Db 237 SEDSSNV 244

RESULT 15
PCT-US96-01314-53

;; Sequence 53, Application PC/TUS9601314
;; GENERAL INFORMATION:
;; APPLICANT: M. Amin Arnaut
;; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM PS/2 Model 50Z or 55SX
;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/01314
;; FILING DATE: 30-JAN-96
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/380,167
;; FILING DATE: 30-JAN-95
;; ATTORNEY/AGENT INFORMATION:
;; NAME: John W. Freeman
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 00786/267001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 253 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US96-01314-53

Query Match 76.9%; Score 30; DB 5; Length 253;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
Db 238 SEDSSNV 245

Search completed: June 8, 2004, 18:31:52
Job time : 10.375 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 26.625 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	9	US-09-832-312-66
2	39	100.0	8	11	US-09-829-495-66
3	39	100.0	161	14	US-10-106-698-6785
4	33	84.6	75	12	US-10-424-599-256961
5	33	84.6	110	12	US-10-371-942-88
6	33	84.6	282	12	US-10-427-805-1
7	33	84.6	397	12	US-10-427-805-3
8	33	84.6	418	12	US-10-427-805-2
9	33	84.6	617	14	US-10-205-342-11
10	33	84.6	934	12	US-10-282-122A-54603
11	32	82.1	166	10	US-09-797-464A-5
12	32	82.1	168	12	US-10-425-114-63711
13	32	82.1	174	10	US-09-797-464A-9
14	32	82.1	363	10	US-09-797-464A-11
15	32	82.1	395	10	US-09-797-464A-2

16	32	82.1	893	13	US-10-014-436-4	Sequence 4, Appli
17	32	82.1	1398	13	US-10-014-436-2	Sequence 2, Appli
18	32	82.1	4327	15	US-10-369-493-10178	Sequence 10178, A
19	31	79.5	10	10	US-09-972-656-23	Sequence 23, Appl
20	31	79.5	62	12	US-10-424-599-183368	Sequence 183368,
21	31	79.5	98	12	US-10-453-698-117	Sequence 117, App
22	31	79.5	98	15	US-10-308-817-117	Sequence 117, App
23	31	79.5	103	10	US-09-972-656-130	Sequence 130, App
24	31	79.5	122	12	US-10-282-122A-61463	Sequence 61463, A
25	31	79.5	217	10	US-09-972-656-88	Sequence 88, Appl
26	31	79.5	290	12	US-10-282-122A-62681	Sequence 62681, A
27	31	79.5	318	14	US-10-029-386-32107	Sequence 32107, A
28	31	79.5	411	12	US-10-282-122A-64019	Sequence 64019, A
29	31	79.5	413	12	US-10-282-122A-64927	Sequence 64927, A
30	31	79.5	558	12	US-10-425-114-54053	Sequence 54053, A
31	31	79.5	595	14	US-10-074-475-257	Sequence 257, App
32	31	79.5	862	16	US-10-149-310-132	Sequence 132, App
33	31	79.5	963	9	US-09-801-368-74	Sequence 74, Appl
34	31	79.5	963	15	US-10-369-493-1436	Sequence 1436, Ap
35	31	79.5	1420	15	US-10-369-493-11250	Sequence 11250, A
36	31	79.5	1610	14	US-10-155-533-9	Sequence 9, Appli
37	30	76.9	241	10	US-09-805-354-14	Sequence 14, Appl
38	30	76.9	241	12	US-09-758-493-14	Sequence 14, Appl
39	30	76.9	241	14	US-10-144-259-14	Sequence 14, Appl
40	30	76.9	242	10	US-09-805-354-15	Sequence 15, Appl
41	30	76.9	242	12	US-09-758-493-15	Sequence 15, Appl
42	30	76.9	242	14	US-10-144-259-15	Sequence 15, Appl
43	30	76.9	341	15	US-10-240-145-146	Sequence 146, App
44	30	76.9	354	16	US-10-616-624-4	Sequence 4, Appli
45	30	76.9	423	15	US-10-080-334-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-09-832-312-66
; Sequence 66, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-66

Query Match 100.0%; Score 39; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8

Db 1 SYDSSNVV 8

RESULT 2

US-09-829-495-66
; Sequence 66, Application US/09829495

Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-66

Query Match 100.0%; Score 39; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
|||
Db 1 SYDSSNVV 8

RESULT 3
US-10-106-698-6785
; Sequence 6785, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6785
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6785

Query Match 100.0%; Score 39; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
|||
Db 114 SYDSSNVV 121

RESULT 4
US-10-424-599-256961
; Sequence 256961, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 256961
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_74059C.1.pep
US-10-424-599-256961

Query Match 84.6%; Score 33; DB 12; Length 75;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
|||
Db 54 SYDSSNML 61

RESULT 5
US-10-371-942-88
; Sequence 88, Application US/10371942
; Publication No. US2003023994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-88

Query Match 84.6%; Score 33; DB 12; Length 110;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
|||
Db 93 SYDSSNVQ 100

RESULT 6
US-10-427-805-1
; Sequence 1, Application US/10427805
; Publication No. US20040063632A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: McLean, Kirk
; TITLE OF INVENTION: No. US20040063632A1 Tissue Factor Targeted Thrombomodulin Fusi
; FILE REFERENCE: 52295AUSMI

; CURRENT APPLICATION NUMBER: US/10/427,805
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,566
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10 antibody
US-10-427-805-1

Query Match 84.6%; Score 33; DB 12; Length 282;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 245 SYDSNNLV 252

RESULT 7
US-10-427-805-3
; Sequence 3, Application US/10427805
; Publication No. US20040063632A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: McLean, Kirk
; TITLE OF INVENTION: No. US20040063632A1 Tissue Factor Targeted Thrombomodulin Fusion
; FILE REFERENCE: 52295AUSM1
; CURRENT APPLICATION NUMBER: US/10/427,805
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,566
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456delta fusione protein
US-10-427-805-3

Query Match 84.6%; Score 33; DB 12; Length 397;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 242 SYDSNNLV 249

RESULT 8
US-10-427-805-2
; Sequence 2, Application US/10427805
; Publication No. US20040063632A1
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: McLean, Kirk
; TITLE OF INVENTION: No. US20040063632A1 Tissue Factor Targeted Thrombomodulin Fusion
; FILE REFERENCE: 52295AUSM1
; CURRENT APPLICATION NUMBER: US/10/427,805
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,566
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

; LENGTH: 418
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of scFv(TF)3e10-TM1456 fusion protein
US-10-427-805-2

Query Match 84.6%; Score 33; DB 12; Length 418;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 245 SYDSNNLV 252

RESULT 9
US-10-205-342-11
; Sequence 11, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Protein: vacuolar adenosine triphosphatase subunit A
US-10-205-342-11

Query Match 84.6%; Score 33; DB 14; Length 617;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 184 NYDASNVV 191

RESULT 10
US-10-282-122A-54603
; Sequence 54603, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078

```
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54603
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (181)..(181)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-54603
```

```
Query Match      84.6%; Score 33; DB 12; Length 934;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 SYDSSNV 8
      ||| |||:
Db      714 SYDSSNV 721
```

```
RESULT 11
US-09-797-464A-5
; Sequence 5, Application US/09797464A
; Publication No. US20030022807A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-5
```

```
Query Match      82.1%; Score 32; DB 10; Length 166;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 SYDSSNV 8
      ||| |||:
Db      108 SYDSSNV 115
```

```
RESULT 12
US-10-425-114-63711
```

```
; Sequence 63711, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63711
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-261-G2_FLI.pep
US-10-425-114-63711
```

```
Query Match      82.1%; Score 32; DB 12; Length 168;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SYDSSNV 7
      : ||| |||
Db      26 TYDSSNV 32
```

```
RESULT 13
US-09-797-464A-9
; Sequence 9, Application US/09797464A
; Publication No. US20030022807A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-9
```

```
Query Match      82.1%; Score 32; DB 10; Length 174;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 SYDSSNV 8
      ||| |||:
Db      117 SYDSSNV 124
```

```
RESULT 14
US-09-797-464A-11
; Sequence 11, Application US/09797464A
; Publication No. US20030022807A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schulein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
```

; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-11

Query Match 82.1%; Score 32; DB 10; Length 363;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
|||
Db 299 SYDSSNVV 306

RESULT 15
US-09-797-464A-2
; Sequence 2, Application US/09797464A
; Publication No. US20030022807A1
; GENERAL INFORMATION:
; APPLICANT: Wilting, Reinhard
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Kauppinen, Markus Sakari
; APPLICANT: Schuelein, Martin
; TITLE OF INVENTION: Family 5 Xyloglucanases
; FILE REFERENCE: 6073.200-US
; CURRENT APPLICATION NUMBER: US/09/797,464A
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Paenibacillus pabuli
US-09-797-464A-2

Query Match 82.1%; Score 32; DB 10; Length 395;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
|||
Db 331 SYDSSNVV 338

Search completed: June 8, 2004, 18:53:00
Job time : 27.625 secs

mis Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 36.375 Seconds
(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	39	100.0	8	4	AAB61298	Aab61298 Anti-TANG
2	39	100.0	8	6	ABU11264	Abu11264 Human TAN
3	39	100.0	161	4	AAG76011	Aag76011 Human col
4	35	89.7	402	2	AAR60578	Aar60578 Osteogeni
5	33	84.6	110	6	ADA89244	Ada89244 Human ant
6	33	84.6	261	8	ADE11153	Adel1153 scFv(TF)3
7	33	84.6	282	8	ADE11151	Adel1151 scFv(TF)3
8	33	84.6	617	6	ABR41350	Abra41350 Mouse ATP
9	33	84.6	730	3	AAG29582	Aag29582 Arabidops
10	33	84.6	752	3	AAG29581	Aag29581 Arabidops
11	33	84.6	934	6	ABU26679	Abu26679 Protein e
12	33	84.6	1945	4	ABE65449	Abbe65449 Drosophil
13	32	82.1	110	5	AAO18434	Aao18434 Anti-GD2
14	32	82.1	113	4	AAU02522	Aau02522 Anti-adip
15	32	82.1	166	4	AAE09787	Aae09787 Paenibaci
16	32	82.1	174	4	AAE09790	Aae09790 Paenibaci
17	32	82.1	363	4	AAE09791	Aae09791 Paenibaci
18	32	82.1	395	4	AAE09784	Aae09784 Paenibaci
19	32	82.1	515	7	ADC95690	Adc95690 E. faeciu
20	32	82.1	521	4	ABE61042	Abbe61042 Drosophil
21	32	82.1	542	4	ABE58491	Abbe58491 Drosophil
22	32	82.1	798	2	AAW73552	Aaw73552 Fullulana
23	32	82.1	893	2	AAW09257	Aaw09257 Bacillus
24	32	82.1	1938	2	AAW09255	Aaw09255 Bacillus
25	32	82.1	1938	2	AAW73553	Aaw73553 Full leng

ALIGNMENTS

RESULT 1

AAB61298
ID AAB61298 standard; peptide; 8 AA.
XX
AC AAB61298;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 66.
XX
KW Human; antibody; scFv; CDR; complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200100810-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018152.
XX
PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;
Gill DS, Qian MD, Kingsbury G;
XX
WPI; 2001-080877/09.

New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.

Claim 32; Page 102; 227pp; English.

The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,

Abbr1894 P. papata
Abbr1916 P. papata
Abbr1914 P. papata
Abbr1918 P. papata
Abbr1920 P. papata
Abbr1923 P. papata
Abbr1923 P. papata
Abbr56510 Human ant
Abbr97094 Recombina
Abbr33539 Protein e
Abbr62470 Drosophil
Abbr69449 Drosophil
Aar42340 Subunit o
Aap90386 Alpha sub
Abu97145 Recombina
Abbe66563 Drosophil
Abbr34757 Protein e
Aay02465 Polypepti
Abbr74296 Mycobacte
Abbr11192 P. papata
Abbr25918 Streptoco

26 31 79.5 28 6 ABR91894
27 31 79.5 36 6 ABR91316
28 31 79.5 36 6 ABR91914
29 31 79.5 40 6 ABR91918
30 31 79.5 44 6 ABR91920
31 31 79.5 57 6 ABR91923
32 31 79.5 98 6 ABR56510
33 31 79.5 109 6 ABR97094
34 31 79.5 122 6 ABR33539
35 31 79.5 131 4 ABR62470
36 31 79.5 192 4 ABR69449
37 31 79.5 220 2 AAR42340
38 31 79.5 245 1 AAP90386
39 31 79.5 249 6 ABU97145
40 31 79.5 272 4 ABB66563
41 31 79.5 290 6 ABU34757
42 31 79.5 325 2 AAY02465
43 31 79.5 382 7 ABR74296
44 31 79.5 394 6 ABR91192
45 31 79.5 395 5 ABP25918

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver

XX
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 39; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
 |||||
 Db 1 SYDSSNVV 8

RESULT 2
 ABU11264
 ID ABU11264 standard; peptide; 8 AA.

AC ABU11264;

DT 06-FEB-2003 (first entry)

XX Human TANGO 268 VLCDRI Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW deglutination; thrombocytopenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 12; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention

XX
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 39; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
 |||||
 Db 1 SYDSSNVV 8

RESULT 3
 AAG76011
 ID AAG76011 standard; protein; 161 AA.

AC AAG76011;

XX 03-SEP-2001 (first entry)

XX Human colon cancer antigen protein SEQ ID NO:6775.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 22.

XX Homo sapiens.

XX WO200122920-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-US026524.

XX 29-SEP-1999; 99US-0157137P.

XX 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI; 2001-235357/24.

XX N-PSDB; AAH35416.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX Claim 11; Page 8234-8235; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the

CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAR37196 to AAR37204 and AAR77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922

XX SQ Sequence 161 AA;

Query Match 100.0%; Score 39; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 114 SYDSSNVV 121
|||||

RESULT 4
AAR60578
ID AAR60578 standard; protein; 402 AA.

AC AAR60578;

XX 25-MAR-2003 (revised)
DT 30-MAR-1995 (first entry)
XX Osteogenic protein OP2.

XX Osteogenic protein.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Cleavage-site 239..242
FT /note="proteolytic cleavage site"
FT 260..263
FT /note="proteolytic cleavage site"

XX WO9420539-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US002335.

XX 04-MAR-1993; 93US-00027070.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX Rueger DC, Jones WK, Tucker RF, Oppermann H, Ozkaynak E;
PI Sampath KT;

XX WPI; 1994-302971/37.
DR N-PSDB; AAQ71426.

XX Binding partners, esp. antibodies, specific for different forms of
PT osteogenic protein - for differentiating between mature and soluble
PT complexed forms of the protein in culture media or serum.

XX Disclosure; Page 50-52; 70pp; English.

XX The osteogenic protein is produced recombinantly in mammalian cell
CC cultures, and may be provided to a site for bone induction in a mammal

CC with a suitable matrix to allow infiltration, proliferation and
CC differentiation of migrating progenitor cells. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX SQ Sequence 402 AA;

Query Match 89.7%; Score 35; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNVV 8
Db 380 YDSSNVV 386
|||||

RESULT 5
ADA89244

ID ADA89244 standard; protein; 110 AA.

XX ADA89244;

XX 20-NOV-2003 (first entry)

XX Human antibody 4B4 light chain amino acid sequence SEQ ID NO:88.

XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.

XX Synthetic.

XX Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.
XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.

XX N-PSDB; ADA89243.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.

XX Disclosure; Fig 21A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that

CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents the light chain of an antibody which binds to an MHC-
 CC peptide complex where the peptide component in as peptide fragment of
 CC hTERT.

XX SQ Sequence 110 AA;

Query Match 84.6%; Score 33; DB 6; Length 110;
 Best Local Similarity 87.5%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSNNV 8
 Db 93 SYDSNNV 100
 |||||

RESULT 6

AD11153
 ID ADE11153 standard; protein; 261 AA.

XX AC ADE11153;

XX DT 29-JAN-2004 (first entry)

XX DE scFv(TF)3e10delta antibody #SEQ ID 3.

XX KW Gene therapy; anticoagulant; antibody; factor VIIa/tissue factor;
 KW FVIIa/TF; deep vein thrombosis; DVT;
 KW disseminated intravascular coagulation; DIC; acute coronary syndrome;
 KW cancer; coagulopathy; scFv(TF)3e10delta.

XX OS Synthetic.

XX PN WO2003093422-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-US013521.

XX PR 01-MAY-2002; 2002US-0376566P.

XX FA (SCHD) SCHERING AG.

XX PI Light D, McLean K;

XX DR WPI; 2004-011886/01.

XX DR N-PSDB; ADE11154.

XX PT New anticoagulant antibody that binds with greater affinity to the factor
 PT VIIa/tissue factor complex than to tissue factor alone, useful in
 PT preparing a composition for treating e.g., deep vein thrombosis or
 PT intravascular coagulation.

XX PS Claim 24; SEQ ID NO 3; 58pp; English.

XX CC The invention relates to a new anticoagulant antibody that binds with
 CC greater affinity to the factor VIIa/tissue factor (FVIIa/TF) complex than
 CC to tissue factor (TF) alone. The antibody of the invention is useful in
 CC preparing a composition for reducing and treating deep vein thrombosis
 CC (DVT), disseminated intravascular coagulation (DIC), acute coronary
 CC syndrome or cancer with evidence of coagulopathy in a patient. The
 CC current sequence represents the amino acid sequence of scFv(TF)3e10delta
 CC antibody.

XX SQ Sequence 261 AA;

Query Match 84.6%; Score 33; DB 8; Length 261;

Best Local Similarity 75.0%; Pred. No. 88;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSNNV 8

Db 242 SYDSNNV 249
 |||||

RESULT 7

AD11151
 ID ADE11151 standard; protein; 282 AA.

XX AC ADE11151;

XX DT 29-JAN-2004 (first entry)

XX DE scFv(TF)3e10 antibody #SEQ ID 1.

XX KW Gene therapy; anticoagulant; antibody; factor VIIa/tissue factor;
 KW FVIIa/TF; deep vein thrombosis; DVT;
 KW disseminated intravascular coagulation; DIC; acute coronary syndrome;
 KW cancer; coagulopathy; scFv(TF)3e10.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 273

XX FT /note= "encoded by GAT"

XX PN WO2003093422-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-US013521.

XX PR 01-MAY-2002; 2002US-0376566P.

XX FA (SCHD) SCHERING AG.

XX PI Light D, McLean K;

XX DR WPI; 2004-011886/01.

XX DR N-PSDB; ADE11152.

XX PT New anticoagulant antibody that binds with greater affinity to the factor
 PT VIIa/tissue factor complex than to tissue factor alone, useful in
 PT preparing a composition for treating e.g., deep vein thrombosis or
 PT intravascular coagulation.

XX PS Claim 24; SEQ ID NO 1; 58pp; English.

XX CC The invention relates to a new anticoagulant antibody that binds with
 CC greater affinity to the factor VIIa/tissue factor (FVIIa/TF) complex than
 CC to tissue factor (TF) alone. The antibody of the invention is useful in
 CC preparing a composition for reducing and treating deep vein thrombosis
 CC (DVT), disseminated intravascular coagulation (DIC), acute coronary
 CC syndrome or cancer with evidence of coagulopathy in a patient. The
 CC current sequence represents the amino acid sequence of scFv(TF)3e10
 CC antibody.

XX SQ Sequence 282 AA;

Query Match 84.6%; Score 33; DB 8; Length 282;

Best Local Similarity 75.0%; Pred. No. 96;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSNNV 8

Db 245 SYDSNNV 252
 |||||

RESULT 8

ABR41950

ID ABR41950 standard; protein; 617 AA.

XX

AC ABR41950;
XX DT 11-AUG-2003 (first entry)
XX DE Mouse ATP synthase subunit A, implicated in pain.
XX KW Mouse; ATP synthase; enzyme; pain; nociceptive; analgesic;
XX KM signal transduction; transgenic animal.
XX OS Mus musculus.
XX PN EP1281775-A2.
XX PD 05-FEB-2003.
XX PF 26-JUL-2002; 2002EP-00255231.
XX PR 27-JUL-2001; 2001GB-00018354.
XX PR 07-FEB-2002; 2002GB-00002892.
XX PA (WARN) WARNER LAMBERT CO.
XX PI Brooksbank RA, Dixon AK, Lee K, Finnock RD;
XX DR N-PSDB; ACC48817.
XX DR WPI; 2003-335009/32.
XX PT Use of isolated gene or nucleic acid sequence, recombinant vector, host
PT cell, non-human animal, polypeptide encoded by the nucleic acid sequence,
PT or antibody, for screening of compounds for the treatment of pain, or for
PT diagnosing pain.
XX PS Disclosure, Page 47-48; 87pp; English.
XX CC The present sequence is the protein sequence of murine vacuolar ATP
CC synthase subunit A. This protein is encoded by a gene that has been
CC identified as being up-regulated in 2 models of chronic pain, i.e.
CC streptozocin-induced diabetes and chronic constrictive injury to a nerve
CC leading to the spine. The expression products of such genes can be used
CC to screen libraries for compounds and peptide agonists and antagonists of
CC gene product activity that may be useful in the treatment or prevention
CC of chronic pain, and in the development of diagnostic tools for the
CC identification and characterisation of pain
XX CC Sequence 617 AA;
SQ Query Match 84.6%; Score 33; DB 6; Length 617;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDSSNVV 8
DB 184 NYDASNVV 191
RESULT 9
AAG29582
ID AAG29582 standard; protein; 730 AA.
XX AC
XX AAG29582;
DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 35222.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PR

PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
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PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.

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PR 04-OCT-1999; 99US-0157117P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 84.6%; Score 33; DB 3; Length 730;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDSSNV 8
|||:::
Db 511 YDSSNII 517

RESULT 10

AAG29581
ID AAG29581 standard; protein; 752 AA.

XX AAG29581;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 35221.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 16-APR-1999; 99US-0129845P.
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PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151068P.
PR 27-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 07-SEP-1999; 99US-0151930P.
PR 10-SEP-1999; 99US-0152363P.
PR 13-SEP-1999; 99US-0153070P.
PR 15-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154039P.
PR 22-SEP-1999; 99US-0154779P.
PR 23-SEP-1999; 99US-0155139P.
PR 24-SEP-1999; 99US-0155486P.
PR 28-SEP-1999; 99US-0155659P.
PR 29-SEP-1999; 99US-0156458P.
PR 04-OCT-1999; 99US-0156596P.
PR 05-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.

PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 25-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 84.6%; Score 33; DB 3; Length 752;

Best Local Similarity 71.4%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0;

Qy 2 YDSSNV 8
 |||||:
 Db 533 YDSSNII 539

RESULT 11
 ABU26679
 ID ABU26679 standard; protein; 934 AA.

AC ABU26679;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #12206.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Campylobacter jejuni.

PN WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.

DR N-ESDB; ACA30549.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 54603; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 934 AA;

Query Match 84.6%; Score 33; DB 6; Length 934;

Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSNV 8

Db 714 SYDSSNII 721

RESULT 12

ABB65449

ID ABB65449 standard; protein; 1945 AA.

AC ABB65449;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 23139.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656960/75.
XX N-PSDB; ABL09552.
DR
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 23139; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1945 AA;
SQ
Query Match 84.6%; Score 33; DB 4; Length 1945;
Best Local Similarity 62.5%; Pred. No. 8.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDSSNVV 8
DB 1266 SYESSNII 1273
RESULT 13
AAO18434
ID AAO18434 standard; protein; 110 AA.
XX
AC AAO18434;
XX
DT 11-OCT-2002 (first entry)
XX
DE Anti-GD2 antibody light chain #11.
XX
KW Anti-GD2 antibody; neuroectodermal tumour; cancer; neuroblastoma;
KW melanoma; vaccine; gene therapy; cytostatic; disialoganglioside GD2.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX DE10059930-A1.
XX
XX 29-MAY-2002.
XX
XX 23-NOV-2000; 2000DE-01059930.
XX
XX 23-NOV-2000; 2000DE-01059930.
XX
XX (FISC/) FISCHER P.
XX (UTTE/) UTTE/REUTHER-FISCHER M.
XX
XX Uttenreuther-Fischer M, Krueger J;
XX WPI; 2002-510006/55.
XX
XX Composition for treating tumors that produce disialoganglioside GD2,
XX comprises human antibody fragment able to induce anti-idiotypic
XX antibodies.
XX
XX Claim 3; Fig 7A; 14pp; German.
PS

XX The present invention relates to a composition for treating tumours
XX positive for disialoganglioside GD2 which is based on human antibody
XX fragments that activate the immune system against GD2, specifically by
XX inducing anti-GD2 antibodies. The composition can be used in the
XX treatment of neuroblastoma and melanoma. The present sequence is an anti-
XX GD2 antibody light chain
XX
SQ Sequence 110 AA;
Query Match 82.1%; Score 32; DB 5; Length 110;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDSSNV 7
DB 91 SYDSSNLI 97
RESULT 14
AAU02522
ID AAU02522 standard; protein; 113 AA.
XX
AC AAU02522;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 13.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX N-PSDB; AAS03422.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 106; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX

Search completed: June 8, 2004, 18:26:57

Job time : 38.375 secs

SQ Sequence 113 AA;
Query Match 82.1%; Score 32; DB 4; Length 113;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SYDSSNVV 8
Db 95 SYDSSNRV 102

RESULT 15
AAE09787
ID AAE09787 standard; protein; 166 AA.
XX
AC AAE09787;
XX
DT 29-NOV-2001 (first entry)
XX
DE Paenibacillus pabuli xyloglucanase XYG1035 enzyme C-terminal sequence.
XX
KW Xyloglucanase; XYG1035; glycosyl hydrolase; textile industry; detergent;
XX cellulose fibre; hemp; jute; flax; linen; garment manufacture.
XX
OS Paenibacillus pabuli.
XX
FN WO200164853-A1.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-DK000132.
XX
PR 01-MAR-2000; 2000DK-00000326.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Wilting R, Bjornvad ME, Kauppinen MS, Schuelein M;
XX WPI; 2001-565502/63.
XX
PT Novel xyloglucanase enzyme for use in textile, detergent and cellulose
PT fiber processing industries comprises family 5 of glycosyl hydrolases and
PT is derived from strains of Paenibacillus.
XX
PS Example 2; Page 91-92; 99pp; English.
XX
CC The present sequence is Paenibacillus pabuli xyloglucanase XYG1035 enzyme
CC C-terminal sequence which belongs to the family 5 of glycosyl hydrolase.
CC Xyloglucanase is useful for machine treatment of fabrics during a washing
CC cycle of a machine washing process with a washing solution. Xyloglucanase
CC is useful in textile industry for improving the properties of cellulosic
CC fibres, yarn, woven or non-woven fabric and in scouring process step, in
CC cellulose fibre processing industry for ratting of fibres such as hemp,
CC jute, flax and linen. Xyloglucanase is useful for treatment of cellulosic
CC material during the processing of cellulosic material into a material
CC ready for garment manufacture or fabric manufacture, e.g. in the desizing
CC or scouring or during industrial or household laundering of such fabric
CC or garment. Xyloglucanase is also useful in detergent compositions for
CC removing or bleaching certain soils or stains present on laundry,
CC especially soils and spots resulting from xyloglucan-containing food and
CC plants. Xyloglucanase prevents binding of certain soils to the xyloglucan
CC left on the cellulosic material and shows high performance in
CC conventional liquid detergent compositions
XX
SQ Sequence 166 AA;
Query Match 82.1%; Score 32; DB 4; Length 166;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SYDSSNVV 8
Db 108 SYDSSNRV 115

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 7.875 Seconds

(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Piri:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	84.6	505	2 AC1469	internalin like pr
2	33	84.6	680	2 T08080	probable myrosinase
3	33	84.6	730	2 F96559	hypothetical prote
4	33	84.6	934	2 C81298	probable formate d
5	33	84.6	1037	2 A60163	glycoprotein Iib -
6	33	84.6	1945	2 T13937	plexin A - fruit f
7	32	82.1	112	1 L6H048	Ig lambda chain V-
8	32	82.1	469	2 B37837	probable alpha-amy
9	32	82.1	527	2 E88040	protein F47F6.3 [i
10	32	82.1	571	2 S58356	hypothetical prote
11	31	79.5	130	2 T20762	pept protein - Sta
12	31	79.5	245	2 A30154	hypothetical prote
13	31	79.5	249	2 G84781	IgE receptor alpha
14	31	79.5	261	2 T15520	hypothetical prote
15	31	79.5	271	2 JC4584	hypothetical prote
16	31	79.5	304	2 H90095	insulin-like growt
17	31	79.5	358	2 C96923	hypothetical prote
18	31	79.5	374	2 T21513	similar to chlorom
19	31	79.5	411	2 B87200	hypothetical prote
20	31	79.5	413	2 A70795	probable ligase [i
21	31	79.5	450	2 T21515	hypothetical prote
22	31	79.5	783	2 B84823	hypothetical prote
23	31	79.5	876	2 B96693	probable isoamylas
24	31	79.5	963	2 S45167	Probable receptor
25	30	76.9	229	2 S49494	chitin synthase [E
26	30	76.9	232	2 AH0954	replication protei
27	30	76.9	293	2 T23806	probable membrane
28	30	76.9	311	2 T17613	hypothetical prote
29	30	76.9	344	2 H97223	hypothetical prote

ALIGNMENTS

RESULT 1

AC1469

internalin like protein (LPXTG motif) [imported] - Listeria innocua (strain Clip11262)
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: AC1469
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouran, A.; Me
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AC1469

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-505 <GLA>

A/Cross-references: GB:AL592022; PIDN:CAC95523.1; PID:gl16412719; GSPDB:GN00178

A/Experimental source: strain Clip11262

A/Genetics:

A/Gene: lin0290

Query Match 84.6%; Score 33; DB 2; Length 505;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
:|||||
DB 319 TYDSSNVV 326

RESULT 2

T08080

probable myrosinase-binding protein - rape

N/Alternate names: jasmonate inducible protein

C/Species: Brassica napus (rape)

C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000

C/Accession: T08080

A/Geshi, N.; Brandt, A.

Planta 204, 295-304, 1998

A/Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L. seed

A/Reference number: Z16340; MUID:98192006; PMID:9530873

A/Accession: T08080

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-680 <GES>

A/Cross-references: EMBL:Y11483; NID:ei023101; PIDN:CAA72271.1; PID:e304150

A/Experimental source: cv. Global; isolate a4; young seedlings

A/Note: jasmonate inducible

Query Match 84.6%; Score 33; DB 2; Length 680;

Best Local Similarity 71.4%; pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDSSNVV 8
 |||||::
 db 308 YDSSNII 314

RESULT 3
F96559
hypothetical protein F5F19.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96559
R,Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96559
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-730 <STO>
A:Cross-references: GB:AE005173; NID:g4220464; PIDN:AA012691.1; GSPDB:GN00141
C:Genetics:
A:Gene: F5F19.6
A:Map position: 1

```
Query Match      84.6%; Score 33; DB 2; Length 730;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5: Conservative 2: Mismatches 0: Indels
```

QY 2 YDSSNV 8
|||
|||:
511 YDSSNV 517

RESULT 4

C81298
probable formate dehydrogenase (EC 1.2.1.2) large chain Cj1511c [similarity] - Campylobacter
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002
C:Accession: C81298
R:Carroll, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.W.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: C81298
A:Molecule type: DNA
A:Cross-References: GB:AL11168; GB:AL139078; MID:96968723; PIDN:CAB73932.1; PID:9696893
A:Experimental source: serotype O2, strain NCTC 11168
A:Note: a translation exception was noted by the authors
A:Note: in Genbank entry AL139078, release 117.0, PIDN:CAB73932.1, the selenocysteine U
C:Genetics:
A:Gene: fdhA; Cj1511c
C:Superfamily: formate dehydrogenase
C:Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; NAD;
F:57,60,64,92/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F:94,182/Active site: lys, His #status predicted
F:181/Binding site: molybdopterin guanine dinucleotide (Cys) (covalent) #status predicted
F:181/Modified site: selenocysteine #status predicted

Query Match 84.6%; Score 33; DB 2; Length 934;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5: Conservative 2: Mismatches 1: Indels

QY 1 SYDSSNVV 8
||| ||::
pb 714 SYDSSNIT 721

RESULT 5

A60163
glycoprotein IIb - rat
C:Species: Rattus sp. (rat)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1998
C:Accession: A60163; B60163
C:Accession: Newman, P.J.
R; Poncz, M.; Newman, P.J.
Blood 75, 1282-1289, 1990
A:Title: Analysis of rodent platelet glycoprotein IIb: evidence for evolutionarily cons
A:Reference number: A60163; PMID:90181615; PMID:2310828
A:Accession: A60163
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1037 <PON>
A:Accession: B60163
A:Molecule type: protein
A:Residues: 32-50 <PON2>
C:Comment: This protein is proteolytically processed into a heavy chain and a light cha
C:Superfamily: integrin alpha-2b chain
C:Keywords: calcium, disulfide bond, glycoprotein

Query Match	84.6%	Score 33;	DB 2;	Length 1037;
Best Local Similarity	87.5%;	Pred. No. 82;		
Matches	7.	Conservative	0:	Mismatches
			1:	Indels
			0:	Gaps
			0:	Gaps

Qy 1 SYDSSNVV 8
252 SYDSSNPV 259

RESULT 6
T13937
plexin A - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-
C/Accession: T13937
R/Winberg, M.L.; Noordermeer, J.N.; Tamagnone,
Cell 95, 903-916, 1998
A/Title: Plexin A is a neuronal semaphorin rec
A/Reference number: Z17621; MUID:99091049; P
A/Accession: T13937
A/Status: preliminary; translated from GB/EMBL
A/Molecule type: mRNA
A/Residues: 1-1945 <WIN>
A/Cross-references: EMBL:AF106932; NID:g405667
C/Genetics:

A;Gene: plexA

A: Cross-reference
A: Man position. 4

C;Function:

A;Description: may function as repellents during axon guidance
C;Keywords: cell adhesion; nerve

Query Match 84.6%; Score 33; DB 2; Length 1945;
Best Local Similarity 62.5%; Pred. NO. 1.6e+02;
Matches 5: Conservative 3; Mismatches 0. Indels

Qy 1 SYDSSNVV 8
|||:::
Db 1266 SYESSNII 11

RESULT 7

L6HU48

L6HU48
 Iα lambda chain V-VT region (N1α-48) - human

C;Species: Homo sapiens (man)

```
C:\Date: 28-Feb-1980 #sequence revision 28-Feb-1980 #text_change 02-Sep-1997
```


C:Accession: A01991
 R:Takahashi, N.; Takayasu, T.; Isobe, T.; Shinoda, T.; Okuyama, T.; Shimizu, A.
 J. Biochem. 86, 1523-1535, 1979
 A:Title: Comparative study on the structure of the light chains of human immunoglobulins
 A:Reference number: A01991, MUID:80094390; PMID:118171
 A:Accession: A01991
 A:Molecule type: protein
 A:Residues: 1-112 <PAK>
 A:Note: this is the first sequenced V region of lambda chain subgroup VI
 C:Comment: This is a Bence Jones protein.
 C:Genetics:
 A:Gene: GDB:IGLV8
 A:Cross-references: GDB:119342; OMIM:147240
 A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:15-33/Domain: immunoglobulin homology <IMM>
 F:22-91/Disulfide bonds: #status predicted

Query Match 82.1%; Score 32; DB 1; Length 112;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
 DB 93 SYDSSNL 99

RESULT 8
 B37837
 probable alpha-amylase (EC 3.2.1.1) - Clostridium acetobutylicum (fragment)
 C:Species: Clostridium acetobutylicum
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999
 A:Accession: B37837
 R:Gerischer, U.; Duerre, P.
 J. Bacteriol. 172, 6907-6918, 1990
 A:Title: Cloning, sequencing, and molecular analysis of the acetoacetate decarboxylase gene
 A:Reference number: A37837; MUID:91072241; PMID:2254264
 A:Accession: B37837
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-469 <GER>
 A:Cross-references: GB:M55392; GB:M34078; NID:G144708; PIDN:AAA63759.1; PID:G144709
 C:Superfamily: alpha-amylase, subtilisin type; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase

Query Match 82.1%; Score 32; DB 2; Length 469;
 Best Local Similarity 85.7%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNV 8
 DB 286 YDSSNLV 292

RESULT 9
 E88040
 protein P47F6.3 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: E88040
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: E88040
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-527 <STO>

A:Cross-references: GB:chr_II; PIDN:ACT1112.1; PID:G1707160; GSPDB:GN00020; CESP:F47F6.3
 C:Genetics:
 A:Gene: F47F6.3
 A:Map position: 2

Query Match 82.1%; Score 32; DB 2; Length 527;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
 DB 337 SYDSSNAL 344

RESULT 10
 S58356
 pept protein - Staphylococcus epidermidis
 C:Species: Staphylococcus epidermidis
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
 R:Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Ker
 Eur. J. Biochem. 232, 478-489, 1995
 A:Title: Nucleotide sequence of the lantibiotic Pep5 biosynthetic gene cluster and function
 A:Reference number: S6651; MUID:96035882; PMID:7556197
 A:Accession: S6651
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-571 <ME2>
 A:Cross-references: EMBL:Z49865; NID:G945014; PIDN:CAA90021.1; PID:G945015
 C:Genetics:
 A:Gene: pept

C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:348-543/Domain: ATP-binding cassette homology <ABC>
 F:365-372/Region: nucleotide-binding motif A (P-loop)

Query Match 82.1%; Score 32; DB 2; Length 571;
 Best Local Similarity 75.0%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
 DB 341 SYDSKNVL 348

RESULT 11
 T20762
 hypothetical protein F11C1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T20762
 R:Palmer, S.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: Z19321
 A:Accession: T20762
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-130 <WIL>
 A:Cross-references: EMBL:Z54270; PIDN:CAA91026.1; GSPDB:GN00028; CESP:F11C1.2
 A:Experimental source: clone F11C1
 C:Genetics:
 A:Gene: CESP:F11C1.2
 A:Map position: x
 A:Introns: 23/3; 63/3; 89/1

Query Match 79.5%; Score 31; DB 2; Length 130;
 Best Local Similarity 85.7%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
 DB 68 SFDSSNV 74

```

RESULT 12
A30154
Igf receptor alpha chain precursor - rat
N/Alternate names: Fc-epsilon-R alpha chain precursor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
C/Accession: C31327; A30154; A27116; I55304
R/Liu, F.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A/Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ig
A/Reference number: A94203; MUID:88289772; PMID:2969594
A/Accession: C31327
A/Molecule type: mRNA
A/Residues: 1-245 <LIU>
A/Cross-references: GB:M21622; GB:J03811
A/Experimental source: basophilic leukemia cell line, clone R3-4
A/Accession: A31327
A/Molecule type: mRNA
A/Residues: 21-245 <LI3>
A/Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811
A/Experimental source: basophilic leukemia cell line
R/Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A/Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization
A/Reference number: A94191; MUID:88158102; PMID:2964640
A/Accession: A30154
A/Molecule type: mRNA
A/Residues: 1-245 <SHI>
A/Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332
R/Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A/Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff
A/Reference number: A27116; MUID:88024987; PMID:2959318
A/Accession: A27116
A/Molecule type: mRNA
A/Residues: 1, 'G', 3-236, 'N', 238-244, 'RLKPNs' <KIN>
R/Tepler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A/Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur
A/Reference number: I55304; MUID:89174653; PMID:2522441
A/Accession: I55304
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391
C/Superfamily: Fc gamma receptor III; immunoglobulin homology
C/Keywords: immunoglobulin receptor; transmembrane protein
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-245/Product: IgE receptor alpha chain #status predicted <MAT>
F/42-93/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 31; DB 2; Length 245;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSNV 7
|||||
Db 153 SYDSNNI 159

RESULT 13
G84781
hypothetical protein At2g36540 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: G84781
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

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A/Accession: G84781
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <STO>
A/Cross-references: GB:AE002093; NID:G4581152; PIDN:AAD24636.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g36540
A/Map position: 2

```

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Query Match 79.5%; Score 31; DB 2; Length 249;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 SYDSNV 7
|||||
Db 187 SYDASNI 193

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RESULT 14
TI5520
hypothetical protein C15H9.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C/Accession: TI5520
R/Bentley, D.
submitted to the EMBL Data Library, April 1996
A/Description: The sequence of C. elegans cosmid C15H9.
A/Reference number: Z18364
A/Accession: TI5520
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-261 <BN>
A/Cross-references: EMBL:U56965; NID:G1945492; PID:G1293841; PIDN:AA852662.1; GSPDB:GN0
A/Experimental source: strain Bristol N2; clone C15H9
C/Genetics:
A/Gene: CHSP:C15H9.2
A/Map position: X
A/Introns: 16/3; 40/2; 78/3; 109/2; 137/3; 192/1; 244/3

```

```

Query Match 79.5%; Score 31; DB 2; Length 261;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 YDSSNV 8
|||||
Db 122 FDSSNV 128

```

```

RESULT 15
JC4584
insulin-like growth factor binding protein-5 precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 07-Jul-2003
C/Accession: JC4584; G23734
R/White, M.E.; Diao, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R.
Biochem. Biophys. Res. Commun. 218, 248-253, 1996
A/Title: Molecular cloning and sequence analysis of the porcine insulin-like growth fac
A/Reference number: JC4584; MUID:96136309; PMID:8573141
A/Accession: JC4584
A/Molecule type: mRNA
A/Residues: 1-271 <WHI>
A/Cross-references: GB:U41340; NID:G1173906; PIDN:AAA87859.1; PID:G1173907
R/Experimental source: skeletal muscle
R/Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A/Title: Isolation and molecular cloning of insulin-like growth factor-binding protein
A/Reference number: A23734; MUID:92049376; PMID:1719383
A/Accession: G23734
A/Molecule type: protein
A/Residues: 20-25, 'X', 27-28, 'X', 30-36, 'X', 38-39 <SHI>
C/Comment: This protein has essential roles in the regulation and coordination of insul
lays a role during myoblast proliferation and differentiation, and is important in the
C/Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat

```

C:Keywords: differentiation; skeletal muscle
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: insulin-like growth factor binding protein-5 #status experimental <MAI
F:191-262/Domain: thyroglobulin type I repeat homology <THYI>

Query Match 79.5%; Score 31; DB 2; Length 271;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
|:|||||
Db 264 SFDSSNV 270

Search completed: June 8, 2004, 18:54:17
Job time : 9.875 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 4.5 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	84.6	617	1 VAAL_MOUSE	P0516 mus musculus
2	32	82.1	112	1 LV6B_HUMAN	P01722 homo sapien
3	32	82.1	460	1 COAA_BF1L	O80297 bacterioph
4	32	82.1	760	1 AMY_CLOAB	P23671 clostridium
5	31	79.5	245	1 FCBL_RAT	P12371 rattus norv
6	31	79.5	271	1 IBP5_PIG	Q28985 sus scrofa
7	31	79.5	272	1 SER3_DROME	P17207 drosophila
8	31	79.5	514	1 FOLE_CANAL	Q94893 candida alb
9	31	79.5	548	1 PRZN_RENSA	P55111 renibacteri
10	31	79.5	963	1 CHS2_YEAST	P14180 saccharomyc
11	31	79.5	964	1 CTA2_BACCI	P70873 bacillus ci
12	30	76.9	332	1 REGA_CLOSA	Q45831 clostridium
13	30	76.9	429	1 YN8H_YEAST	P53729 saccharomyc
14	30	76.9	462	1 MB12_ARATH	Q9sav0 arabidopsis
15	30	76.9	624	1 VP97_NEVOP	P17930 oryza pseu
16	30	76.9	630	1 V109_FOWPV	P36317 foalpoix vir
17	30	76.9	754	1 MES3_CAEEL	Q10665 caenorhabdi
18	30	76.9	769	1 ITB7_HUMAN	P05107 homo sapien
19	30	76.9	798	1 GYRB_BUCAL	P26010 homo sapien
20	30	76.9	803	1 GYRB_MOUSE	P57126 buchnera ap
21	30	76.9	806	1 ITB7_MOUSE	P26011 mus musculu
22	30	76.9	816	1 COLA_VIBPA	Q58696 vibrio para
23	30	76.9	1483	1 YCD4_DROME	Q9vgw1 drosophila
24	29	74.4	294	1 YHDI_ECOLI	P28638 escherichia
25	29	74.4	469	1 IA13_LYCES	Q24881 lycopersico
26	29	74.4	483	1 YCU2_YEAST	P25632 saccharomyc
27	29	74.4	501	1 ACHB_HUMAN	P11230 homo sapien
28	29	74.4	501	1 ACHB_MOUSE	P05690 mus musculu
29	29	74.4	501	1 ACHB_RAT	P25109 rattus norv
30	29	74.4	505	1 ACHB_BOVIN	P04758 bos taurus
31	29	74.4	528	1 FOLE_NEUCR	O13492 neurospora
32	29	74.4	758	1 YP58_YEAST	Q99299 saccharomyc
33	29	74.4	762	1 SLAP_ACEKI	P22258 acetogenium

34	29	74.4	771	1 ITB2_MOUSE	P11835 mus musculu
35	29	74.4	775	1 CDR2_SCHPO	P87050 schizosacch
36	29	74.4	784	1 LON_RICPR	Q9zd92 rickettsia
37	29	74.4	803	1 GYRB_ECOLI	P06982 escherichia
38	29	74.4	803	1 GYRB_SALTY	Q60008 salmonella
39	29	74.4	907	1 NUOG_BUCBP	Q89aul buchnera ap
40	29	74.4	1916	1 RIFI_YEAST	P29539 saccharomyc
41	28	71.8	173	1 LEC2_MEGRO	P17346 megabalanus
42	28	71.8	209	1 RH01_YEAST	P06780 saccharomyc
43	28	71.8	221	1 EPD2_ONCMY	P28771 oncorhynchu
44	28	71.8	230	1 Y920_HELPJ	Q9zkt1 helicobacte
45	28	71.8	230	1 Y920_HELPY	O25578 helicobacte

ALIGNMENTS

RESULT 1
VAAL_MOUSE STANDARD; PRT; 617 AA.
AC P50516;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform
DE (EC 3.6.3.14) (V-ATPase A subunit 1) (Vacuolar proton pump alpha
DE subunit 1) (V-ATPase 69 kDa subunit 1).
GN ATP6V1A OR ATP6V1A1 OR ATP6A1 OR ATP6A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=96362668; PubMed=8741845;
RA Laitala T., Howell M.L., Dean G.E., Vaananen H.K.;
RT "Resorption-cycle-dependent polarization of mRNAs for different
RL Mol. Biol. Cell 7:129-142(1996).
CC -!- FUNCTION: Catalytic subunit of the peripheral V1 complex of
CC vacuolar ATPase. V-ATPase vacuolar ATPase is responsible for
CC acidifying a variety of intracellular compartments in eukaryotic
CC cells.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: V-ATPase is an heteromultimeric enzyme composed of a
CC peripheral catalytic V1 complex (main components: subunits A, B,
CC C, D, E, and F) attached to an integral membrane V0 proton pore
CC complex (main component: the proteolipid protein).
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC
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CC EMBL; U13837; AAC52410.1; -;
CC MGD; MGI:1201780; Atp6vial.
CC InterPro; IPR005725; ATP_synthV A.
CC InterPro; IPR000793; ATPase a/b C.
CC InterPro; IPR000194; ATPase a/bcentre.
CC InterPro; IPR004100; ATPase a/bN.
CC InterPro; IPR009005; F1_ATPase_a/bN.
CC Pfam; PF00006; ATP-synt_ab; 1.
CC Pfam; PF00306; ATP-synt ab C; 1.
CC TIGRFAMs; TIGR01042; V-ATPase V1 A; 1.
CC PROSITE; PS00152; ATPASE ALPHA BETA; 1.
CC ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
CC Multigene family.

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FT NP BIND 250 257 ATP (POTENTIAL).
SQ SEQUENCE 617 AA; 68268 MW; 778D2843070200CF CRC64;

Query Match 84.6%; Score 33; DB 1; Length 617;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 8
Db 184 NYDASNV 191

RESULT 2
LV6B HUMAN STANDARD; PRT; 112 AA.
ID - LV6B_HUMAN
AC P01722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG lambda chain V-VI region NIG-48.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80094390; PubMed=118171;
RA Takahashi N., Takayasu T., Isobe T., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative study on the structure of the light chains of human
RL J. Biochem. 86:1523-1535(1979).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01991; L6HU48.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 107 IG-LIKE.
FT NON TER 112
SQ SEQUENCE 112 AA; 12152 MW; CFB307BC527A384 CRC64;

Query Match 82.1%; Score 32; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
Db 93 SYDSSNV 99

RESULT 3
COAA BP1F1 STANDARD; PRT; 460 AA.
ID - COAA_BP1F1
AC O80297;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Coat protein A precursor (Attachment protein).
GN III OR 3.
OS Bacteriophage Ifi.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10868;
RN [1]
RP SEQUENCE FROM N.A.
RA Hill D.P., Hughes G., McNaughton J.C., Stockwell P.A., Petersen G.B.;

"DNA sequence of the filamentous coliphage Ifi.";
Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Coat protein A is necessary for adsorption of the virion
onto the F-pilus of the host cell (By similarity).
-----
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CC EMBL; U02303; AAC62155.1; -.
DR HSSP; P03661; IFGP.
DR InterPro; IPR008021; Phage Coat A.
DR Pfam; PF05357; Phage Coat A; 1.
KW Phage recognition; Coat protein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 460 COAT PROTEIN A.
SQ SEQUENCE 460 AA; 48790 MW; 9AD651968C715AE2 CRC64;

Query Match 82.1%; Score 32; DB 1; Length 460;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
Db 229 SYDSSNV 235

RESULT 4
AMY CLOAB STANDARD; PRT; 760 AA.
ID - AMY_CLOAB
AC P23671; Q9S429;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanhydrolase).
GN AMYA OR AMYP OR CAP0168.
OS Clostridium acetobutylicum.
OG Plasmid pSOLI.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RA Schaffer S., Duerre P.;
RT "Nucleotide sequence analysis and ECF sigma factor-dependent
RT expression of an alpha-amylase gene from Clostridium acetobutylicum
RT DSM 792.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RA Sabathe F., Cornillot E., Croux C., Soucaille P.;
RT "Molecular characterization of amyP, a pSOLI located gene coding the
RT major alpha-amylase of Clostridium acetobutylicum ATCC824, and its use
RT as a reporter system for strain degeneration.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).

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RN RP SEQUENCE OF 292-760 FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=91072241; PubMed=2254264;
RA Gerischer U., Duerre P.;
RT "Cloning, sequencing, and molecular analysis of the acetate
RL J. Bacteriol. 172:6907-6918(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
DR EMBL; M55392; AAA63759.2; -
DR EMBL; AF164199; AAD47072.1; -
DR EMBL; AB001438; AAK76913.1; -
DR PIR; B37837; B37837.
DR HSP; P00691; LBAG.
DR InterPro; IPR006048; Alpha_amyl C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR005085; CBM 25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase; 1.
DR Pfam; PF03423; CBM 25; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00632; Amy C; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Plasmid; Complete proteome.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 760 ALPHA-AMYLASE.
FT ACT_SITE 222 222 BY SIMILARITY.
FT ACT_SITE 262 262 BY SIMILARITY.
FT ACT_SITE 321 321 BY SIMILARITY.
FT METAL 143 143 CALCIUM (BY SIMILARITY).
FT METAL 184 184 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT METAL 192 192 CALCIUM (BY SIMILARITY).
FT METAL 226 226 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT CONFLICT 213 213 D -> H (IN REF. 1).
FT CONFLICT 222 222 D -> H (IN REF. 1).
FT CONFLICT 571 571 A -> G (IN REF. 1).
SQ SEQUENCE 760 AA; 83045 MW; 10E146F40252F6D0 CRC64;

Query Match 82.1%; Score 32; DB 1; Length 760;
Best Local Similarity 85.7%; Pred.No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNVV 8
Db 577 YDSSNLV 583

RESULT 5
ID FCE1 RAT STANDARD; PRT; 245 AA.
AC P12371.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor precursor
DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN FCER1A OR FCE1A.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakimi J., Kochan J.;
RT "A cDNA presumptively coding for the alpha subunit of the receptor
RL with high affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RN [2]
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Mast cells;
RX MEDLINE=88158102; PubMed=2964640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [4]
RP SEQUENCE OF 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;
RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IGE receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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CC
DR EMBL; M17153; AAA42045.1; -
DR EMBL; J03606; AAA41582.1; -
DR EMBL; M21622; AAA41146.1; -
DR PIR; C31327; A30154.
DR HSP; P12319; IAL5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 245 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT RECEPTOR ALPHA-SUBUNIT.
FT DOMAIN 24 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 245 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 103 IG-LIKE 1.
FT DOMAIN 113 181 IG-LIKE 2.
FT DISULFID 49 91 BY SIMILARITY.
FT DISULFID 130 174 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 245 AA; 27793 MW; AOE67DD363B72197 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 245;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
 Db 153 SYDSSNV 159
 |||||

RESULT 6
 IBP5_PIG STANDARD; PRT; 271 AA.
 AC Q28985;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Insulin-like growth factor binding protein 5 precursor (IGFBP-5)
 DE (IBP-5) (IGF-binding protein 5).
 GN IGFBP5.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=96136309; PubMed=8573141;
 RA White M.E., Diao R., Hathaway M.R., Mickelson J., Dayton W.R.;
 RA "Molecular cloning and sequence analysis of the porcine insulin-like
 RT growth factor binding protein-5 complementary deoxyribonucleic
 RT acid.";
 RL Biochem. Biophys. Res. Commun. 218:248-253 (1996).
 CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs
 CC and have been shown to either inhibit or stimulate the growth
 CC promoting effects of the IGFs on cell culture. They alter the
 CC interaction of IGFs with their cell surface receptors.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 IGFBP domain.
 CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
 CC
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 CC
 CC -----
 CC EMBL; U41340; AAA87859.1; --
 CC PIR; JC4584; JC4584.
 CC HSSP; P24593; 180E.
 CC InterPro; IPR009030; Grow_fac_recep.
 CC InterPro; IPR000867; Insl_gro_fac_pr.
 CC InterPro; IPR000716; Thyroglobulin_1.
 CC Pfam; PF00219; IGFBP; 1.
 CC Pfam; PF00086; thyroglobulin_1; 1.
 CC PIRSF; PIRSF001969; IGFBP1-67; 1.
 CC SMART; SM00121; IB; 1.
 CC SMART; SM00211; TY; 1.
 CC PROSITE; PS00222; IGF BINDING; 1.
 CC PROSITE; PS00484; THYROGLOBULIN_1; 1.
 KW Growth factor binding; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 271 INSULIN-LIKE GROWTH FACTOR BINDING
 FT PROTEIN 5.

FT DOMAIN 214 262 THYROGLOBULIN TYPE-I.
 SQ SEQUENCE 271 AA; 30323 MW; 95C254E95DC4ED8D CRC64;

Query Match 79.5%; Score 31; DB 1; Length 271;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNV 7
 Db 264 SFDSNV 270
 |||||

RESULT 7
 SER3_DROME STANDARD; PRT; 272 AA.
 AC P17207; O9VAD8;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Serine protease 3 precursor (EC 3.4.21.-).
 GN SER9DC OR SER3 OR CG17951.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.B., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fogle C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Mazny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE OF 212-272 FROM N.A.
 RX MEDLINE=89219063; PubMed=2469005;
 RA Yun Y., Davis R.L.;
 RT "Levels of RNA from a family of putative serine protease genes are

RT reduced in *Drosophila melanogaster* dunce mutants and are regulated by
 RT cyclic AMP.";
 RL Mol. Cell. Biol. 9:692-700(1989).
 CC -!- FUNCTION: Its major function may be to aid in digestion.
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in the larval gut.
 CC -!- DEVELOPMENTAL STAGE: Began to appear at late embryo stage and
 CC continued to increase in abundance throughout the larval stage.
 CC They are not present in pupae but reappeared in the adult.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
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 CC -----
 DR EMBL; AE003771; AAF56973.1; -.
 DR EMBL; M24380; AAB02551.1; -.
 DR PIR; PS0049; PS0049.
 DR HSSP; P00734; 1B7X.
 DR MEROPS; S01.00A; -.
 DR FlyBase; FBgn0003358; Ser-99Dc.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal; Zymogen; Multigene family.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 40 BY SIMILARITY.
 FT CHAIN 41 272 SERINE PROTEASE 3.
 FT ACT_SITE 84 84 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 127 127 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 69 85 BY SIMILARITY.
 FT DISULFID 193 208 BY SIMILARITY.
 FT DISULFID 218 246 BY SIMILARITY.
 FT CONFLICT 212 212 P -> M (IN REF. 2).
 SQ SEQUENCE 272 AA; 29620 MW; A61E9DE3AFC93AF CRC64;
 Query Match 79.5%; Score 31; DB 1; Length 272;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YDSSNVV 8
 Db 171 YDGSNVV 177
 RESULT 8
 FOIE CANAL STANDARD; PRT; 514 AA.
 ID FOIE CANAL
 AC Q9Y893;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Folylpolylglutamate synthase (EC 6.3.2.17) (Folylpolyl-gamma-glutamate
 DE synthetase) (FPGS).
 GN MET7.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Subramanian M., Li C., Desouza L., Bognar A.L.;
 RT "Sequencing of a Candida albicans genomic library plasmid which

RT encodes the complete open reading frame of folylpolylglutamate
 RT synthetase.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Conversion of folates to polyglutamate derivatives (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + {tetrahydrofolyl-(Glu)} (N) + L-glutamate
 CC = ADP + phosphate + {tetrahydrofolyl-(Glu)} (N+1).
 CC -!- PATHWAY: Folate biosynthesis.
 CC -!- SIMILARITY: Belongs to the folylpolylglutamate synthase family.
 CC -----
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 CC -----
 DR EMBL; AF156928; AAD40312.1; -.
 DR HSSP; P15925; 1FGS.
 DR InterPro; IPR001645; Fpolygl_synthase.
 DR TIGRFAMs; TIGR01499; foic; 1.
 DR PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; FALSE_NEG.
 DR PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1.
 KW Ligase; One-carbon metabolism; ATP-binding.
 FT NP_BIND 78 84 ATP (POTENTIAL).
 SQ SEQUENCE 514 AA; 57907 MW; EA8F3C8CC79A12A CRC64;
 Query Match 79.5%; Score 31; DB 1; Length 514;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDSSNVV 8
 Db 192 TYDSTNII 199
 RESULT 9
 PRZN RENSA STANDARD; PRT; 548 AA.
 ID PRZN RENSA
 AC P5511;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Zinc metalloproteinase precursor (EC 3.4.24.-) (Hemolysin).
 GN HLY.
 OS Renibacterium salmoninarum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; Renibacterium.
 OX NCBI_TaxID=1646;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT444;
 RX MEDLINE=95400487; PubMed=7545509;
 RA Grayson T.H., Evenden A.J., Gilpin M.L., Martin K.L., Munn C.B.;
 RT "A gene from Renibacterium salmoninarum encoding a product which
 RT shows homology to bacterial zinc-metalloproteases.";
 RL Microbiology 141:1331-1341(1995).
 RN [2]
 RP REVISIONS TO 149-170.
 RA Grayson T.H.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ZINC METALLOPROTEASE WITH HEMOLYTIC PROPERTIES.
 CC HEMOLYTIC ACTIVITY IS OBSERVED FROM 6 TO 37 DEGREES CELSIUS FOR
 CC MAMMALIAN ERYTHROCYTES.
 CC -!- COFACTOR: Binds 1 zinc ion and 4 calcium ions per subunit (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: NOT SECRETED, BUT PROBABLY REMAINS ATTACHED
 CC OR ASSOCIATED WITH THE CELL WALL.
 CC -!- INDUCTION: EXPRESSION OF THE HEMOLYSIN IS MODULATED BY THE
 CC AVAILABILITY OF IRON.
 CC -!- SIMILARITY: Belongs to peptidase family M4.
 CC -----

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 48.1 kDa protein in SEC12-SXK2 intergenic region.
 GN YNR029C OR N3260.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 [1]
 RP SEQUENCE FROM N.A.
 RA Pohl T.M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO P.DENITRIFICANS COBW.
 CC
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 CC
 CC EMBL; Z71644; CAA96309.1; -.
 DR PIR; S63360; S63360.
 DR GerMOnline; 143374; -.
 DR SGD; S0005312; YNR029C.
 DR InterPro; IPR003495; COBW.
 DR Pfam; PF02492; COBW; 1.
 KW Hypothetical protein; ATP-binding.
 FT NP BIND 78 85 ATP (POTENTIAL).
 SQ SEQUENCE 429 AA; 48121 MW; 5BE033E6885EF764 CRC64;

 Query Match 76.9%; Score 30; DB 1; Length 429;
 Best Local Similarity 62.5%; Pred. No. 63;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 SYDSSNVV 8
 |||||:
 Db 36 SYDGGNIV 43

 RESULT 14
 MB12 ARATH
 ID MB12 ARATH STANDARD; PRT; 462 AA.
 AC Q9SAV0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Myrosinase binding protein-like At1G52040.
 GN AT1G52040 OR F5F19.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA STEAIN-cv. Columbia;
 RC MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gil J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 CC -!- SIMILARITY: Belongs to the jacalin lectin family.
 CC
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 CC
 CC EMBL; AC006216; AAD12678.1; -.
 DR PIR; B96560; B96560.
 DR HSSP; P18670; IJAC.
 DR InterPro; IPR001229; Jacalin_lectin.
 DR Pfam; PF01419; Jacalin; 3.
 KW Lectin; Repeat; Multigene family.
 SQ SEQUENCE 462 AA; 50167 MW; 0A86DC8AF4B72319 CRC64;

 Query Match 76.9%; Score 30; DB 1; Length 462;
 Best Local Similarity 57.1%; Pred. No. 68;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 YDSSNVV 8
 |||||:
 Db 87 YDSTNII 93

 RESULT 15
 VP87_NPVOP
 ID VP87_NPVOP STANDARD; PRT; 624 AA.
 AC P17930;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Capsid protein p87.
 GN P87.
 OS Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNVPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolydnavirus.
 OX NCBI_TaxID=164623;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90232722; PubMed=2184573;
 RA Mueller R., Pearson M.N., Russell R.L.Q., Rohrmann G.F.;
 RA "A capsid-associated protein of the multicapsid nuclear polyhedrosis
 RT virus of Orgyia pseudotsugata: genetic location, sequence,
 RT transcriptional mapping, and immunocytochemical characterization.";
 RL Virology 176:133-144 (1990).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97271300; PubMed=9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohrmann G.F.;
 RT "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
 RT polyhedrosis virus genome.";
 RL Virology 229:381-399 (1997).
 CC -!- SUBCELLULAR LOCATION: CAPSID-ASSOCIATED.
 CC
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 CC
 CC EMBL; D13959; BAA03061.1; -.

DR EMBL; U75930; AAC59104.1; -.
KW PIR; A34602; VCNV87.
FT Coat protein; Repeat.
FT DOMAIN 256 280 2 X 13 AA TANDEM REPEATS, MOTIF A.
FT REPEAT 256 288 MOTIF A.
FT REPEAT 269 280 MOTIF A.
FT DOMAIN 283 324 3 X 11 AA REPEATS, MOTIF B.
FT REPEAT 283 293 MOTIF B.
FT REPEAT 296 306 MOTIF B.
FT REPEAT 314 324 MOTIF B.
SQ SEQUENCE 624 AA; 70696 MW; 8573D00964C9157B CRC64;

Query Match 76.9%; Score 30; DB 1; Length 624;

Best Local Similarity 62.5%; Pred. No. 95;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8

DB 352 SYDTSVI 359

Search completed: June 8, 2004, 18:56:18

Job time : 5.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 23.125 Seconds
(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-66
Perfect score: 39
Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	89.7	218	2 Q7WRF3	Q7wrf3 neisseria m
2	35	89.7	350	2 Q7X4S0	Q7x4s0 neisseria m
3	34	87.2	644	16 Q8A3E1	Q8a3e1 bacteroides
4	33	84.6	505	16 Q92F18	Q92ff18 listeria in
5	33	84.6	600	5 Q8ITJ3	Q8itj3 heterodera
6	33	84.6	680	10 P93658	P93658 brassica na
7	33	84.6	730	10 Q9ZU23	Q9zu23 arabidopsis
8	33	84.6	934	16 Q9PWF2	Q9pmf2 campylobact
9	33	84.6	951	5 Q7YU07	Q7yu07 drosophila
10	33	84.6	1505	5 Q8IM99	Q8im99 drosophila
11	33	84.6	1945	5 Q96681	Q96681 drosophila
12	33	84.6	1945	5 Q9V491	Q9v491 drosophila
13	32	82.1	238	12 Q993S3	Q993s3 banana mild
14	32	82.1	507	12 Q8QHV1	Q8qhv1 spartina mo
15	32	82.1	521	5 Q9VDQ3	Q9vqd3 drosophila
16	32	82.1	523	5 Q8MT85	Q8mt85 drosophila

17	32	82.1	527	5	P91310	P91310 caenorhabdi
18	32	82.1	542	5	Q9V9K0	Q9v9k0 drosophila
19	32	82.1	547	10	Q7XIM1	Q7xim1 oryza sativ
20	32	82.1	557	5	Q95XY3	Q95xy3 caenorhabdi
21	32	82.1	571	2	Q54121	Q54121 staphylococ
22	32	82.1	840	3	Q876C9	Q876c9 saccharomyc
23	32	82.1	1938	2	P70983	P70983 bacillus vuln
24	32	82.1	4654	16	Q8D418	Q8d418 vibrio vuln
25	32	82.1	7149	5	Q8IM09	Q8im09 plasmodium
26	31	79.5	105	2	Q7WUM5	Q7wum5 actinoplan
27	31	79.5	158	5	Q19343	Q19343 caenorhabdi
28	31	79.5	192	5	Q9V8A2	Q9v8a2 drosophila
29	31	79.5	249	10	Q9SJQ4	Q9sjq4 arabidopsis
30	31	79.5	261	5	Q18030	Q18030 caenorhabdi
31	31	79.5	274	5	Q17086	Q17086 anopheles s
32	31	79.5	304	10	Q98RQ1	Q98rg1 guillardia
33	31	79.5	317	5	Q8WP58	Q8wp58 plasmodium
34	31	79.5	326	5	Q8WP98	Q8wp98 plasmodium
35	31	79.5	333	12	Q8JKJ2	Q8jkj2 heliothis z
36	31	79.5	358	16	Q97MK4	Q97mk4 clostridium
37	31	79.5	374	5	Q17852	Q17852 caenorhabdi
38	31	79.5	393	16	Q8D4N4	Q8d4n4 vibrio vuln
39	31	79.5	395	5	Q95WD9	Q95wd9 phlebotomus
40	31	79.5	398	16	Q9A1Z8	Q9a1z8 streptococ
41	31	79.5	398	16	Q8P318	Q8p318 streptococ
42	31	79.5	400	2	O08342	O08342 bacillus sp
43	31	79.5	411	16	O89522	O69522 mycobacteri
44	31	79.5	413	16	O89679	O69679 mycobacteri
45	31	79.5	413	16	Q7TVV4	Q7tvv4 mycobacteri

ALIGNMENTS

RESULT 1
Q7WRF3 PRELIMINARY; PRT; 218 AA.
AC Q7WRF3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Xcbb (Fragment).
GN Xcbb.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M9592, M9601, M9554, M8210, and M2526;
RA Sacchi C.T., Whitney A.M., Mayer L.W., Popovic T.;
RT "Neisseria meningitidis xccb gene.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY281038; AAP34761.1; -
DR EMBL; AY281039; AAP34762.1; -
DR EMBL; AY281040; AAP34763.1; -
DR EMBL; AY281041; AAP34764.1; -
DR EMBL; AY281042; AAP34765.1; -
FT NON TER 1
FT NON TER 218
SQ SEQUENCE 218 AA; 24876 MW; FF55F1E3E3A8A178 CRC64;

Query Match 89.7%; Score 35; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. NO. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDSSNVV 8
Db 75 YDSSNVV 81

RESULT 2
Q7X4S0

```

ID Q7X4S0 PRELIMINARY; PRT; 350 AA.
AC Q7X4S0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xcbb.
GN Xcbb.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W7575;
RA Tzeng Y.-L., Noble C., Stephens D.;
RT "Genetic basis for biosynthesis of the (alpha-1-4) linked N-acetyl-D-
RT glucosamine 1-phosphate capsule of serogroup X Neisseria
RT meningitidis.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY289931; AAP44501.1; -.
SQ SEQUENCE 350 AA; 39735 MW; 0CC5BDE0C3793019 CRC64;

Query Match 89.7%; Score 35; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNVV 8
DB 161 YDSSNVV 167

RESULT 3
ID Q8A3E1 PRELIMINARY; PRT; 644 AA.
AC Q8A3E1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN BT3013.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016938; AA078119.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 644 AA; 73170 MW; AD84BE7590892390 CRC64;

Query Match 87.2%; Score 34; DB 16; Length 644;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
DB 87 SYDSSNVV 94

RESULT 4
ID Q92F18 PRELIMINARY; PRT; 505 AA.
AC Q92F18
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Internalin like protein (LPXTG motif).

```

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GN LIN0290.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo P., Garrido P.,
RA Gautier L.-M., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkart G.,
RA Madueno E., Maltournan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001)
DR EMBL; AL596164; CAC35523.1; -.
DR PIR; AC1469; AC1469.
DR ListList; LIN00290; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007092; LRR_SDS22.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF00560; LRR; 7.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 505 AA; 54909 MW; BCE8B477E36780C CRC64;

Query Match 84.6%; Score 33; DB 16; Length 505;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
DB 319 TYDSSNVV 326

RESULT 5
ID Q8ITJ3 PRELIMINARY; PRT; 600 AA.
AC Q8ITJ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutaryl transpeptidase.
OS Heterodera glycines (soybean cyst nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=51029;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao B., Maier T., Davis E.L., Baum T.J., Hussey R.S.;
RT "Cloning of Heterodera glycines glutaryl transpeptidase gene Hg-
RT gt.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469056; AAN32885.1; -.
DR GO; GO:0003840; F:gamma-glutamyltransferase activity; IPA.
DR InterPro; IPR000101; Peptidase_T3.
DR Pfam; PF01019; G_glu_transpept; 1.
DR PRINTS; PR01210; GGTRANSPASE.
SQ SEQUENCE 600 AA; 66232 MW; 67069EF6C12445A3 CRC64;

Query Match 84.6%; Score 33; DB 5; Length 600;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```



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QY 1 SYDSSNVV 8
Db 564 SYDNNVV 571

RESULT 6
P93658
ID P93658 PRELIMINARY; PRT; 680 AA.
AC P93658;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Jasmonate inducible protein.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Global;
RA Geshi N., Brandt A.;
RT "Two jasmonate inducible proteins from Brassica napus seedlings
RL homologous to myosinase binding proteins and jacalin.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11483; CAA72271.1; -.
DR PIR; T08080; T08080.
DR HSP; P18670; LJAC.
DR InterPro; IPR001229; Jacalin_lectin.
DR Pfam; PF01419; Jacalin; 4.
SQ SEQUENCE 680 AA; 69937 MW; 8CD0CF16C30CA1E2 CRC64;

Query Match 84.6%; Score 33; DB 10; Length 680;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNVV 8
Db 308 YDSSNII 314

RESULT 7
Q9ZU23
ID Q9ZU23 PRELIMINARY; PRT; 730 AA.
AC Q9ZU23;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F5F19.6 protein.
GN F5F19.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Lenz C., Liu S.,
RA Li J., Kremenetskaia I., Luros J., Gonzalez A., Altafi H., Araujo R.,
RA Buehler E., Conway A.B., Conn L., Dunn P., Hansen N., Huizar L.,
RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F5F19 sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006216; AAD12691.1; -.
DR PIR; F96559; F96559.
DR HSP; P18670; LJAC.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001229; Jacalin_lectin.
DR Pfam; PF01419; Jacalin; 3.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 730 AA; 73939 MW; E4323AF993B1D95E CRC64;

Query Match 84.6%; Score 33; DB 10; Length 730;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDSSNVV 8
Db 511 YDSSNII 517

RESULT 8
Q9PMF2
ID Q9PMF2 PRELIMINARY; PRT; 934 AA.
AC Q9PMF2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative formate dehydrogenase large subunit (Selenocysteine
containing) (EC 1.2.1.2).
GN FDHA OR CJ1511C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10689204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668 (2000).
DR EMBL; AL139078; CAB73932.1; -.
DR PIR; C81298; C81298.
DR HSP; P07658; 1FDO.
DR GO; GO:0008963; F:formate dehydrogenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR009010; Asp decarb fold.
DR InterPro; IPR006656; Molybdopterin.
DR InterPro; IPR006963; Molybdop_Fe4S4.
DR InterPro; IPR006657; Molydinuc_bind.
DR InterPro; IPR006655; ProK_Mboxred.
DR InterPro; IPR006311; Tat.
DR Pfam; PF00384; molybdopterin; 1.
DR Pfam; PF04879; Molybdop_Fe4S4; 1.
DR Pfam; PF01568; Molybdop_Binding; 1.
DR TIGRFAMs; TIGR01409; TAT signal seq; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
KW Complete proteome.
SQ SEQUENCE 934 AA; 103906 MW; 5613822028D643DA CRC64;

Query Match 84.6%; Score 33; DB 16; Length 934;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 714 SYDSSNII 721

RESULT 9
Q7YU07
ID Q7YU07 PRELIMINARY; PRT; 951 AA.
AC Q7YU07;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE L015833p.
GN PLEXA.
OS Drosophila melanogaster (Fruit fly).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX STRAIN-Berkley;
RP SEQUENCE FROM N.A.
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT010060; AAQ22529.1; -
SQ SEQUENCE 951 AA; 105937 MW; F42ACC394B8AAD9F CRC64;

Query Match      84.6%; Score 33; DB 5; Length 951;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 826 SYESSNII 833

RESULT 10
Q8IM99 PRELIMINARY; PRT; 1505 AA.
AC Q8IM99;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG11081-PB.
GN PLEXA OR CG11081.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX STRAIN-Berkley;
RP SEQUENCE FROM N.A.
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT010060; AAQ22529.1; -
SQ SEQUENCE 951 AA; 105937 MW; F42ACC394B8AAD9F CRC64;

Query Match      84.6%; Score 33; DB 5; Length 951;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 826 SYESSNII 833

RESULT 10
Q8IM99 PRELIMINARY; PRT; 1505 AA.
AC Q8IM99;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG11081-PB.
GN PLEXA OR CG11081.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX STRAIN-Berkley;
RP SEQUENCE FROM N.A.
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT010060; AAQ22529.1; -
SQ SEQUENCE 951 AA; 105937 MW; F42ACC394B8AAD9F CRC64;

Query Match      84.6%; Score 33; DB 5; Length 1505;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSSNVV 8
Db 826 SYESSNII 833

RESULT 11
O96681 PRELIMINARY; PRT; 1945 AA.
ID O96681

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AC 096681;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PLEXA A
 DE PLEXA OR CG11081.
 GN Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99091049; PubMed=9875845;
 RA Winberg M.L., Noordermeer J.N., Tanagnone L., Comoglio P.M.,
 RA Spriggs M.K., Tessier-Lavigne M., Goodman C.S.;
 RT "Plexin A is a neuronal semaphorin receptor that controls axon
 RT guidance.";
 RL Cell 95:903-916 (1998).
 DR EMBL; AF106932; AAD09425.1; -.
 DR PIR; T13937; T13937.
 DR FlyBase; FBgn0025741; plexA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR002909; IPT TIG.
 DR InterPro; IPR002165; plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF01437; PSI; 3.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF01833; TIG; 3.
 DR SMART; SM00429; IPT; 3.
 DR SMART; SM00423; PSI; 3.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 SQ SEQUENCE 1945 AA; 218278 MW; 09D3565598DBEF1 CRC64;
 Query Match 84.6%; Score 33; DB 5; Length 1945;
 Best Local Similarity 62.5%; Pred. No. 5.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDSNNV 8
 Db 1266 SYESSNII 1273
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 DE PLEXA protein.
 GN PLEXA OR CG11081.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., P.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-f., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 DR EMBL; AE003846; AAF59394.1; -.
 DR FlyBase; FBgn0025741; plexA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR002909; IPT TIG.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF01437; PSI; 3.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF01833; TIG; 3.
 DR SMART; SM00429; IPT; 3.
 DR SMART; SM00423; PSI; 3.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 SQ SEQUENCE 1945 AA; 218356 MW; 4C032CA07C83A745 CRC64;
 Query Match 84.6%; Score 33; DB 5; Length 1945;
 Best Local Similarity 62.5%; Pred. No. 5.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDSNNV 8
 Db 1266 SYESSNII 1273
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 DE PLEXA protein.
 GN PLEXA OR CG11081.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,

RESULT 13

Q99383

ID Q99383

AC Q99383

DT 01-JUN-2001

DT 01-JUN-2001

DE Coat protein (Capid protein).

OS Banana mild mosaic virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.

OX NCBI_TaxID=148079;

RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21440425; PubMed=11556712;
RA Gambley C.F., Thomas J.E.;
RT "Molecular characterisation of Banana mild mosaic virus, a new
RL filamentous virus in Musa spp.";
RN Arch. Virol. 146:1369-1379(2001).
[2]
RP SEQUENCE FROM N.A.
RA Gambley C.F., Thomas J.E.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SELF-ASSEMBLES WITH THE RNA TO FORM INFECTIOUS PARTICLES
CC -!- (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POTEXVIRUSES COAT PROTEIN FAMILY.
DR EMBL; AF314662; AAK28493.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR000052; Plevix coat.
DR Pfam; PF00286; virus_p-coat; 1.
DR PRINTS; PR00232; POTXCARLCOAT.
KW Coat protein.
SQ SEQUENCE 238 AA; 26825 MW; 38E7599DB1CDE27A CRC64;

Query Match
Best Local Similarity 82.1%; Score 32; DB 12; Length 238;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDSSNVV 8
Db |||||:|
31 YDSSNVV 37

RESULT 14
Q8QHV1 PRELIMINARY; PRT; 507 AA.
AC Q8QHV1;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DE Polyprotein (Fragment).
OS Spartina mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae.
OX NCBI_TaxID=190503;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Assisi;
RX MEDLINE=21887386; PubMed=11890529;
RA Goetz R., Huth W., Lesemann D.E., Maiss E.;
RT "Molecular and serological relationships of Spartina mottle virus
RT (SPMV) strains from Spartina spec. and from Cynodon dactylon to other
RL members of the Potyviridae.";
RN Arch. Virol. 147:379-391(2002).
DR EMBL; AF491352; AAM12550.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0003968; P:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001592; Poty_coat.
DR Pfam; PF00767; Poty_coat; 1.
FT NON_TER
KW Coat protein.
SQ SEQUENCE 507 AA; 57114 MW; DA8184C7DC94CA31 CRC64;

Query Match
Best Local Similarity 75.0%; Score 32; DB 12; Length 507;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SYDSSNVV 8
Db |||||:|
57 SYDSSNVV 64

RESULT 15

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Q9VDQ3
ID Q9VDQ3 PRELIMINARY; PRT; 521 AA.
AC Q9VDQ3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE CG4936 protein (LD08906P).
GN CG4936.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Xu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003728; AAF55737.1; -.
DR EMBL; AY061100; AAL28648.1; -.
DR Flybase; FBgn0030768; CG4936.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR SMART; SM00355; Znf_C2H2; 5.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.

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DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
KW Metal-binding; Zinc; Zinc-finger.
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Query Match 82.1%; Score 32; DB 5; Length 521;
Best Local Similarity 62.5%; Pred.No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDSSNVV 8
Db 510 SYDTANIV 517
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Job time : 25.125 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 9.07812 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/prodata/2/iaa/5B COMB.pap:*

3: /cgn2_6/prodata/2/iaa/6A COMB.pap:*

4: /cgn2_6/prodata/2/iaa/6B COMB.pap:*

5: /cgn2_6/prodata/2/iaa/PCITUS COMB.pap:*

6: /cgn2_6/prodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	106	1	US-08-259-372A-16
2	34	89.5	106	1	US-08-468-671-16
3	33	86.8	112	2	US-08-665-202-39
4	33	86.8	112	4	US-09-315-574-39
5	32	84.2	108	1	US-08-259-372A-10
6	32	84.2	108	1	US-08-468-671-10
7	32	84.2	192	4	US-09-252-991A-27287
8	31	81.6	64	2	US-08-765-179B-19
9	31	81.6	108	4	US-09-025-769B-20
10	31	81.6	109	3	US-09-157-370-5
11	31	81.6	249	4	US-10-039-785-53
12	30	78.9	109	4	US-09-025-769B-32
13	30	78.9	109	4	US-09-025-769B-51
14	30	78.9	234	4	US-09-372-425A-4
15	30	78.9	462	3	US-08-875-944B-5
16	30	78.9	462	3	US-09-116-049-4
17	30	78.9	462	4	US-09-602-868A-5
18	30	78.9	462	4	US-09-884-363-4
19	30	78.9	555	2	US-08-780-835B-2
20	30	78.9	555	3	US-09-303-268-2
21	30	78.9	555	3	US-09-116-049-2
22	30	78.9	555	4	US-09-884-363-2
23	30	78.9	555	4	US-09-328-925-47
24	30	78.9	620	4	US-08-426-509A-9
25	30	78.9	620	4	US-08-232-545-9
26	30	78.9	620	5	PCT-US95-05008-9
27	30	78.9	631	4	US-09-489-039A-10289

28 29 76.3 71 4 US-09-621-976-6566 Sequence 6566, Ap

29 29 76.3 109 1 US-08-478-039-91 Sequence 91, Appl

30 29 76.3 109 1 US-08-476-349A-91 Sequence 91, Appl

31 29 76.3 111 3 US-08-983-607-35 Sequence 35, Appl

32 29 76.3 112 3 US-08-983-607-31 Sequence 31, Appl

33 29 76.3 132 1 US-08-534-975-4 Sequence 4, Appl

34 29 76.3 132 3 US-09-129-855A-4 Sequence 4, Appl

35 29 76.3 132 3 US-09-129-855A-4 Sequence 4, Appl

36 29 76.3 132 3 US-09-247-154-4 Sequence 4, Appl

37 29 76.3 132 4 US-09-480-718-4 Sequence 4, Appl

38 29 76.3 132 4 US-09-610-833-4 Sequence 4, Appl

39 29 76.3 132 4 US-09-129-855A-4 Sequence 4, Appl

40 29 76.3 139 4 US-09-252-991A-19245 Sequence 19245, A

41 29 76.3 475 4 US-09-252-991A-29248 Sequence 29248, A

42 29 76.3 491 4 US-09-543-681A-8251 Sequence 8251, Ap

43 29 76.3 519 4 US-09-719-919A-17 Sequence 17, Appl

44 29 76.3 633 4 US-09-489-039A-11853 Sequence 11853, A

45 29 76.3 739 4 US-09-543-681A-6437 Sequence 6437, Ap

ALIGNMENTS

RESULT 1

US-08-259-372A-16
; Sequence 16, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/259,372A

FILING DATE: 14-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/871,426

FILING DATE: 21-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676,036

FILING DATE: 27-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/538,796

FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/192,754

FILING DATE: 11-MAY-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/925,196

FILING DATE: 31-OCT-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/904,517

FILING DATE: 05-SEP-1986

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-50-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-16

Query Match 89.5%; Score 34; DB 1; Length 106;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|||:||||
Db 49 EDNRPS 55

RESULT 2
US-08-468-671-16
; Sequence 16, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-671-16

Query Match 89.5%; Score 34; DB 1; Length 106;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|||:||||
Db 49 EDNRPS 55

RESULT 3
US-08-665-202-39
; Sequence 39, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 86.8%; Score 33; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQPS 7
|||||
Db 52 DNQPS 57

RESULT 4
US-09-315-574-39
; Sequence 39, Application US/09315574


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; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 86.8%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7
Db 52 DNORPS 57

RESULT 5
US-08-259-372A-10
; Sequence 10, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-10

Query Match 84.2%; Score 32; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 49 DDNRPS 55

RESULT 6
US-08-468-671-10
; Sequence 10, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US 08/468,671
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/259,372
 FILING DATE: 14-JUN-1994
 APPLICATION NUMBER: US 07/871,426
 FILING DATE: 21-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/676,036
 FILING DATE: 27-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/538,796
 FILING DATE: 15-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/192,754
 FILING DATE: 11-MAY-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/925,196
 FILING DATE: 31-OCT-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/904,517
 FILING DATE: 05-SEP-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-50-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-468-671-10

Query Match 84.2%; Score 32; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels

QY 1 EDNQRP 7
:|:|:|
pb 49 DDNERPS 55

RESULT 7
US-09-252-991A-27287
; Sequence 27287, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27287
; LENGTH: 192
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27287

Query Match	84.2%;	Score 32;	DB 4;	Length 192;
Best Local Similarity	85.7%;	Pred. NO. 36;		
Matches 6;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;

Qy 1 EDNQRP 7
Dy 4 EDNQRP 10

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RESULT 8
US-08-765-179B-19
; Sequence 19, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; OF ANTIBODIES
; NUMBER OF INVENTIONS: 1
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765.179B
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115.7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PS-08-765-179B-19

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Query Match 81.6%; Score 31; DB 2; Length 64;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels

QY 1 EDNQ RPS 7
: : : :
pb 19 DDNK RPS 25

RESULT 9
US-09-025-769B-20
; Sequence 20, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York

; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-20

Query Match 81.6%; Score 31; DB 4; Length 108;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
:|||||
Db 48 DDKRPS 54

RESULT 10
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; FILE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; TITLE OF INVENTION: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-157-370-5

Query Match 81.6%; Score 31; DB 3; Length 109;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
:|||||
Db 49 DDKRPS 55

RESULT 11

US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
; US-10-039-785-53

Query Match 81.6%; Score 31; DB 4; Length 249;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
:|||||
Db 190 QDKRPS 196

RESULT 12
US-09-025-769B-32
; Sequence 32, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-32

Query Match 78.9%; Score 30; DB 4; Length 109;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 51 DNNQRPS 57

RESULT 13
US-09-025-769B-51
Sequence 51, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-025-769B-51

Query Match 78.9%; Score 30; DB 4; Length 109;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 51 DNNQRPS 57

RESULT 14
US-09-372-425A-4
Sequence 4, Application US/09372425A
Patent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
APPLICANT: Ramon Montano
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Light chain - AA
US-09-372-425A-4

Query Match 78.9%; Score 30; DB 4; Length 234;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 69 DNNQRPS 75

RESULT 15
US-08-875-944B-5
Sequence 5, Application US/08875944B
Patent No. 6096542
GENERAL INFORMATION:
APPLICANT: FUJINAGA, Kei
APPLICANT: YOSHIDA, Koichi
APPLICANT: HIGASHINO, Fumihito

;; TITLE OF INVENTION: CANCER CONTROL
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
;; STREET: 624 Ninth Street N.W., Ste. 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20001
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/875,944B
;; FILING DATE: 07-AUG-1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 07-020173
;; FILING DATE: 08-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP96/00016
;; FILING DATE: 09-JAN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: FUJINAGA=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-5197
;; TELEFAX: (202) 737-3528
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 462 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-875-944B-5

Query Match 78.9%; Score 30; DB 3; Length 462;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7
Db 412 DNORPA 417

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Job time : 10.0781 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 23.2969 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

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Searched: 1155919 seqs, 281338677 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	9	US-09-832-312-65
2	38	100.0	7	10	US-09-972-656-13
3	38	100.0	7	11	US-09-829-495-65
4	38	100.0	98	12	US-10-453-698-117
5	38	100.0	98	15	US-10-308-817-117
6	38	100.0	103	10	US-09-972-656-130
7	38	100.0	110	12	US-10-371-942-56
8	38	100.0	110	14	US-10-269-805-42
9	38	100.0	110	14	US-10-269-805-52
10	38	100.0	110	14	US-10-269-805-58
11	38	100.0	112	12	US-10-371-942-48
12	38	100.0	161	14	US-10-106-698-6785
13	38	100.0	216	10	US-09-972-656-108
14	38	100.0	258	10	US-09-880-748-1234
15	38	100.0	258	12	US-10-293-418-1234

16 34 89.5 7 15 US-10-425-855-13 Sequence 13, Appl
17 34 89.5 109 15 US-10-425-855-9 Sequence 9, Appl
18 34 89.5 114 9 US-09-925-299-1194 Sequence 1194, Ap
19 34 89.5 114 10 US-09-925-299-1194 Sequence 1194, Ap
20 34 89.5 233 16 US-10-312-354-38 Sequence 38, Appl
21 34 89.5 243 14 US-10-322-673-55 Sequence 55, Appl
22 34 89.5 244 10 US-09-880-748-1842 Sequence 1842, Ap
23 34 89.5 244 12 US-10-293-418-1842 Sequence 1842, Ap
24 33 86.8 7 10 US-09-972-656-14 Sequence 14, Appl
25 33 86.8 7 10 US-09-972-656-20 Sequence 20, Appl
26 33 86.8 110 12 US-10-371-942-88 Sequence 88, Appl
27 33 86.8 161 15 US-10-364-743-65 Sequence 65, Appl
28 33 86.8 165 15 US-10-364-743-33 Sequence 33, Appl
29 33 86.8 216 10 US-09-972-656-90 Sequence 90, Appl
30 33 86.8 218 10 US-09-972-656-102 Sequence 102, App
31 33 86.8 248 10 US-09-880-748-1273 Sequence 1273, Ap
32 33 86.8 248 12 US-10-293-418-1273 Sequence 1273, Ap
33 33 86.8 252 10 US-09-880-748-1128 Sequence 1128, Ap
34 33 86.8 252 12 US-10-293-418-1128 Sequence 1128, Ap
35 33 86.8 253 10 US-09-880-748-1227 Sequence 1227, Ap
36 33 86.8 253 12 US-10-293-418-1227 Sequence 1227, Ap
37 33 86.8 259 10 US-09-880-748-1277 Sequence 1277, Ap
38 33 86.8 259 12 US-10-293-418-1277 Sequence 1277, Ap
39 33 86.8 282 12 US-10-427-805-1 Sequence 1, Appli
40 33 86.8 397 12 US-10-427-805-3 Sequence 3, Appli
41 33 86.8 418 12 US-10-427-805-2 Sequence 2, Appli
42 32 84.2 99 12 US-10-282-122A-47570 Sequence 47570, A
43 32 84.2 99 12 US-10-282-122A-50272 Sequence 50272, A
44 32 84.2 110 12 US-10-251-085B-166 Sequence 166, App
45 32 84.2 110 14 US-10-269-805-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-832-312-65
; Sequence 55, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-65

Query Match 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred.No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
Db 1 EDNQRPS 7

RESULT 2

US-09-972-656-13
; Sequence 13, Application US/09972656

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; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-13

Query Match      100.0%; Score 38; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 1 EDNORPS 7

RESULT 3
US-09-829-495-65
; Sequence 65, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-65

Query Match      100.0%; Score 38; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 1 EDNORPS 7

RESULT 4
US-10-453-698-117
; Sequence 117, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
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; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-117

Query Match      100.0%; Score 38; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 51 EDNORPS 57

RESULT 5
US-10-308-817-117
; Sequence 117, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Davang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-117

Query Match      100.0%; Score 38; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 51 EDNORPS 57

RESULT 6
US-09-972-656-130
; Sequence 130, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc.
; LOCATION: (7)..(7)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (33)..(33)
; OTHER INFORMATION: Unidentified
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; NAME/KEY: Misc.
; LOCATION: (34)..(34)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (35)..(35)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (36)..(36)
; OTHER INFORMATION: Unidentified
US-09-972-656-130

Query Match      100.0%; Score 38; DB 10; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNRPS 7
Db      56 EDNRPS 62

RESULT 7
US-10-371-942-56
; Sequence 56, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-56

Query Match      100.0%; Score 38; DB 12; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNRPS 7
Db      51 EDNRPS 57

RESULT 8
US-10-269-805-42
; Sequence 42, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-42

Query Match      100.0%; Score 38; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNRPS 7
Db      51 EDNRPS 57

RESULT 9
US-10-269-805-52
; Sequence 52, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-52

Query Match      100.0%; Score 38; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNRPS 7
Db      51 EDNRPS 57

RESULT 10
US-10-269-805-58
; Sequence 58, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-58

Query Match      100.0%; Score 38; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNRPS 7
Db      51 EDNRPS 57

RESULT 11
US-10-371-942-48
; Sequence 48, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
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; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-48

Query Match 100.0%; Score 38; DB 12; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 51 EDNORPS 57

RESULT 12

US-10-106-698-6785
; Sequence 6785, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005F1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6785
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6785

Query Match 100.0%; Score 38; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 72 EDNORPS 78

RESULT 13

US-09-972-656-108
; Sequence 108, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108

; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-108

Query Match 100.0%; Score 38; DB 10; Length 216;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 51 EDNORPS 57

RESULT 14

US-09-880-748-1234
; Sequence 1234, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1234

Query Match 100.0%; Score 38; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
Db 198 EDNORPS 204

RESULT 15

US-10-293-418-1234
; Sequence 1234, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1234

Query Match      100.0%; Score 38; DB 12; Length 258;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNQRPS 7
      |||||
Db      198 EDNQRPS 204
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Search completed: June 8, 2004, 18:52:59
Job time : 23.2969 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 6.89062 Seconds
(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	112	1	L6HUAR
2	34	89.5	109	1	L1HUWA
3	34	89.5	111	1	L1HUNW
4	34	89.5	131	1	L6HUEB
5	34	89.5	266	2	S72947
6	34	89.5	704	2	T02558
7	33	86.8	111	1	L6HULT
8	32	84.2	111	1	L6HUST
9	32	84.2	460	2	T27770
10	32	84.2	471	2	T20690
11	32	84.2	603	2	AC0674
12	31	81.6	107	2	PC4283
13	31	81.6	161	2	E81447
14	30	78.9	108	1	L5HUDL
15	30	78.9	158	2	C95159
16	30	78.9	158	2	C98025
17	30	78.9	232	2	C84706
18	30	78.9	332	2	A45710
19	30	78.9	361	2	T30402
20	30	78.9	371	1	E64821
21	30	78.9	371	2	E90743
22	30	78.9	371	2	A85594
23	30	78.9	420	2	B86217
24	30	78.9	462	1	S35534
25	30	78.9	522	2	B82195
26	30	78.9	555	1	S24061
27	30	78.9	620	1	S33253
28	30	78.9	664	2	T01368
29	30	78.9	885	1	A55453

ALIGNMENTS

RESULT 1

L6HUAR

Ig lambda chain V-VI region (AR) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000

C;Accession: A01987

R;Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.

Biochem. J. 195, 561-572, 1981

A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-chain

A;Reference number: A01987; MUID:82091000; PMID:6797401

A;Contents: amyloid protein AR

A;Accession: A01987

A;Molecule type: protein

A;Residues: 1-112 <SLE>

A;Note: about half of the lambda chain C region is missing from this protein

C;Comment: This protein was isolated from the spleen of a patient with amyloidosis.

C;Genetics:

A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: amyloid; heterotetramer; immunoglobulin

F;15-93/Domain: immunoglobulin homology <IMM>

F;22-91/Disulfide bonds: #status predicted

Query Match 92.1%; Score 35; DB 1; Length 112;

Best Local Similarity 85.7%; Pred. No. 2.2;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7

Db 51 DDNQRPS 57

RESULT 2

L1HUWA

Ig lambda chain V-I region (Wah) - human

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Sep-1997

C;Accession: A01967

R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983

A;Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda

A;Reference number: A01967; MUID:83221661; PMID:6407018

A;Accession: A01967

A;Molecule type: protein

A;Residues: 1-109 <TAK>

C;Genetics:

A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240

Ig lambda chain -
Ig lambda chain -
Ig lambda chain V1
genome polyprotein
Ig lambda chain pr
cyclin-dependent k
helix-destabilizin
matrix protein - r
matrix protein - r
matrix protein - r
matrix protein - r
Ig lambda chain -
hypothetical prote
pyruvate synthase
hypothetical prote
hypothetical prote

29 76.3 98 2 S36068
31 29 76.3 106 2 S38495
32 29 76.3 111 2 S47009
33 29 76.3 112 2 S51125
34 29 76.3 117 2 S04525
35 29 76.3 132 2 I39004
36 29 76.3 195 2 A27241
37 29 76.3 202 1 MFVNAV
38 29 76.3 202 1 MFVNAV
39 29 76.3 202 1 MFVNAV
40 29 76.3 202 1 MFVNAV
41 29 76.3 232 2 S25742
42 29 76.3 243 2 A96744
43 29 76.3 312 1 S22397
44 29 76.3 312 2 E84268
45 29 76.3 318 2 H69959

A;Map position: 22q11.2-22q11.2
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;20-131/Product: Ig lambda chain V region (EB4) #status predicted <MAT>
 F;20-412/Region: framework 1
 F;34-112/Domain: immunoglobulin homology <IMM>
 F;42-54/Region: complementarity-determining 1
 F;55-69/Region: framework 2
 F;70-76/Region: complementarity-determining 2
 F;77-110/Region: framework 3
 F;111-118/Region: complementarity-determining 3
 F;119-131/Region: framework 4
 F;41-110/Disulfide bonds: #status predicted

Query Match 89.5%; Score 34; DB 1; Length 109;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 :|||||
 Db 51 KDNQRPS 57

RESULT 3
 L1HUNW
 Ig lambda chain V-I region (New) - human
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999
 C;Accession: A01964
 R;Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
 A;Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
 A;Reference number: A01964; MUID:69060892; PMID:4177823
 A;Accession: A01964
 A;Molecule type: protein
 A;Residues: 1-111 <LAN>
 C;Comment: This is a Bence Jones protein.
 C;Genetics:
 A;Gene: GDB:IGLV@
 A;Cross-references: GDB:119342; OMIM:147240
 A;Map position: 22q11.2-22q11.2
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: blocked amino end; heterotetramer
 F;15-91/Domain: immunoglobulin homology <IMM>
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
 F;22-89/Disulfide bonds: #status predicted

Query Match 89.5%; Score 34; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred. No. 3.6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 :|||||
 Db 51 EDNQRPS 57

RESULT 4
 L6HUEB
 Ig lambda chain precursor V-VI region (EB4) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
 R;Anderson, M.L.M.; Brown, L.; McKenzie, E.; Kellow, J.E.; Young, B.D.
 Nucleic Acids Res. 13, 2931-2941, 1985
 A;Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in the
 A;Reference number: A01990; MUID:85215660; PMID:3923440
 A;Accession: A01990
 A;Molecule type: mRNA
 A;Residues: 1-131 <AND>
 C;Genetics:
 A;Gene: GDB:IGLV@
 A;Cross-references: GDB:119342; OMIM:147240
 A;Map position: 22q11.2-22q11.2
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-131/Product: Ig lambda chain V-VI region (EB4) #status predicted <MAT>
 F;20-412/Region: framework 1
 F;34-112/Domain: immunoglobulin homology <IMM>
 F;42-54/Region: complementarity-determining 1
 F;55-69/Region: framework 2
 F;70-76/Region: complementarity-determining 2
 F;77-110/Region: framework 3
 F;111-118/Region: complementarity-determining 3
 F;119-131/Region: framework 4
 F;41-110/Disulfide bonds: #status predicted

Query Match 89.5%; Score 34; DB 1; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRP 6
 :|||||
 Db 70 EDNQRP 75

RESULT 5
 S72947
 hypothetical protein B2235_F2_77 - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
 C;Accession: S72947
 R;Smith, D.R.; Robison, K.
 submitted to the EMBL Data Library, November 1993
 A;Description: Mycobacterium leprae cosmid B2235.
 A;Reference number: S72587
 A;Accession: S72947
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <SMT>
 A;Cross-references: EMBL:U00019; NID:9467079; PIDN:AAAL7283.1; PID:9467100

Query Match 89.5%; Score 34; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRP 6
 :|||||
 Db 103 EDNQRP 108

RESULT 6
 T02558
 hypothetical protein At2g32590 [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein T26B15.15
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 25-Aug-2003
 R;Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, July 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.
 A;Reference number: Z14678
 A;Accession: T02558
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-704 <ROU>
 A;Cross-references: EMBL:AC004681; NID:G3298532; PID:G3298547
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84735
 A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-704 <STO>
A;Cross-references: GB:AB002093; NID:g3298547; PIDN:AAC25941.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g32590; T26B15.15
A;Map position: 2
A;Introns: 89/3; 123/3; 163/1; 184/3; 205/1; 400/3; 449/1; 543/1; 594/3; 631/3
C;Superfamily: chromosome condensation complex Condensin, subunit H

Query Match 89.5%; Score 34; DB 2; Length 704;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|:|||||
DB 330 EENQPS 336

RESULT 7
L6HULT
Ig lambda chain V-VI region (WLT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01989
R;Dwulet, F.E.; Strako, K.; Benson, M.D.
Scand. J. Immunol. 22, 653-660, 1985
A;Title: Amino acid sequence of a lambda VI primary (AL) amyloid protein (WLT).
A;Reference number: A01989; MUID:86122667; PMID:4089539
A;Accession: A01989
A;Molecule type: protein
A;Residues: 1-111 <DWU>
C;Genetics:
A;Gene: GDB:IGLV6

A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-101/Region: complementarity-determining 3
F;102-111/Region: framework 4
F;22-91/Disulfide bonds: #status predicted

Query Match 86.8%; Score 33; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|:|||||
DB 51 EENQPS 57

RESULT 8
L6HUST
Ig lambda chain V-VI region (SUT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01988
R;Solomon, A.; Kyle, R.A.; Frangione, B.
in Amyloidosis, Glenner, G.G.; Osserman, E.F.; Benditt, E.P.; Calkins, E.; Cohn, A.S.; et al
A;Title: Light chain variable region subgroups of monoclonal immunoglobulins in amyloidosis
A;Reference number: A01988
A;Accession: A01988
A;Molecule type: protein
A;Residues: 1-111 <SOL>
C;Genetics:
A;Gene: GDB:IGLV6

A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-100/Region: complementarity-determining 3
F;101-111/Region: framework 4
F;22-91/Disulfide bonds: #status predicted

Query Match 84.2%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|:|||||
DB 51 EDTQPS 57

RESULT 9
T27770
hypothetical protein ZK177.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T27770
R;Anderson, K.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid ZK177.
A;Reference number: Z20416
A;Accession: T27770
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-460 <AND>
A;Cross-references: EMBL:U21321; PIDN:AAB36965.1; GSPDB:GN00020; CESP:ZK177.1
A;Experimental source: strain Bristol N2; clone ZK177
C;Genetics:
A;Gene: CESP:ZK177.1
A;Map position: 2
A;Introns: 20/1; 31/3; 71/3; 111/1; 127/1; 294/1; 323/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK177.1

Query Match 84.2%; Score 32; DB 2; Length 460;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
|:|||||
DB 153 QDNQPS 159

RESULT 10
T20690
hypothetical protein F10B5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20690
R;Sims, M.
submitted to the EMBL Data Library, February 1995
A;Reference number: Z19310
A;Accession: T20690
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-471 <WIL>
A;Cross-references: EMBL:Z48334; PIDN:CAA88310.1; GSPDB:GN00020; CESP:F10B5.3
A;Experimental source: clone F10B5
C;Genetics:
A;Gene: CESP:F10B5.3

RESULT
E81447


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Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95159
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75468.1; PID:gi4972855; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1370
C:Superfamily: shikimate kinase; shikimate kinase homology

Query Match      78.9%; Score 30; DB 2; Length 158;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNQRP 6
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Db      109 KDNQRP 114

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Job time : 8.89062 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 16.8594 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Issued Patents AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	62.9	13	1	US-07-988-925-4
2	39	62.9	13	2	US-08-362-780-4
3	39	62.9	110	1	US-07-988-925-16
4	39	62.9	110	2	US-08-362-780-16
5	39	62.9	110	2	US-08-362-780-26
6	38	61.3	505	4	US-08-426-509A-17
7	38	61.3	505	4	US-08-232-545-17
8	38	61.3	505	5	PCT-US95-05008-17
9	36	58.1	373	4	US-09-543-681A-5564
10	36	58.1	503	4	US-09-679-263-5
11	36	58.1	522	4	US-09-446-301A-49
12	36	58.1	522	4	US-09-099-932-49
13	35	56.5	58	4	US-08-630-915A-131
14	35	56.5	132	2	US-08-649-991-91
15	35	56.5	132	2	US-08-649-991-92
16	35	56.5	431	4	US-09-071-035-344
17	35	56.5	474	4	US-09-071-035-342
18	35	56.5	496	4	US-09-134-000C-5286
19	35	56.5	512	4	US-08-426-509A-16
20	35	56.5	512	4	US-08-232-545-16
21	35	56.5	512	5	PCT-US95-05008-16
22	35	56.5	1129	4	US-09-252-991A-22330
23	34	54.8	29	3	US-09-070-504-1
24	34	54.8	30	3	US-09-070-504-2
25	34	54.8	37	1	US-08-233-389C-9
26	34	54.8	37	2	US-08-801-863-9
27	34	54.8	37	2	US-08-486-596A-9

28 34 54.8 37 2 US-09-004-713-9 Sequence 9, Appli
29 34 54.8 37 2 US-08-619-841-2 Sequence 2, Appli
30 34 54.8 37 2 US-08-446-929A-2 Sequence 2, Appli
31 34 54.8 37 3 US-09-070-504-3 Sequence 3, Appli
32 34 54.8 37 3 US-09-070-504-8 Sequence 8, Appli
33 34 54.8 37 3 US-09-070-504-9 Sequence 9, Appli
34 34 54.8 37 6 5424221-4 Patent No. 5424221
35 34 54.8 38 1 US-07-776-272-20 Sequence 20, Appl
36 34 54.8 73 4 US-09-461-325-222 Sequence 222, App
37 34 54.8 73 4 US-10-012-542-222 Sequence 222, App
38 34 54.8 98 1 US-08-211-202-111 Sequence 111, App
39 34 54.8 98 2 US-08-665-202-38 Sequence 38, Appl
40 34 54.8 98 4 US-09-315-574-38 Sequence 38, Appl
41 34 54.8 107 4 US-08-635-109-5 Sequence 5, Appli
42 34 54.8 109 1 US-08-276-852-147 Sequence 147, App
43 34 54.8 109 1 US-08-899-575-147 Sequence 147, App
44 34 54.8 109 1 US-08-899-575-147 Sequence 147, App
45 34 54.8 109 3 US-09-240-274-59 Sequence 59, Appli

ALIGNMENTS

RESULT 1
US-07-988-925-4
; Sequence 4, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L
; APPLICANT: Clark, Michael R
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,925
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206422.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB92/01933
; FILING DATE: 21-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 13 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-925-4

Query Match 62.9%; Score 39; DB 1; Length 13;

Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
| | | | : | | |
Db 1 TLSSGNIENYV 12

RESULT 2
US-08-362-780-4
; Sequence 4, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,780
; FILING DATE:

CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-4

Query Match 62.9%; Score 39; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
| | | | : | | |
Db 1 TLSSGNIENYV 12

RESULT 3
US-07-988-925-16
; Sequence 16, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L
; APPLICANT: Clark, Michael R

; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,925
; FILING DATE:

CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206422.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB92/01933
; FILING DATE: 21-OCT-1992

ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-925-16

Query Match 62.9%; Score 39; DB 1; Length 110;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
| | | | : | | |
Db 23 TLSSGNIENYV 34

RESULT 4
US-08-362-780-16
; Sequence 16, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/362,780
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/862,543
;; FILING DATE: 23-JUNE-1992
;; APPLICATION NUMBER: GB 9021679.7
;; FILING DATE: 05-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/GB91/01726
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mitchard, Leonard C.
;; REGISTRATION NUMBER: 29009
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 7038164000
;; TELEFAX: 7038164100
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-362-780-16

Query Match 62.9%; Score 39; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
Db 23 TLSSGNIENNYV 34

RESULT 5

US-08-362-780-26
;; Sequence 26, Application US/08362780
;; Patent No. 5968509
;; GENERAL INFORMATION:
;; APPLICANT: Gorman, Scott D
;; APPLICANT: Routledge, Edward G
;; APPLICANT: Waldmann, Herman
;; TITLE OF INVENTION: Antibody Preparation
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon and Vanderhye pc
;; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/362,780
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/862,543
;; FILING DATE: 23-JUNE-1992
;; APPLICATION NUMBER: GB 9021679.7
;; FILING DATE: 05-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/GB91/01726
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mitchard, Leonard C
;; REGISTRATION NUMBER: 29009

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 7038164000
;; TELEFAX: 7038164100
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-362-780-26

Query Match 62.9%; Score 39; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
Db 23 TLSSGNIENNYV 34

RESULT 6

US-08-426-509A-17
;; Sequence 17, Application US/08426509A
;; Patent No. 6326469
;; GENERAL INFORMATION:
;; APPLICANT: Ullrich, Axel
;; APPLICANT: Gishizky, Mikhail
;; APPLICANT: Sures, Iman G.
;; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
;; TITLE OF INVENTION: TYROSINE KINASES
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York,
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/426,509A
;; FILING DATE: 21-APR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/232,545
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7883-0074-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 505 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
US-08-426-509A-17

Query Match 61.3%; Score 38; DB 4; Length 505;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYV 12
Db 23 TLSSGNIENNYV 34

Db 101 TRKEGYIPSNV 112

RESULT 7

US-08-232-545-17
; Sequence 17, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; PCT-US95-05008-17

Query Match 61.3%; Score 38; DB 4; Length 505;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy 1 TRSGSGSIASNV 12
Db 101 TRKEGYIPSNV 112

RESULT 8

PCT-US95-05008-17
; Sequence 17, Application PC/TUS9505008
; GENERAL INFORMATION:
; APPLICANT: Sugen, Inc.
; APPLICANT: 515 Galveston Drive
; APPLICANT: Redwood City, California 94063-4720
; APPLICANT: United States of America
; APPLICANT: Wissenschaften E.V.
; APPLICANT: Hofgarten Str. 2
; APPLICANT: Munchen 80539
; APPLICANT: Germany
; TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05008
; FILING DATE: 24-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; PCT-US95-05008-17

Query Match 61.3%; Score 38; DB 5; Length 505;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy 1 TRSGSGSIASNV 12
Db 101 TRKEGYIPSNV 112

RESULT 9

US-09-543-681A-5564
; Sequence 5564, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5564
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-5564

Query Match 58.1%; Score 36; DB 4; Length 373;
Best Local Similarity 63.6%; Pred. No. 86;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SSGSIASNVQ 13
Db 131 NSAQIAANYVQ 141

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RESULT 10
US-09-679-263-5
; Sequence 5, Application US/09679263
; Patent No. 6600091
; GENERAL INFORMATION:
; APPLICANT: Mok, David
; TITLE OF INVENTION: Enzymes Responsible for the Metabolism of Zeatin
; FILE REFERENCE: 51524
; CURRENT APPLICATION NUMBER: US/09/679,263
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/080852
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Phaseolus lunatus
US-09-679-263-5

Query Match      58.1%; Score 36; DB 4; Length 503;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TRSSGSIASNY 11
Db      30 TRASGSIASCY 40

RESULT 11
US-09-446-301A-49
; Sequence 49, Application US/09446301A
; Patent No. 6506893
; GENERAL INFORMATION:
; APPLICANT: EL SOLH, NEVINE
; APPLICANT: ALLIGNET, JEANINE
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 03715-0059
; CURRENT APPLICATION NUMBER: US/09/446,301A
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-446-301A-49

Query Match      58.1%; Score 36; DB 4; Length 522;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches      5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      79 TKSGGVTNRVIR 91

RESULT 12
US-09-099-932-49
; Sequence 49, Application US/09099932
; Patent No. 6570001
; GENERAL INFORMATION:
; APPLICANT: El Solh, Nevine
; APPLICANT: Allignet, Jeanine
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 03495-0173-00000
; CURRENT APPLICATION NUMBER: US/09/099,932
; CURRENT FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/050,380
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; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Staphylococcus
US-09-099-932-49

Query Match      58.1%; Score 36; DB 4; Length 522;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches      5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      79 TKSGGVTNRVIR 91

RESULT 13
US-08-630-915A-131
; Sequence 131, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-131

Query Match      56.5%; Score 35; DB 4; Length 58;
Best Local Similarity 58.3%; Pred. No. 15;
Matches      7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYV 12
Db      44 TKEGFIPSNIV 55
```

RESULT 14

US-08-649-991-91
; Sequence 91, Application US/08649991
; Patent No. 5919462
; GENERAL INFORMATION:
; APPLICANT: Narwa, Remy
; APPLICANT: Roques, Pierre
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
; TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
; TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
; TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,991
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9505914
; FILING DATE: 18-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: ORES-5003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-991-91

Query Match 56.5%; Score 35; DB 2; Length 132;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNY 11

Db 122 TRSSQVSQNY 132

RESULT 15

US-08-649-991-92
; Sequence 92, Application US/08649991
; Patent No. 5919462
; GENERAL INFORMATION:
; APPLICANT: Narwa, Remy
; APPLICANT: Roques, Pierre
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
; TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
; TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
; TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 3.9375 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38
Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	112	1 LV6A HUMAN	P01721 homo sapien
2	34	89.5	109	1 LV1F HUMAN	P04208 homo sapien
3	34	89.5	111	1 LV1C HUMAN	P01701 homo sapien
4	34	89.5	131	1 LV6E HUMAN	P06319 homo sapien
5	33	86.8	111	1 LV6D HUMAN	P06318 homo sapien
6	33	86.8	494	1 PE33 BRARE	Q9pug1 brachydanio
7	32	84.2	111	1 LV6C HUMAN	P06317 homo sapien
8	32	84.2	460	1 YS41 CAEEL	Q09370 caenorhabdi
9	31	81.6	161	1 LV5A HUMAN	Q9pik9 campylobact
10	30	78.9	108	1 GREA CAMJE	P01719 homo sapien
11	30	78.9	265	1 SEPB BRARE	Q98sv0 brachydanio
12	30	78.9	332	1 Y1E2 HSVB4	Q02484 bovine herp
13	30	78.9	371	1 Y1I1 ECOLI	P75804 escherichia
14	30	78.9	551	1 ETV4 HUMAN	P43268 homo sapien
15	30	78.9	555	1 ETV4 MOUSE	P28322 mus musculu
16	30	78.9	620	1 ITK HUMAN	Q08981 homo sapien
17	30	78.9	862	1 NPP2 MOUSE	Q9rie6 m etonucle
18	30	78.9	885	1 NPP2 RAT	P64610 r etonucle
19	29	76.3	195	1 ROA1 BOVIN	Q9967 bos taurus
20	29	76.3	202	1 VMAT RABVA	P15200 rabies viru
21	29	76.3	202	1 VMAT RABVC	P25223 rabies viru
22	29	76.3	202	1 VMAT RABVE	P13616 rabies viru
23	29	76.3	202	1 VMAT RABVN	P25224 rabies viru
24	29	76.3	202	1 VMAT RABVP	P08671 rabies viru
25	29	76.3	318	1 YHQH BACSU	P54515 bacillus su
26	29	76.3	319	1 ROA1 MACMU	Q28521 macaca mula
27	29	76.3	319	1 ROA1 MOUSE	P49312 mus musculu
28	29	76.3	319	1 ROA1 RAT	P04256 rattus norv
29	29	76.3	371	1 ROA1 HUMAN	P09651 homo sapien
30	29	76.3	473	1 DNPE MOUSE	Q922w0 mus musculu
31	29	76.3	475	1 PRIG ERWCH	Q07162 erwinia chr
32	29	76.3	477	1 ETVI HUMAN	P50549 homo sapien
33	29	76.3	477	1 ETVI MOUSE	P41164 mus musculu

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34 29 76.3 510 1 ERM HUMAN P41161 homo sapien
35 29 76.3 519 1 KCG4 HUMAN Q8tdn1 homo sapien
36 29 76.3 578 1 YDV8 SCHPO O14226 schizosacch
37 29 76.3 871 1 SYA_AQUPY Q9xdm3 aquifex pyr
38 29 76.3 924 1 ORC1 DROME O16810 drosophila
39 29 76.3 1131 1 PHYA SORBI P53692 sorghum bic
40 29 76.3 1140 1 RA18 SCHPO P87503 human adeno
41 29 76.3 1193 1 DPOL ADR04 P03189 epstein-bar
42 29 76.3 1239 1 V120 EBV Q01118 homo sapien
43 29 76.3 1682 1 CIN7 HUMAN P07210 h genome po
44 29 76.3 2164 1 POLG_HRV89 O98799 mus musculu
45 29 76.3 5376 1 ZAN_MOUSE

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ALIGNMENTS

```

RESULT 1
LV6A_HUMAN
ID LV6A_HUMAN STANDARD; PRT; 112 AA.
AC P01721;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-VI region AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (AMYL0ID PROTEIN AR).
RX MEDLINE=82091000; PubMed=6797401;
RA Sletten K., Natvig J.B., Husby G., Juul J.;
RT "The complete amino acid sequence of a prototype
RT immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";
RL Biochem J 195;561-572(1981).
CC -!- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING
CC FROM THIS PROTEIN.
CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A
CC PATIENT WITH AMYLOIDOSIS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01987; L6HUR.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 107 IG-LIKE.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;

```

```

Query Match 92.1%; Score 35; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 0.84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EDNQRPS 7
Db :|||||
51 DDNQRPS 57

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RESULT 2
LV1F_HUMAN
ID LV1F_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain."
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690 (1983).
DR PIR; A01967; LIHUNA.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 89.5%; Score 34; DB 1; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNRPS 7
DB 51 KDNQPS 57

RESULT 3
ID LV1C HUMAN STANDARD; PRT; 111 AA.
AC P01701.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69060892; PubMed=4177823;
RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type."
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951 (1968).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01964; LIHUNW.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyridolone carboxylic acid.
FT DOMAIN 1 105 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11453 MW; AAECBCA3C49F2AD3 CRC64;
Query Match 89.5%; Score 34; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;
OY 1 EDNRPS 7
DB 51 EDNRPS 57

RESULT 4
ID LV6E HUMAN STANDARD; PRT; 131 AA.
AC P06319;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region EB4 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215660; PubMed=3923440;
RA Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in the Burkitt's lymphoma cell line EB4."
RL Nucleic Acids Res. 13:2931-2941 (1985).
DR PIR; A01990; L6HUEB.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 110 FRAMEWORK-3.
FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 131 FRAMEWORK-4.
FT DISULFID 41 110 BY SIMILARITY.
FT NON TER 131 131
SQ SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

Query Match 89.5%; Score 34; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNRPS 6
DB 70 EDNRPS 75

RESULT 5
ID LV6D HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region WLT.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86122667; PubMed=4089539;
RA Dwulet F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
  (WLT).";
RL Scand J. Immunol. 22:653-660(1985).
DR PR; A01989; L6HULT.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 22 FRAMEWORK-1.
FT DOMAIN 23 35 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 36 50 FRAMEWORK-2.
FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 58 91 FRAMEWORK-3.
FT DOMAIN 92 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 22 91 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 86.8%; Score 33; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 51 ENNRPS 57

RESULT 6
PEA3 BRARE
ID PEA3 BRARE STANDARD; PRT; 494 AA.
AC 9PU01; O57586;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE ETS-domain transcription factor PEA3.
GN PEA3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, DNA-BINDING, AND REGULATION OF
  ACTIVITY.
RC TISSUE=Embryo;
RX MEDLINE=9834393; PubMed=9671318;
RA Brown L.A., Amores A., Schilling T.F., Jowett T., Baert J.-L.,
  de Launoy Y., Sharrocks A.D.;
RT "Molecular characterisation of the zebrafish PEA3 ETS-domain
  transcription factor";
RL Oncogene 17:93-104(1998).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Gastrula;
RX MEDLINE=20005800; PubMed=10534622;
RA Muenchberg S.R., Ober E.A., Steinbeisser H.;
RT "Expression of the Ets transcription factors erm and pea3 in early
  zebrafish development.";

```

```

RL Mech. Dev. 88:233-236 (1999).
RN [3]
RP TISSUE SPECIFICITY, AND INDUCTION BY FGF8.
RX MEDLINE=21305906; PubMed=11413000;
RA Roehl H., Nusslein-Volhard C.;
RT "Zebrafish pea3 and erm are general targets of FGF8 signaling.";
RL Curr. Biol. 11:503-507(2001).
RN [4]
RP TISSUE SPECIFICITY, AND INDUCTION BY FGF3 AND FGF8.
RX MEDLINE=21412239; PubMed=11520667;
RA Raible F., Brand M.;
RT "Tight transcriptional control of the ETS domain factors Erm and Pea3
  by Fgf signaling during early zebrafish development.";
RL Mech. Dev. 107:105-117(2001).
CC -!- FUNCTION: Binds to the (5'-CGGGA[AT]-3') motif. May control the
  acquisition of specific cell fates at an early stage during the
  development of the somites and nervous system. May mediate the
  cellular effects of the fibroblast growth factors on
  embryogenesis.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: In the embryo, expressed ubiquitously until
  in the late blastula stage, in the marginal zone of gastrula stages,
  in the presumptive forebrain and hindbrain and in the trunk region
  of early somite stages. In later stages, also expressed in Rohon-
  Bead neurons, epiphysis, lateral line placodes, pectoral fin
  buds, developing lens and heart.
CC -!- DEVELOPMENTAL STAGE: First detected in the embryo after 4.3
  hours.
CC -!- INDUCTION: By the fibroblast growth factors FGF3 and FGF8.
CC -!- PTM: Phosphorylated (Probable).
CC -!- MISCELLANEOUS: Transcriptional activation activity is enhanced by
  Raf1, ERK and PKA.
CC -!- SIMILARITY: Belongs to the ETS family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ003200; CA05980.1; -.
DR EMBL; AF168008; AAD50434.1; -.
DR HSP; P14921; 2STT.
DR ZFIN; ZDB-GENE-990415-71; pea3.
DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0016563; F:transcriptional activator activity; IDA.
DR GO; GO:0009790; P:embryonic development; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR006715; ETS_PEA3_N.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF04621; ETS_PEA3_N; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS50063; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein; Activator; Transcription regulation;
  Phosphorylation.
FT DOMAIN 47 78 ASP/GLU-RICH (ACIDIC).
FT DNA BIND 350 430 ETS-DOMAIN
FT CONFLICT 148 148 A -> G (IN REF. 2).
FT CONFLICT 177 177 ID -> A (IN REF. 2).
FT CONFLICT 217 218 ID -> MH (IN REF. 2).
FT CONFLICT 224 226 MISSING (IN REF. 2).
FT CONFLICT 392 393 IE -> MQ (IN REF. 2).
SQ SEQUENCE 494 AA; 55621 MW; 81492553EA25C362 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 494;
Best Local Similarity 100.0%; Pred. No. 12;

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNORPS 7
Db 443 DNORPS 448

RESULT 7
LV6C HUMAN
ID LV6C HUMAN STANDARD; PRT; 111 AA.
AC P06317;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-VI region SUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Solomon A., Kyle R.A., Frangione B.;
RT "Light chain variable region subgroups of monoclonal immunoglobulins
in amyloidosis AL".
RL (In) Glenner G.G., Osseman E.F., Benditt E.P., Calkins E.,
Cohen A.S., Zucker-Franklin D. (eds.); New York (1986).
RL Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR PIR; A01988; L6HUST.
DR PDB; 1CD0; 06-MAR-00.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 22
FT DOMAIN 23 35
FT DOMAIN 36 50
FT DOMAIN 51 57
FT DOMAIN 58 91
FT DOMAIN 92 100
FT DOMAIN 101 111
FT DISULFID 22 91
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 EDNRPS 7
Db 51 EDNRPS 57

RESULT 8
YS41 CAEEL
ID YS41 CAEEL STANDARD; PRT; 460 AA.
AC Q09370;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 52.5 kDa protein ZK177.1 in chromosome II.
GN ZK177.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Anderson K.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

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EMBL; U21321; AAG00044.1; -.
DR PIR; T27770; T27770.
DR WormPep; ZK177.1; CE02089.
KW Hypothetical protein.
SQ SEQUENCE 460 AA; 52498 MW; F5E2958CE6CC6F58 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 460;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 153 QDNORPA 159

RESULT 9
GREA CAMJE
ID GREA CAMJE STANDARD; PRT; 161 AA.
AC Q9PIK9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription elongation factor greA (transcript cleavage factor
greA).
GN GREA OR CU0287C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RC MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feitwell T., Holroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -!- FUNCTION: Necessary for efficient RNA polymerase transcription
elongation past template-encoded arresting sites. The arresting
sites in DNA have the property of trapping a certain fraction of
elongating RNA polymerases that pass through, resulting in locked
ternary complexes. Cleavage of the nascent transcript by cleavage
factors such as greA or greB allows the resumption of elongation
from the new 3' terminus. GreA releases sequences of 2 to 3
nucleotides (By similarity).
CC -!- SIMILARITY: Belongs to the greA/greB family.

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EMBL; AL139074; CAB72754.1; -.
DR PIR; E81447; E81447.
DR HSSP; P21346; IGRJ.
DR HAMAP; MF 00105; -; 1.
DR InterPro; IPR006359; GreA.

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DR InterPro; IPR001437; GreA_Greb.
DR Pfam; PF01272; GreA_Greb_1.
DR Pfam; PF03449; GreA_Greb_N; 1.
DR ProDom; PD004918; GreA_Greb; 1.
DR TIGRFAMs; TIGR01462; GreA; 1.
DR PROSITE; PS00829; GREAB 1; 1.
DR PROSITE; PS00830; GREAB 2; 1.
DR PROSITE; PS00830; GREAB 2; 1.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 43 74 COILED COIL (POTENTIAL).
SQ SEQUENCE 161 AA; 18010 MW; 132C7DEC962A3239 CRC64;

Query Match
Best Local Similarity 81.6%; Score 31; DB 1; Length 161;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 22 KDNQRP 28

RESULT 10
LVSA HUMAN
ID LVSA HUMAN STANDARD; PRT; 108 AA.
AC F01719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-V region DEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75112179; PubMed=4452363;
RA Bultz M.;
RT "A new subgroup of human L-chains of the lambda-type. Primary
RT structure of Bence-Jones protein DEL.";
RL Eur. J. Biochem. 50:49-69(1974).
CC -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC CHAIN SUBGROUP V.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01985; L5HIDL.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 97
FT NON TER 108 108 IG-LIKE.
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09C9E451 CRC64;

Query Match
Best Local Similarity 78.9%; Score 30; DB 1; Length 108;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 48 EDNDRPA 54

RESULT 11
SEPB BRARE
ID SEPB BRARE STANDARD; PRT; 265 AA.
AC Q98SV0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

DR InterPro; IPR001437; GreA_Greb.
DR Pfam; PF01272; GreA_Greb_1.
DR Pfam; PF03449; GreA_Greb_N; 1.
DR ProDom; PD004918; GreA_Greb; 1.
DR TIGRFAMs; TIGR01462; GreA; 1.
DR PROSITE; PS00829; GREAB 1; 1.
DR PROSITE; PS00830; GREAB 2; 1.
DR PROSITE; PS00830; GREAB 2; 1.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 43 74 COILED COIL (POTENTIAL).
SQ SEQUENCE 161 AA; 18010 MW; 132C7DEC962A3239 CRC64;

Query Match
Best Local Similarity 71.4%; Score 30; DB 1; Length 108;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 48 EDNDRPA 54

RESULT 12
YIE2 HSVB4
ID YIE2 HSVB4 STANDARD; PRT; 332 AA.
AC Q02484;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in IE2 5' region (Fragment).
OS Bovine herpesvirus type 4 (isolate DN-599).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OC NCBI_TaxID=10355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93124571; PubMed=8380465;
RA van Santen V.L.;
RT "Characterization of a bovine herpesvirus 4 immediate-early RNA

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RT encoding a homolog of the Epstein-Barr virus R transactivator.";
RL J. Virol. 67:773-784(1993).
CC -!- SIMILARITY: TO EBV BRRF2.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L01099; AAA45056.1; --
CC PIR; A45710; A45710.
CC InterPro; IPR008550; DUF832.
CC Pfam; PF05734; DUF832; 1.
CC Hypothetical protein.
CC NON_TER 1
CC SEQUENCE 332 AA; 37951 MW; E0B6FAF287CC5315 CRC64;
CC -----
Query Match 78.9%; Score 30; DB 1; Length 332;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDNORP 6
DB 11 EENORP 16
|:|||||
|:|||||

RESULT 13
YLII_ECOLI STANDARD; PRT; 371 AA.
AC P75804; Q9R7R6;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ylii precursor.
GN YLII OR B0837.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Miobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RA "A 718-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -!- COFACTOR: PQQ (Potential).
CC -!- SIMILARITY: Belongs to the PQQ oxidoreductase gdhB family.
CC -----
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CC -----
EMBL; AF000186; AAC73924.1; --
EMBL; D90721; BAA35532.1; --
EMBL; D90722; BAA35540.1; --
PIR; E64821; E64821.
DR ECoGene; EG13480; ylii.
KW Hypothetical protein; Oxidoreductase; PQQ; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 371 HYPOTHETICAL PROTEIN YLII.
SQ SEQUENCE 371 AA; 41054 MW; 99D808FA302F50B9 CRC64;
CC -----
Query Match 78.9%; Score 30; DB 1; Length 371;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDNORPS 7
DB 166 ENNQRP 172
|:|||||
|:|||||

RESULT 14
ETV4_HUMAN STANDARD; PRT; 551 AA.
AC P43268;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Adenovirus E1A enhancer binding protein (E1A-F) (BTS translocation
DE variant 4) (Fragment).
GN ETV4 OR E1AF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293380; PubMed=7774926;
RA Friedman L.S., Ostermeyer E.A., Lynch E.D., Szabo C.I., Meza J.E.,
RA Anderson L.A., Dowd P., Lee M.K., Rowell S.E., Ellison J.,
RA Boyd J., King M.-C.;
RA "22 genes from chromosome 17q21: cloning, sequencing, and
RT characterization of mutations in breast cancer families and tumors.";
RL Genomics 25:256-263 (1995).
RN [2]
RP SEQUENCE OF 90-551 FROM N.A.
RX MEDLINE=93181246; PubMed=8441666;
RA Higashino F., Yoshida K., Fujinaga K., Kamio K., Fujinaga K.;
RA "Isolation of a cDNA encoding the adenovirus E1A enhancer binding
RT protein: a new human member of the ets oncogene family.";
RL Nucleic Acids Res. 21:547-553(1993).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
CC 5' (AC)GG(A)TGT-3'.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the ETS family.
CC -----
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CC -----
EMBL; U18018; AAA95991.1; --
EMBL; D12765; BAA02234.1; --
HSSP; P28324; 1BC8.
DR TRANSFAC; T00685; --
DR Genew; HGNC:3493; ETV4.
DR MIM; 600711; --
DR GO; GO:0005634; C:nucleus; NAS.
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DR GO: 0016563; F:transcriptional activator activity; NAS.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR00418; ETS.
DR InterPro; IPR006715; ETS_PEA3_N.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00178; Ets; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS00661; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein; Activator; Transcription regulation.
FT NON_TER 1 1
FT DOMAIN 116 142 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 215 311 GLN-RICH.
FT DNA_BIND 408 488 ETS-DOMAIN.
FT CONFLICT 91 94 GNGS -> EMSD (IN REF. 2).
SQ SEQUENCE 551 AA; 60570 MW; 9D649C8A1FBD8DB CRC64;

Query Match 78.9%; Score 30; DB 1; Length 551;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQRPS 7
Db 501 DNORPA 506

RESULT 15
ETV4 MOUSE
ID ETV4 MOUSE STANDARD; PRT; 555 AA.
AC P28322;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymavirus enhancer activator 3 (PEA3 protein) (ETS translocation
DE variant 4).
GN ETV4 OR PEA3 OR PEA-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92192459; PubMed=1547944;
RA Xin J.-H., Cowie A., Lachance P., Hassell J.A.;
RT "Molecular cloning and characterization of PEA3, a new member of the
RT Ets oncogene family that is differentially expressed in mouse
RT embryonic cells.";
RL Genes Dev. 6:481-496(1992).
CC -!- FUNCTION: BINDS TO THE PEA3 MOTIF (5'-AGGAAG-3'). MAY PLAY A
CC REGULATORY ROLE DURING EMBRYOGENESIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Epididymis and brain.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the ETS family.
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DR EMBL; X63190; CAA44872.1; -.
DR PIR; S24061; S24061.
DR HSSP; P28324; 1BC8.
DR TRANSFAC; T00684; -.
DR MGD; MGI:99423; Etv4.
DR GO: 0008045; P:motor axon guidance; IMP.
DR InterPro; IPR000418; Ets.
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DR InterPro; IPR006715; ETS_PEA3_N.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00178; Ets; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS00661; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein; Activator; Transcription regulation;
KW Phosphorylation.
FT DOMAIN 124 150 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 217 315 GLN-RICH.
FT DNA_BIND 412 492 ETS-DOMAIN.
SQ SEQUENCE 555 AA; 60846 MW; 278D76BA8A4D4B2 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 555;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNQRPS 7
Db 505 DNORPA 510
```

Search completed: June 8, 2004, 18:56:17
Job time : 5.9375 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 20.2344 Seconds
(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38
Sequence: 1 EDNQRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum Match 100%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rviro:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	112	4 Q96JD1	Q96jd1 homo sapien
2	38	100.0	116	4 Q96JD0	Q96jd0 homo sapien
3	35	92.1	614	3 Q7Z863	Q7z863 emericella
4	35	92.1	614	3 Q7Z862	Q7z862 emericella
5	34	89.5	248	4 Q8WW18	Q8ww18 homo sapien
6	34	89.5	266	2 Q49849	Q49849 mycobacteri
7	34	89.5	704	10 Q80896	Q80896 arabidopsis
8	34	89.5	1564	10 Q7Y0A9	Q7y0a9 oryza sativ
9	33	86.8	112	4 Q96JD2	Q96jd2 homo sapien
10	33	86.8	222	2 Q93D14	Q93d14 acinetobact
11	33	86.8	478	5 Q43955	Q43955 leishmania
12	32	84.2	392	5 Q7Z1F3	Q7z1f3 tribolium c
13	32	84.2	471	5 Q09534	Q09534 caenorhabdi
14	32	84.2	603	16 Q8Z722	Q8z722 salmonella
15	32	84.2	691	16 Q8ZPF2	Q8zpf2 salmonella
16	31	81.6	193	16 Q8EQ75	Q8eq75 oceanobacil

17	31	81.6	221	13 Q90X42	Q90x42 brachydanio
18	31	81.6	233	4 Q8TEC9	Q8tbc9 homo sapien
19	31	81.6	250	16 Q8DV81	Q8dv81 streptococc
20	31	81.6	395	2 Q7WY19	Q7wy19 bifidobacte
21	31	81.6	395	16 Q8G873	Q8g873 bifidobacte
22	31	81.6	450	2 Q8VQV1	Q8vqv1 rhodococcus
23	31	81.6	848	11 Q80Z32	Q80z32 rattus norv
24	31	81.6	1097	5 Q9V4C9	Q9v4c9 drosophila
25	30	78.9	85	2 Q919B7	Q919b7 chlamydia t
26	30	78.9	114	4 Q7Z6T1	Q7z6t1 homo sapien
27	30	78.9	125	16 Q882H6	Q882h6 pseudomonas
28	30	78.9	150	16 Q8EXI6	Q8exi6 leptoospira
29	30	78.9	158	16 Q97Q60	Q97q60 streptococc
30	30	78.9	158	16 Q8DPD4	Q8dpd4 streptococc
31	30	78.9	190	2 Q8GHN3	Q8ghn3 pseudomonas
32	30	78.9	202	12 Q98VM3	Q98vm3 rabies viru
33	30	78.9	207	4 Q96IU0	Q96iu0 homo sapien
34	30	78.9	232	10 Q22922	Q22922 arabidopsis
35	30	78.9	234	4 Q7Z2U7	Q7z2u7 homo sapien
36	30	78.9	312	16 Q83S24	Q83s24 shigella fl
37	30	78.9	336	13 Q9YHW5	Q9yhw5 gallus gall
38	30	78.9	355	16 Q9F3F6	Q9f3f6 streptomyc
39	30	78.9	361	12 Q9YMR9	Q9ymr9 lymantria d
40	30	78.9	366	2 Q98GR0	Q9xgr0 neisseria m
41	30	78.9	371	16 Q8X6U6	Q8x6u6 escherichia
42	30	78.9	371	16 Q8CW87	Q8cw87 escherichia
43	30	78.9	381	16 Q88KU1	Q88ku1 pseudomonas
44	30	78.9	390	9 Q9FZR6	Q9fzr6 mycoplasma
45	30	78.9	400	5 Q963B5	Q963b5 loligo peal

ALIGNMENTS

RESULT 1

ID	Q96JD1	PRELIMINARY;	PRT;	112 AA.
AC	Q96JD1;			
DT	01-DEC-2001 (TREMREL. 19, Created)			
DT	01-DEC-2001 (TREMREL. 19, Last sequence update)			
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)			
DE	Amyloid lambda 6 light chain variable region PIP (Fragment).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;			
RT	"Amyloid lambda 6 light chain variable region PIP.";			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF267874; AAK58586.1; -			
DR	PIR; A30323; A30323.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER 1			
FT	NON_TER 112			
SQ	SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;			

Query Match 100.0%; Score 38; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.89; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 EDNQRPS 7

Db 51 EDNQRPS 57

RESULT 2

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Q96JDO ID Q96JDO PRELIMINARY; PRT; 116 AA.
AC Q96JDO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid lambda 6 light chain variable region SAR (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL "Amyloid lambda 6 light chain variable region SAR.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267875; AAKS5857.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT TER 116
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 100.0%; Score 38; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 51 EDNRPS 57

RESULT 3
Q7Z863 ID Q7Z863 PRELIMINARY; PRT; 614 AA.
AC Q7Z863;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pot1-like protein.
OS NIMU.
OC Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RA Pitt C.W., Moreau E., Lunness P.A., Doonan J.H.;
RT "A telomere end binding protein homologue is required for ordering
RT mitotic events in Aspergillus nidulans.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ567920; CAE00178.1; -.
SQ SEQUENCE 614 AA; 69567 MW; 0873BC14CC9A86AE CRC64;

Query Match 92.1%; Score 35; DB 3; Length 614;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 353 EDNRPS 359

RESULT 4
Q7Z862 ID Q7Z862 PRELIMINARY; PRT; 614 AA.
AC Q7Z862;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pot1-like protein.
GN NIMU.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RA Pitt C.W., Moreau E., Lunness P.A., Doonan J.H.;
RT "A telomere end binding protein homologue is required for ordering
RT mitotic events in Aspergillus nidulans.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ567922; CAE00179.1; -.
SQ SEQUENCE 614 AA; 69552 MW; 09D90DBDF62B2C1E CRC64;

Query Match 92.1%; Score 35; DB 3; Length 614;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRPS 7
Db 353 EDNRPS 359

RESULT 5
Q8WW18 ID Q8WW18 PRELIMINARY; PRT; 248 AA.
AC Q8WW18;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to RIKEN cDNA 1700020L24 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021727; AAH21727.1; -.
SQ SEQUENCE 248 AA; 27236 MW; A988860B81AA530D CRC64;

Query Match 89.5%; Score 34; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNRP 6
Db 37 EDNRP 42

RESULT 6
Q49849 ID Q49849 PRELIMINARY; PRT; 266 AA.
AC Q49849;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE B2235.F2.77.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.;

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RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00019; AAA17283.1; -.
DR F01; S72947; S72947.
DR InterPro; IPR007139; DUF349.
DR Pfam; PF03993; DUF349; 1.
SQ SEQUENCE 266 AA; 29602 MW; 02C50A1B4E36EC82 CRC64;

Query Match      89.5%; Score 34; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORP 6
Db 103 EDNORP 108

RESULT 7
O80896 PRELIMINARY; PRT; 704 AA.
AC O80896;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AT2G32590 protein.
GS AT2G32590.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004681; AAC25941.1; -.
DR F01; T02558; T02558.
DR InterPro; IPR008418; Barren.
DR Pfam; PF05786; Barren; 1.
SQ SEQUENCE 704 AA; 79017 MW; 69C8E8FD56C040FA CRC64;

Query Match      89.5%; Score 34; DB 10; Length 704;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORPS 7
Db 330 EDNORPS 336

RESULT 8
Q7Y0A9 PRELIMINARY; PRT; 1564 AA.
AC Q7Y0A9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative polypeptide.
GN OSUNBA0075A22.5.

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OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBA0075A22 genomic sequence.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC133859; AAP50978.1; -.
KW Polyprotein.
SQ SEQUENCE 1564 AA; 178940 MW; CD2394D233D5E0A CRC64;

Query Match      89.5%; Score 34; DB 10; Length 1564;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORP 6
Db 388 EDNORP 393

RESULT 9
O96JD2 PRELIMINARY; PRT; 112 AA.
AC O96JD2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region NEG.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK58585.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match      86.8%; Score 33; DB 4; Length 112;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORPS 7
Db 51 EDNORPS 57

RESULT 10
Q93D14

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ID Q93D14 PRELIMINARY; PRT; 222 AA.
 AC Q93D14;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE O-methyltransferase-like protein.
 DE O-methyltransferase-like protein.
 OS Acinetobacter sp. ADP1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=62977;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ADP1;
 RX MEDLINE=21555098; PubMed=11698371;
 RA Young D.M., Ornston L.N.;
 RT "Functions of the Mismatch Repair Gene mutS from Acinetobacter sp.
 RT Strain ADP1.";
 RL J. Bacteriol. 183:6822-6831(2001).
 DR EMBL; AF400582; AAK92498.1; -;
 DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR InterPro; IPR002935; Methyltransferase_3.
 DR InterPro; IPR000051; SAM bind.
 DR Pfam; PF01596; Methyltransferase_3; 1.
 KW Methyltransferase; Transferase.
 SQ SEQUENCE 222 AA; 24730 MW; E8C020F41AD3CF67 CRC64;

Query Match 86.8%; Score 33; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNORPS 7
 Db 177 DNORPS 182

RESULT 11
 O43955 PRELIMINARY; PRT; 478 AA.
 ID O43955
 AC O43955;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DE NupM1.
 DE NupM1.
 GN TOR.
 OS Leishmania mexicana.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LV 78;
 RX MEDLINE=98135664; PubMed=9476797;
 RA Detke S.;
 RT "Identification of a transcription factor like protein at the TOR
 RT locus in Leishmania mexicana amazonensis.";
 RL Mol. Biochem. Parasitol. 90:505-511(1997).
 DR EMBL; AF016581; AAC38851.1; -;
 SQ SEQUENCE 478 AA; 52237 MW; 60363D4E0210CFA1 CRC64;

Query Match 86.8%; Score 33; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNORPS 7
 Db 342 DNORPS 347

RESULT 12
 Q7Z1F3 PRELIMINARY; PRT; 392 AA.
 ID Q7Z1F3
 AC Q7Z1F3;

DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Glass protein.
 OS Tribolium castaneum (Red flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tribolium.
 OX NCBI_TaxID=7070;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Friedrich M.;
 RT "The Tribolium homolog of the photoreceptor specific transcription
 RT factor glass and the evolutionary origin of larval eyes in
 RT holometabolous insects.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY293621; AAF46182.1; -;
 DR EMBL; AY293621; AAF46182.1; -;
 SQ SEQUENCE 392 AA; 43494 MW; D8D325DF9140AB96 CRC64;

Query Match 84.2%; Score 32; DB 5; Length 392;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
 Db 244 EDNORPS 250

RESULT 13
 Q09534 PRELIMINARY; PRT; 471 AA.
 ID Q09534
 AC Q09534;
 DT 01-JAN-1999 (TREMBlrel. 09, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DE F10B5.3 protein.
 DE F10B5.3 protein.
 GN F10B5.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sims M.A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z48334; CAA88310.1; -;
 DR F10B5.3 protein.
 DR WormPep; F10B5.3; CE01545.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB POZ.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00097; BTB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 KW Metal-binding; zinc; Zinc-finger.
 SQ SEQUENCE 471 AA; 51751 MW; C9F7B0E3AE882CA CRC64;

Query Match 84.2%; Score 32; DB 5; Length 471;
 Best Local Similarity 85.7%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
 Db 3 EDNORPS 9

RESULT 14

Q8Z722 PRELIMINARY; PRT; 603 AA.
 AC Q8Z722;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative glycosyl debranching protein (EC 3.2.1.-).
 GN STY1505 OR STY4273 OR GLGX OR T1471.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Hoiden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fellwell T., Hamlin N., Haque N., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 DR EMBL; AL627270; CAD01764.1; -.
 DR GO; AE016839; AAO69109.1; -.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_ amyl_cat.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 KW Hypothetical protein; Glycosidase; Hydrolase; Complete proteome.
 SQ SEQUENCE 603 AA; 68588 MW; 0D0B16EB5D6C6BF2 CRC64;

Query Match 84.2%; Score 32; DB 16; Length 603;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EDNRPS 7
 Db 154 EDRQPS 160

RESULT 15

Q8ZPF2 PRELIMINARY; PRT; 691 AA.
 AC Q8ZPF2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative glycosyl hydrolase (EC 3.2.1.-).
 GN STM1558.

OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AE008768; AAL20476.1; -.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_ amyl_cat.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 KW Hydrolase; Glycosidase; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 691 AA; 78569 MW; 318863462PBA531 CRC64;

Query Match 84.2%; Score 32; DB 16; Length 691;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EDNRPS 7
 Db 154 EDRQPS 160

Search completed: June 8, 2004, 18:30:11
 Job time : 23.2344 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 31.8281 Seconds

(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	38	100.0	7	4	AAB61297	Aab61297 Anti-TANG
2	38	100.0	7	6	ABU11263	Abu11263 Human TAN
3	38	100.0	98	6	ABP56510	Abp56510 Human ant
4	38	100.0	110	6	ABR55820	AbR55820 Lambda ch
5	38	100.0	110	6	ABR55826	AbR55826 Lambda ch
6	38	100.0	110	6	ABR55810	AbR55810 Lambda ch
7	38	100.0	110	6	ADA89212	Ada89212 Human ant
8	38	100.0	112	6	ADA89204	Ada89204 Human ant
9	38	100.0	113	4	AUU02522	Auu02522 Anti-adip
10	38	100.0	161	4	AAG76011	Aag76011 Human col
11	38	100.0	258	5	ABP45223	Abp45223 Human Bly
12	34	89.5	7	2	AAW16592	Aaw16592 Anti-RSV
13	34	89.5	101	4	ABB12331	Abb12331 Human bon
14	34	89.5	106	2	AAR54054	Aar54054 Sequence
15	34	89.5	106	2	AAW01529	Aaw01529 Monoclona
16	34	89.5	106	2	AAW24991	Aaw24991 Monoclona
17	34	89.5	109	2	AAW16588	Aaw16588 Anti-RSV
18	34	89.5	109	2	AAW14785	Aaw14785 Human mon
19	34	89.5	114	3	AAW53654	Aaw53654 Human col
20	34	89.5	233	5	AAU82012	Aau82012 Human sec
21	34	89.5	243	6	AAO31149	Aao31149 Human CM0
22	34	89.5	244	5	ABP45831	Abp45831 Human Bly
23	34	89.5	246	4	ABB12413	Abb12413 Human bon
24	33	86.8	88	4	AAU56093	Aau56093 Propionib
25	33	86.8	88	6	ABW52612	Abw52612 Propionib

ALIGNMENTS

RESULT 1

AAB61297
ID AAB61297 standard; peptide; 7 AA.

XX AAB61297;

DT 04-APR-2001 (first entry)

XX Anti-TANGO 268 scFv CDR, SEQ ID NO: 65.

XX Human; antibody; scFv; CDR; complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.

XX Homo sapiens.

XX WO200100810-A1.

XX 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US018152.

XX 30-JUN-1999; 99US-00345468.

XX 06-DEC-1999; 99US-00454824.

XX 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelail J, Jandrot-Perrus M, Vainchenker W;

XX Gill DS, Qian MD, Kingsbury G;

XX WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
diagnosing hemorrhagic disorders, thrombotic diseases and immunological
disorders.

XX Claim 32; Page 102; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
nucleic acid molecule encoding a platelet membrane glycoprotein receptor
glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
and polypeptides and their modulators, e.g. antisense nucleic acids,

26	33	86.8	110	5	AAO18434	Aao18434 Anti-GD2
27	33	86.8	110	6	ADA89244	Ada89244 Human ant
28	33	86.8	112	2	AAW08488	Aaw08488 C6 human
29	33	86.8	114	6	ABP56512	Abp56512 Human ant
30	33	86.8	114	6	ABP56511	Abp56511 Human ant
31	33	86.8	161	7	ADD28287	Add28287 Human het
32	33	86.8	166	7	ADD28255	Add28255 Human het
33	33	86.8	248	5	ABP45262	Abp45262 Human Bly
34	33	86.8	252	5	ABP45117	Abp45117 Human Bly
35	33	86.8	252	8	ADE83876	Ade83876 Chemokine
36	33	86.8	253	5	ABP45216	Abp45216 Human Bly
37	33	86.8	259	5	ABP45266	Abp45266 Human Bly
38	33	86.8	261	8	ADE11153	Ade11153 scFv(TF)3
39	33	86.8	282	8	ADE11151	Ade11151 scFv(TF)3
40	33	86.8	367	6	ABW68331	Abw68331 Photorhab
41	32	84.2	99	6	ABU22348	Abu22348 Protein e
42	32	84.2	99	6	ABU19646	Abu19646 Protein e
43	32	84.2	108	2	AAR54051	Aar54051 Sequence
44	32	84.2	108	2	AAW01523	Aaw01523 Monoclona
45	32	84.2	108	2	AAW24988	Aaw24988 Monoclona

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRP 7
 |||||
 Db 1 EDNQRP 7

RESULT 2

ABU11263
 ID ABU11263 standard; peptide; 7 AA.

XX AC ABU11263;

XX DT 06-FEB-2003 (first entry)

XX DE Human TANGO 268 VLCDRI Peptide #3.

XX KW Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX OS Homo sapiens.

XX FN WO200280968-A1.

XX PD 17-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011122.

XX PR 09-APR-2001; 2001US-00829495.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchenker W;

XX PI Gill DS, Qian DM, Kingsbury G;

XX DR WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX FS Claim 11; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRP 7
 |||||
 Db 1 EDNQRP 7

RESULT 3

ABP56510

ID ABP56510 standard; protein; 98 AA.

XX AC ABP56510;

XX DT 20-MAR-2003 (first entry)

XX DE Human anti-Fc-epsilon-R1 alpha autoantibody light chain VI-22.

XX KW Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;
 KW allergic disease; urticaria; late phase allergic reaction; malignancy;
 KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;
 KW conditional autoimmunity; IgE mediated disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200282085-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-EP003660.

XX PR 04-APR-2001; 2001US-0281024P.

XX PA (ZLBB-) ZLB BIOPLASMA AG.

XX PI Miescher S;

XX DR WPI; 2003-103348/09.

XX Identifying and obtaining inhibitor of a pathological process for
 XX treating e.g. autoimmunity comprises determining if a compound is capable
 XX of modulating the binding of the Fc-epsilon-R1 receptor and an
 XX autoantibody against its alpha-chain.

XX FS Claim 20; Page 22; 29pp; English.

XX The present invention describes a method for identifying and obtaining an
 CC inhibitor of a pathological process. The method comprises determining if
 CC a compound is capable of modulating the binding of the Fc-epsilon-R1
 CC receptor alpha-chain and an autoantibody against its alpha-chain. Also
 CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor
 CC alpha-chain for identifying and obtaining an inhibitor of a pathological
 CC process; (2) use of the identified inhibitor for inhibiting activity of
 CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3)
 CC a compound identified by the method, which binds but does not activate
 CC the receptor; and (4) a polypeptide capable of specific binding to the Fc
 CC -epsilon-R1 receptor alpha-chain. The method is useful for obtaining an
 CC inhibitor of a pathological process e.g. imbalance between cell-bound and
 CC free IgE e.g. allergic disease (urticaria, late phase allergic reactions,
 CC intrinsic asthma, drug intolerance and food intolerance), IgE mediated
 CC disease or malignancy. The compound is useful for treating a pathological
 CC process, particularly conditional autoimmunity. The present sequence
 CC represents a human recombinant anti-Fc-epsilon-R1 alpha autoantibody
 CC light chain protein sequence from the present invention
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 38; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNRPS 7
 Db 51 EDNRPS 57
 RESULT 4
 ABR55820
 ID ABR55820 standard; protein; 110 AA.
 XX
 AC ABR55820;
 XX
 DT 02-SEP-2003 (first entry)
 XX
 DE Lambda chain variable region of anti-Ang-2 antibody GC1E8 lambda.
 XX
 KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /note= "complementarity determining region (CDR) 1"
 FT Region 58..80
 FT /note= "complementarity determining region (CDR) 2"
 FT Region 91..101
 FT /note= "complementarity determining region (CDR) 3"
 FN WO2003030833-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032613.
 XX
 PR 11-OCT-2001; 2001US-0328604P.
 PR 10-OCT-2002; 2002US-00269805.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Oliner JD;
 XX
 DR WPI; 2003-504963/47.
 XX
 XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX Claim 1; Page 95; 161pp; English.
 XX
 CC The invention relates to a specific binding agent, which comprises at
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
 CC fragment. The binding agents are antibodies that recognize and bind to
 CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity,
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
 CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a lambda chain variable region of an anti-Ang-2
 CC antibody
 XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 38; DB 6; Length 110;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNRPS 7
 Db 51 EDNRPS 57
 RESULT 5
 ABR55826
 ID ABR55826 standard; protein; 110 AA.
 XX
 AC ABR55826;
 XX
 DT 02-SEP-2003 (first entry)
 XX
 DE Lambda chain variable region of anti-Ang-2 antibody IF-1C10 lambda.
 XX
 KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /note= "complementarity determining region (CDR) 1"
 FT Region 58..80
 FT /note= "complementarity determining region (CDR) 2"
 FT Region 91..101
 FT /note= "complementarity determining region (CDR) 3"
 FN WO2003030833-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032613.
 XX
 PR 11-OCT-2001; 2001US-0328604P.
 PR 10-OCT-2002; 2002US-00269805.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Oliner JD;
 XX
 DR WPI; 2003-504963/47.
 XX
 XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 XX
 PS Claim 1; Page 95; 161pp; English.
 XX

CC The invention relates to a specific binding agent, which comprises at
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
 CC fragment. The binding agents are antibodies that recognize and bind to
 CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity,
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
 CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a lambda chain variable region of an anti-Ang-2
 CC antibody

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 38; DB 6; Length 110;

Best Local Similarity 100.0%; Pred. No. 4.9; Length 110;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
 |||||
 Db 51 EDNORPS 57

RESULT 6

ID ABR55810 standard; protein; 110 AA.

XX AC ABR55810;

XX DT 02-SEP-2003 (first entry)

XX DE Lambda chain variable region of anti-Ang-2 antibody FD-B2 lambda.

XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 22..36

FT /note= "complementarity determining region (CDR) 1"

FT Region 58..80

FT /note= "complementarity determining region (CDR) 2"

FT Region 91..101

FT /note= "complementarity determining region (CDR) 3"

XX WO2003030833-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032613.

XX 11-OCT-2001; 2001US-0328604P.

XX 10-OCT-2002; 2002US-00269805.

XX (AMGE-) AMGEN INC.

XX Olinier JD;

XX WPI; 2003-504963/47.

XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX Claim 1; Page 95; 161pp; English.

XX The invention relates to a specific binding agent, which comprises at
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
 CC fragment. The binding agents are antibodies that recognize and bind to

CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity,
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
 CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a lambda chain variable region of an anti-Ang-2
 CC antibody

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 38; DB 6; Length 110;

Best Local Similarity 100.0%; Pred. No. 4.9; Length 110;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNORPS 7
 |||||
 Db 51 EDNORPS 57

RESULT 7

ID ADA89212 standard; protein; 110 AA.

XX AC ADA89212;

XX DT 20-NOV-2003 (first entry)

XX DE Human antibody G3F3 light chain amino acid sequence SEQ ID NO:56.

XX immunoglobulin; Ig; heavy chain variable domain;

KW light chain variable domain; major histocompatibility complex; MHC;
 KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
 KW cancer.

XX OS Synthetic.

XX OS Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.

XX N-PSDB; ADA89211.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
 PT and an immunoglobulin light chain variable (VL) domain, useful for
 PT preparing a composition for treating or preventing a cancerous disorder.

XX Disclosure; Fig 13A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin
 CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
 CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
 CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC
 CC in the absence of the bound peptide, and does not substantially bind the

CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the
 CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents the light chain of an antibody which binds to an MHC-
 CC peptide complex where the peptide component in as peptide fragment of
 CC gp100.

XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 38; DB 6; Length 110;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 Db 51 EDNQRPS 57
 |||||

RESULT 8
 ADA89204
 ID ADA89204 standard; protein; 112 AA.

AC ADA89204;

DT 20-NOV-2003 (first entry)

DE Human antibody G2D12 light chain amino acid sequence SEQ ID NO:48.

DE immunoglobulin; Ig; heavy chain variable domain;

KW light chain variable domain; major histocompatibility complex; MHC;
 KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
 KW cancer.

OS Synthetic.

OS Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.
 XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.

XX N-PSDB; ADA89203.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
 PT and an immunoglobulin light chain variable (VL) domain, useful for
 PT preparing a composition for treating or preventing a cancerous disorder.

XX Disclosure; Fig 11A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin
 CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
 CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,

CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC
 CC in the absence of the bound peptide, and does not substantially bind the
 CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the
 CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents the light chain of an antibody which binds to an MHC-
 CC peptide complex where the peptide component in as peptide fragment of
 CC gp100.

XX Sequence 112 AA;

Query Match 100.0%; Score 38; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
 Db 51 EDNQRPS 57
 |||||

RESULT 9
 AAU02522

ID AAU02522 standard; protein; 113 AA.

AC AAU02522;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 13.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03422.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 106; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or

CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 38; DB 4; Length 113;

Best Local Similarity 100.0%; Pred. No. 5.1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 EDNRPS 7

Db 53 EDNRPS 59
|||||

RESULT 10

AAAG76011
ID AAG76011 standard; protein; 161 AA.

XX AC AAG76011;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:6775.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma; chromosome 22.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US026524.

XX PR 29-SEP-1999; 99US-0157137P.

XX PR 03-NOV-1999; 99US-0163280P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CB, Rosen CA;

XX DR WPI; 2001-235357/24.

XX DR N-PSDB; AAH35416.

XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX PS Claim 11; Page 8234-8235; 9803pp; English.

XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX CC proteins are collectively known as colon cancer antigens. The colon
XX CC cancer antigens have cytostatic activity and can be used in gene therapy
XX CC and vaccine production. N and P may be used in the prevention, diagnosis
XX CC and treatment of diseases associated with inappropriate P expression. For
XX CC example, N and P may be used to treat disorders associated with decreased
XX CC expression by rectifying mutations or deletions in a patient's genome
XX CC that affect the activity of P by expressing inactive proteins or to
XX CC supplement the patients own production of P. Additionally, N may be used
XX CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX CC into a host cell and culturing the cell to express the proteins. N and P
XX CC can be used in the prevention, diagnosis and treatment of colorectal

CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1032, 7921 and 7922

XX SQ Sequence 161 AA;

Query Match 100.0%; Score 38; DB 4; Length 161;

Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 EDNRPS 7

Db 72 EDNRPS 78
|||||

RESULT 11

ABP45223
ID ABP45223 standard; protein; 258 AA.

XX AC ABP45223;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1234.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO2000202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 1874-1875; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
XX CC and so may be used to detect and quantitate the presence of Blys in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of Blys. They may also be
XX CC administered to treat diseases associated with aberrant Blys expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 258 AA;

Query Match 100.0%; Score 38; DB 5; Length 258;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORPS 7
 |||||
 Db 198 EDNORPS 204

RESULT 12
 AAW16592
 ID AAW16592 standard; peptide; 7 AA.
 XX
 AC AAW16592;
 XX
 DT 30-NOV-1997 (first entry)
 DE
 DE Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6 CDR2.
 XX
 XX Respiratory syncytial virus; RSV; monoclonal antibody; CDR;
 KW complementarity determining region; pneumonia; bronchiolitis; diagnosis;
 KW therapy; vaccine; RSVF2-5.
 XX
 XX Homo sapiens.
 OS
 XX WO9710846-A1.
 PN
 XX 27-MAR-1997.
 PD
 XX 18-SEP-1996; 96WO-US014937.
 PF
 XX 18-SEP-1995; 95US-0003931P.
 PR
 XX (INTR-) INTRACEL CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Pilkington GR, Gilmour PS, Chanock RM, Crowe JE, Murphy BR;
 XX WPI; 1997-202621/18.
 DR
 XX Composition comprising respiratory syncytial virus antibody - useful for
 PT treatment or prophylaxis of active disease or infection.
 PT
 XX Claim 8; Page 56; 71pp; English.

XX This peptide sequence comprises complementarity determining region 2
 CC (CDR2) of the light chain VL6 region of a novel neutralising human
 CC monoclonal antibody to the respiratory syncytial virus (RSV). The
 CC antibody, designated RSVF2-5 (ATCC 69509), selectively binds to an RSV F
 CC glycoprotein epitope. DNA encoding RSVF2-5 Fd and light chain (see
 CC AAT66556-57) was isolated from a phage library prepared from the RNA of
 CC peripheral blood lymphocytes of an HIV-1 infected donor. A claimed
 CC pharmaceutical preparation comprises a carrier and an antibody that
 CC includes the RSVF2-5 VH3 CDR3 (AAW16586) and which may also include the
 CC VH3 CDR2 (AAW16584) and/or CDR1 (AAW16582) or the entire Fd region
 CC (AAW16580), or is an Fab fragment and includes the RSVF2-5 VL6 CDR3
 CC (AAW16594), CDR2, CDR1 (AAW16590) or entire light chain (AAW16588). The
 CC preparation alternatively comprises a carrier and a vector that includes
 CC a nucleotide sequence encoding the antibody. The preparations can be used
 CC for the treatment or prophylaxis of active RSV disease or infection
 CC (claimed), and may also be used for RSV detection. The antibody binds and
 CC neutralises antigenic subgroups A and B of RSV with high efficiency
 XX
 SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORP 6
 |||||
 Db 1 EDNORP 6

RESULT 13
 ABB12331
 ID ABB12331 standard; protein; 101 AA.

XX
 AC ABB12331;
 XX
 DT 15-JAN-2002 (first entry)
 DE
 DE Human bone marrow expressed protein SEQ ID NO: 85.

XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
 KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
 KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
 KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
 KW nervous system disorder; autoimmune disorder; inflammation; allergy.
 XX
 OS Homo sapiens.
 XX WO200174836-A1.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US010472.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 PR
 XX 30-NOV-2000; 2000US-0250583P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
 PI WPI; 2001-626375/72.
 DR N-PSDB; ABA09575.

XX New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling.
 XX
 PS Claim 10; Page 200-201; 380pp; English.

XX The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC cell disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections, a
 CC allergies and blood coagulation disorders. The present sequence is a
 CC protein of the invention

Sequence 101 AA;

Query Match 89.5%; Score 34; DB 4; Length 101;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORPS 7
 |||||
 Db 25 EDNORPS 31

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RESULT 14
ID AAR54054 standard; protein; 106 AA.
XX AC AAR54054;
XX DT 25-MAR-2003 (revised)
XX DT 08-NOV-1994 (first entry)
XX DE Sequence of the VL region of monoclonal antibody MD3-4 against hepatitis
XX DE B virus surface antigen.
XX KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy; HBsAg;
XX KW diagnosis; HBV.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1. .95
XX FT Region /label= V III
XX FT Region /label= CDR 1
XX FT Region /label= CDR 2
XX FT Region /label= CDR 3
XX FT Region /label= J 3
XX PN WO9411495-A1.
XX PD 26-MAY-1994.
XX PF 06-NOV-1992; 92WO-US009749.
XX PR 06-NOV-1992; 92WO-US009749.
XX PA (SANO ) SANDOZ LTD.
XX PI Ostberg LG;
XX WPI; 1994-183497/22.
XX N-PSDB; AAQ64057.
XX Monoclonal antibodies active against Hepatitis B surface antigen - for
XX diagnosis and treatment of Hepatitis B virus.
XX Example; Page 43; 53pp; English.
XX Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZMI- 2,
XX ZMI-1 and PEI-1 hybridoma cell lines were derived from lymphocytes of
XX individuals immunised with Heptavax (Merck & Co). Antibodies PEI-1, ZMI-
XX 1, ZMI-2 and MD3-4 belong to the IgG1 clas. The cell lines producing PEI-
XX 1, ZMI-1 and ZMI-2 were deposited as ATCC HB9234, 9191 and 9192
XX respectively. The cell lines all behave as typical (mouse x human) x
XX human hybridomas and produce their respective Abs in concs. ranging up to
XX 25 mg/l in standard suspension culture. The heavy variable (VH) and light
XX variable (LH) chains of Abs PEI-1, ZMI-1, ZMI-2 and MD3-4 were isolated
XX and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each
XX cell line. ss DNA was synthesised using AMV-reverse transcriptase and
XX oligo-dT as primer. PCRs were performed and amplified DNA was size
XX selected. ss DNA for sequencing was isolated from each positive clone
XX after superinfection with M13K07. Sequencing was by the dideoxy chain
XX termination method (Sanger et al.). (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 106 AA;
XX Query Match 89.5%; Score 34; DB 2; Length 106;
XX Best Local Similarity 85.7%; Pred. No. 32;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EDNORPS 7
Db 49 EDNKRPS 55

RESULT 15
AAW01529
ID AAW01529 standard; protein; 106 AA.
XX AC AAW01529;
XX DT 25-MAR-2003 (revised)
XX DT 04-MAR-1997 (first entry)
XX DE Monoclonal antibody MD3-4 light chain variable region.
XX KW Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
XX KW xenogeneic hybridoma; SP4Z 4; PEI-1; ZMI-1; ZMI-2; MD3-4; L03-3;
XX KW IgG1 class; heavy chain; light chain; variable region.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 1. .94
XX FT Region /label= V_kappa_III_region
XX FT Region /label= CDR1
XX FT Region /label= CDR2
XX FT Region /label= framework_region
XX FT Region /label= CDR3
XX FT Region /label= J_kappa_3_region
XX PN US5565354-A.
XX PD 15-OCT-1996.
XX PF 14-JUN-1994; 94US-00259372.
XX PR 05-SEP-1986; 86US-00904517.
XX PR 31-OCT-1986; 86US-00925196.
XX PR 11-MAY-1988; 88US-00192754.
XX PR 15-JUN-1990; 90US-00538796.
XX PR 27-MAR-1991; 91US-00676036.
XX PR 21-APR-1992; 92US-00871426.
XX PA (SANO ) SANDOZ LTD.
XX PI Ostberg LG;
XX WPI; 1996-476304/47.
XX N-PSDB; AAT46135.
XX Human monoclonal antibodies specific for hepatitis B surface antigen -
XX are used to treat or prevent infection or in diagnostic assays.
XX Example 9; Col 43-46; 26pp; English.
XX Monoclonal antibodies effective for the diagnosis and treatment of
XX diseases caused by infection with hepatitis B have been prepared from a
XX cell line obtained by fusing a xenogeneic hybridoma designated SP4Z 4
XX with blood cells of a patient immunised with hepatitis B vaccine.
XX Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of
XX these being of the IgG1 class. The present sequence is the light variable
XX chain of MD3-4. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 106 AA;

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Query Match 89.5%; Score 34; DB 2; Length 106;
Best/Local Similarity 85.7%; Pred.No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNQRPS 7
|||:||||
Db 49 EDNKRPS 55

Search completed: June 8, 2004, 18:26:55
Job time : 32.8281 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 43.2656 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	13	9	US-09-832-312-64
2	62	100.0	13	11	US-09-829-495-64
3	62	100.0	98	12	US-10-453-698-117
4	62	100.0	98	15	US-10-308-817-117
5	62	100.0	110	14	US-10-269-805-50
6	62	100.0	110	14	US-10-269-805-52
7	62	100.0	161	14	US-10-106-698-6785
8	59	95.2	110	14	US-10-269-805-42
9	58	93.5	248	14	US-10-120-414-78
10	56	90.3	258	10	US-09-880-748-1234
11	56	90.3	258	12	US-10-293-418-1234
12	55	88.7	13	10	US-09-972-656-2
13	55	88.7	216	10	US-09-972-656-108
14	54	87.1	13	10	US-09-972-656-3
15	54	87.1	161	15	US-10-364-743-76

16	54	87.1	166	15	US-10-364-743-37	Sequence 37, Appl
17	54	87.1	216	10	US-09-972-656-90	Sequence 90, Appl
18	53	85.5	253	10	US-09-880-748-909	Sequence 909, App
19	53	85.5	253	10	US-09-880-748-1125	Sequence 1125, Ap
20	53	85.5	253	10	US-09-880-748-1167	Sequence 1167, Ap
21	53	85.5	253	10	US-09-880-748-1375	Sequence 1375, Ap
22	53	85.5	253	12	US-10-293-418-909	Sequence 909, App
23	53	85.5	253	12	US-10-293-418-1125	Sequence 1125, Ap
24	53	85.5	253	12	US-10-293-418-1167	Sequence 1167, Ap
25	53	85.5	253	12	US-10-293-418-1375	Sequence 1375, Ap
26	53	85.5	282	12	US-10-427-805-1	Sequence 1, Appli
27	53	85.5	397	12	US-10-427-805-3	Sequence 3, Appli
28	53	85.5	418	12	US-10-427-805-2	Sequence 2, Appli
29	52	83.9	257	10	US-09-880-748-1531	Sequence 1531, Ap
30	52	83.9	257	12	US-10-293-418-1531	Sequence 1531, Ap
31	51	82.3	69	12	US-10-363-616-291	Sequence 291, App
32	51	82.3	110	14	US-10-269-805-58	Sequence 58, Appl
33	50	80.6	13	10	US-09-972-656-1	Sequence 1, Appli
34	50	80.6	13	15	US-10-425-855-11	Sequence 11, Appl
35	50	80.6	103	10	US-09-972-656-130	Sequence 130, App
36	50	80.6	109	15	US-10-425-855-9	Sequence 9, Appli
37	50	80.6	217	10	US-09-972-656-88	Sequence 88, Appl
38	49	79.0	243	14	US-10-322-673-55	Sequence 55, Appl
39	48	77.4	110	12	US-10-371-942-88	Sequence 88, Appl
40	47	75.8	13	10	US-09-972-656-9	Sequence 9, Appli
41	47	75.8	218	10	US-09-972-656-102	Sequence 102, App
42	44	71.0	727	15	US-10-108-260A-3060	Sequence 3060, Ap
43	42	67.7	113	12	US-10-424-599-241152	Sequence 241152,
44	40	64.5	116	12	US-10-424-599-193332	Sequence 193332,
45	39	62.9	13	9	US-09-736-371B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-832-312-64
; Sequence 64, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-64

Query Match 100.0%; Score 62; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13

Db 1 TRSSGSIASNYVQ 13

RESULT 2

US-09-829-495-64
; Sequence 64, Application US/09829495

; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeval J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
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; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-64

Query Match 100.0%; Score 62; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 1 TRSSGSIASNYVQ 13

RESULT 3
US-10-453-698-117
; Sequence 117, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-117

Query Match 100.0%; Score 62; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 23 TRSSGSIASNYVQ 35

RESULT 4
US-10-308-817-117
; Sequence 117, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37

; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-117

Query Match 100.0%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 23 TRSSGSIASNYVQ 35

RESULT 5
US-10-269-805-50
; Sequence 50, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-50

Query Match 100.0%; Score 62; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 23 TRSSGSIASNYVQ 35

RESULT 6
US-10-269-805-52
; Sequence 52, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-52

Query Match 100.0%; Score 62; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRSSGSIASNYVQ 13

```
Db      23 TRSSGSIASNYVQ 35
|||||
RESULT 7
US-10-106-698-6785
; Sequence 6785, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6785
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6785

Query Match      100.0%; Score 62; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      44 TRSSGSIASNYVQ 56
|||||
RESULT 8
US-10-269-805-42
; Sequence 42, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-42

Query Match      95.2%; Score 59; DB 14; Length 110;
Best Local Similarity 92.3%; Pred. No. 0.0074;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      23 TRSSGSIATNYVQ 35
|||||
RESULT 9
US-10-120-414-78
; Sequence 78, Application US/10120414
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23P2
```

```
; Publication No. US20030175274A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PFI12P9
; CURRENT APPLICATION NUMBER: US/10/120,414
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,385
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/350,366
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-414-78

Query Match      93.5%; Score 58; DB 14; Length 248;
Best Local Similarity 92.3%; Pred. No. 0.027;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      160 TRSSGSIASNYVQ 172
|||||
RESULT 10
US-09-880-748-1234
; Sequence 1234, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1234

Query Match      90.3%; Score 56; DB 10; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.063;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
Db      170 TRSSGSIASNYVQ 182
|||||
RESULT 11
US-10-293-418-1234
; Sequence 1234, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23P2
```

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1234

Query Match 90.3%; Score 56; DB 12; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.063; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 170 TRSSGSIASNYVQ 182

RESULT 12

US-09-972-656-2
; Sequence 2, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-2

Query Match 88.7%; Score 55; DB 10; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.004; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 1 TGSSGSIASNYVQ 13

RESULT 13

US-09-972-656-108
; Sequence 108, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-108

Query Match 88.7%; Score 55; DB 10; Length 216;
Best Local Similarity 92.3%; Pred. No. 0.079; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 23 TGSSGSIASNYVQ 35

RESULT 14

US-09-972-656-3
; Sequence 3, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-3

Query Match 87.1%; Score 54; DB 10; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.006; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
Db 1 TRSSGSIASNYVQ 13

RESULT 15

US-10-364-743-76
; Sequence 76, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 161
; TYPE: PRT
; ORGANISM: human
US-10-364-743-76

Query Match 87.1%; Score 54; DB 15; Length 161;

Best Local Similarity 84.6%; Pred. No. 0.087; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| | | | | | | | | |
Db 25 TRSSGSIVGNYVQ 37

Search completed: June 8, 2004, 18:52:59
Job time : 44.2656 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 59.1094 Seconds
(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	13	4 AAB61296	Aab61296 Anti-TANG
2	62	100.0	13	6 ABU11262	Abu11262 Human TAN
3	62	100.0	98	6 ABP56510	Abp56510 Human ant
4	62	100.0	110	5 AAO18434	Aao18434 Anti-GD2
5	62	100.0	110	6 ABR55820	Abr55820 Lambda ch
6	62	100.0	110	6 ABR55818	Abr55818 Lambda ch
7	62	100.0	113	4 AAU02522	Aau02522 Anti-adip
8	62	100.0	161	4 AAG76011	Aag76011 Human col
9	59	95.2	110	6 ABR55810	Abr55810 Lambda ch
10	58	93.5	248	6 ABJ19832	Abj19832 Human VEG
11	57	91.9	238	6 ABR62334	Abr62334 Anti-EBV
12	56	90.3	258	5 ABP45223	Abp45223 Human Bly
13	55	88.7	112	6 ABP56513	Abp56513 Human ant
14	54	87.1	161	7 ADD28298	Add28298 Human het
15	54	87.1	166	7 ADD28259	Add28259 Human het
16	53	85.5	253	5 ABP44898	Abp44898 Human Bly
17	53	85.5	253	5 ABP45156	Abp45156 Human Bly
18	53	85.5	253	5 ABP45364	Abp45364 Human Bly
19	53	85.5	253	5 ABP45114	Abp45114 Human Bly
20	53	85.5	261	8 ADE11153	Adel1153 scFv(TF)3
21	53	85.5	282	8 ADE11151	Adel1151 scFv(TF)3
22	52	83.9	257	5 ABP45520	Abp45520 Human Bly
23	51	82.3	69	5 ABP62854	Abp62854 Human pol
24	51	82.3	110	6 ABR55826	Abr55826 Lambda ch
25	50	80.6	13	2 AAW16590	Aaw16590 Anti-RSV

26	50	80.6	109	2 AAW16588	Aaw16588 Anti-RSV
27	50	80.6	109	2 AAW14785	Aaw14785 Human mon
28	49	79.0	243	6 AAO31149	Aao31149 Human CM0
29	48	77.4	110	6 ADA89244	Ada89244 Human ant
30	45	72.6	114	6 ABP56512	Abp56512 Human ant
31	45	72.6	114	6 ABP56511	Abp56511 Human ant
32	44	71.0	677	4 ABG07372	Abg07372 Novel hum
33	44	71.0	3572	5 ABG95659	Abg95659 Human nuc
34	42	67.7	517	4 ABB57957	Abb57957 Drosophil
35	39	62.9	13	2 AAR23736	Aar23736 Ligand CD
36	39	62.9	13	2 AAR50108	Aar50108 CDR (d)
37	39	62.9	13	3 AAY68804	Aay68804 Amino aci
38	39	62.9	13	5 ABG31465	Abg31465 Rat immun
39	39	62.9	13	6 ABP98797	Abp98797 Rat anti-
40	39	62.9	110	5 ABG31476	Abg31476 Light cha
41	39	62.9	110	6 ABP98809	Abp98809 Chimeric
42	39	62.9	111	3 AAY68807	Aay68807 A light c
43	39	62.9	128	2 AAR23778	Aar23778 Recombina
44	39	62.9	128	2 AAR23814	Aar23814 Recombina
45	39	62.9	128	2 AAR23772	Aar23772 Recombina

ALIGNMENTS

RESULT 1

AAB61296
ID AAB61296 standard; peptide; 13 AA.
XX
AC AAB61296;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 64.
XX
KW Human; antibody; scFv; CDR; complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200100810-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018152.
XX
PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX
(MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilelial J, Jandrot-Perrus M, Vainchenker W;
Gill DS, Qian MD, Kingsbury G;
XX
DR WPI; 2001-080877/09.
XX

New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.

Claim 32; Page 102; 227pp; English.

The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 62; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 DB 1 TRSSGSIASNYVQ 13

RESULT 2
 ABU11262
 ID ABU11262 standard; peptide; 13 AA.

XX
 AC ABU11262;

XX
 DT 06-FEB-2003 (first entry)

XX
 DE Human TANGO 268 VLCDR1 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

OS
 PN WO200280968-A1.

XX
 XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchenker W;

PI Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 10; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX

Sequence 13 AA;

Query Match 100.0%; Score 62; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 DB 1 TRSSGSIASNYVQ 13

RESULT 3

ABP56510

ID ABP56510 standard; protein; 98 AA.

XX AC ABP56510;

XX 20-MAR-2003 (first entry)

XX Human anti-Fc-epsilon-R1 alpha autoantibody light chain V1-22.

KW Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;
 KW allergic disease; urticaria; late phase allergic reaction; malignancy;
 KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;
 KW conditional autoimmunity; IgE mediated disease.

XX Homo sapiens.

OS Synthetic.

XX WO200282085-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-EP003660.

XX 04-APR-2001; 2001US-0281024P.

XX (ZLBB-) ZLB BIOPLASMA AG.

XX Miescher S;

XX WPI; 2003-103348/09.

XX Identifying and obtaining inhibitor of a pathological process for
 PT treating e.g. autoimmunity comprises determining if a compound is capable
 PT of modulating the binding of the Fc-epsilon-R1 receptor and an
 PT autoantibody against its alpha-chain.

PS Claim 20; Page 22; 29pp; English.

Query Match 100.0%; Score 62; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
DB 23 TRSSGSIASNYVQ 35

RESULT 6
ABR55818
ID ABR55818 standard; protein; 110 AA.
XX
XX ABR55818;
AC
XX
XX 02-SEP-2003 (first entry)
DT
XX
XX Lambda chain variable region of anti-Ang-2 antibody GLD4 lambda.
DE
XX
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW synaenological; antinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
XX Homo sapiens.
OS

PH Key Location/Qualifiers
FT Region 22..36
FT /note= "complementarity determining region (CDR) 1"
FT Region 58..80
FT /note= "complementarity determining region (CDR) 2"
FT Region 91..101
FT /note= "complementarity determining region (CDR) 3"
XX
XX WO2003030833-A2.

PN
XX
XX 17-APR-2003.
PD
XX
XX 11-OCT-2002; 2002WO-US032613.
PF
XX
XX 11-OCT-2001; 2001US-0328604P.
PR
XX
XX 10-OCT-2002; 2002US-00269805.

XX (AMGE-) AMGEN INC.

XX Oliner JD;

XX WPI; 2003-504963/47.

XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX Claim 1; Page 95; 161pp; English.

XX The invention relates to a specific binding agent, which comprises at
XX least one peptide selected from any of 62 peptides (ABR55769-830) or its
XX fragment. The binding agents are antibodies that recognize and bind to
XX angiotensin-2 (Ang-2). The specific binding agent, particularly the
XX antibody, is useful for inhibiting undesired angiogenesis, treating
XX cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
XX 2 activity, modulating vascular permeability or plasma leakage, or
XX treating a disease (e.g. ocular neovascular disease, obesity,
XX haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
XX inflammatory disorders, atherosclerosis, endometriosis, neoplastic
XX disease, bone-related disease, or psoriasis) in a mammal. The present
XX sequence represents a lambda chain variable region of an anti-Ang-2
XX antibody

XX Sequence 110 AA;

Query Match 100.0%; Score 62; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
DB 23 TRSSGSIASNYVQ 35

RESULT 7
AAU02522
ID AAU02522 standard; protein; 113 AA.
XX

XX AC AAU02522;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, PAT 13.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX N-PSDB; AAS03422.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX Claim 1; Page 106; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease

XX Sequence 113 AA;

Query Match 100.0%; Score 62; DB 4; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| | | | | | | | | | | | | | |
DB 25 TRSSGSIASNYVQ 37

RESULT 8

AAG76011
 ID AAG76011 standard; protein; 161 AA.
 XX
 AC AAG76011;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:6775.
 XX
 DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 22.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US026524.
 XX
 PR 29-SEP-1999; 99US-0157137P.
 PR 03-NOV-1999; 99US-0163280P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI; 2001-235357/24.
 DR N-PSDB; AAH35416.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers.
 XX
 PS Claim 11; Page 8234-8235; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG773514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
 CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated P8, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922
 XX
 SQ Sequence 161 AA;
 Query Match 100.0%; Score 62; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVQ 13
 DB 44 TRSSGSIASNYVQ 56
 |||||
 RESULT 9
 ABR55810
 ID ABR55810 standard; protein; 110 AA.
 XX
 AC ABR55810;
 XX
 DT 02-SEP-2003 (first entry)
 XX

DE Lambda chain variable region of anti-Ang-2 antibody FD-B2 lambda.
 XX
 KW Ang-2; angiopeptin-2; anorectic; cytostatic; antiarteriosclerotic;
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 KW angiogenesis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /note= "complementarity determining region (CDR) 1"
 FT Region 58..80
 FT /note= "complementarity determining region (CDR) 2"
 FT Region 91..101
 FT /note= "complementarity determining region (CDR) 3"
 XX
 PN WO2003030833-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032613.
 XX
 PR 11-OCT-2001; 2001US-0328604P.
 PR 10-OCT-2002; 2002US-00269805.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Oliner JD;
 XX
 DR WPI; 2003-504963/47.
 XX
 PT New specific binding agents (i.e. anti-Angiopeptin-2 antibodies), useful
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 XX
 PS Claim 1; Page 95; 161pp; English.
 XX
 CC The invention relates to a specific binding agent, which comprises at
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
 CC fragment. The binding agents are antibodies that recognize and bind to
 CC angiopeptin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancer, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity,
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
 CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a lambda chain variable region of an anti-Ang-2
 CC antibody
 XX
 SQ Sequence 110 AA;
 Query Match 95.2%; Score 59; DB 6; Length 110;
 Best Local Similarity 92.3%; Pred. No. 0.0039;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVQ 13
 DB 23 TRSSGSIATNYVQ 35
 |||||
 RESULT 10
 ABR19832
 ID ABR19832 standard; protein; 248 AA.
 XX
 AC ABR19832;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Human VEGF-2 related protein SEQ ID No 78.
 XX
 KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic;

KW antiarthritic; antidiabetic; ophthalmological; antiallergic;
 KW immunosuppressive; dermatological; antipsoriatic; vulnery; antibody;
 KW CDR region; VH domain; immunospecific; VEGF-2; cancer;
 KW proliferative disorder; cardiovascular disorder; arrhythmia;
 KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;
 KW infectious disease; autoimmune disease; rheumatoid arthritis;
 KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;
 KW angiogenesis; wound healing; vascular tissue repair; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200283704-A1.
 XX
 XX 24-OCT-2002.
 XX
 XX 12-APR-2002; 2002WO-US011474.
 XX
 XX 13-APR-2001; 2001US-0283385P.
 XX 24-JAN-2002; 2002US-0350366P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Albert VR, Ruben SM, Wager RE;
 XX WPI; 2003-092991/08.
 XX
 XX New isolated polynucleotide encoding an antibody which inhibits a VEGF-2
 PT polypeptide, useful for diagnosing, treating or preventing diseases
 PT associated with aberrant VEGF-2 expression or function, e.g. cancer or
 PT inflammation.
 XX
 XX Disclosure; Page 389-390; 425pp; English.
 XX
 XX The invention relates to an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody comprising an
 CC amino acid sequence selected from at least one, two or three CDR
 CC region(s) of a VH or VL domain where the first antibody
 CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated
 CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,
 CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or
 CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,
 CC such as cancer and other proliferative disorders, cardiovascular
 CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral
 CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases
 CC (e.g. rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),
 CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and
 CC antibodies may also be used to stimulate angiogenesis, wound healing, and
 CC promoting vascular tissue repair. The polynucleotide and polypeptide may
 CC also be used for in vitro purposes related to scientific research,
 CC synthesis of DNA and manufacture of DNA vectors, and for the production
 CC of diagnostics and therapeutics to treat human diseases. This sequence
 CC represents a human VEGF-2 related protein of the invention
 XX
 XX Sequence 248 AA;
 SQ
 Query Match 93.5%; Score 58; DB 6; Length 248;
 Best Local Similarity 92.3%; Pred. No. 0.015;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TRSGSGSIASNVVQ 13
 Db 160 TRSGSGSIASNVVQ 172
 RESULT 11
 ABR62334
 ID ABR62334 standard; protein; 238 AA.
 XX
 XX ABR62334;
 AC ABR62334;
 XX
 XX 22-SEP-2003 (first entry)
 DT
 XX Anti-EBV latent membrane protein scFv antibody FG-47.

XX Latent membrane protein; LMP; antibody; scFv; Epstein-Barr virus; EBV;
 KW lymphoma; lymphoproliferative disease; carcinoma; malignancy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 1..29
 FT /label= VH_FR1
 FT Region 31..35
 FT /label= VH_CDR1
 FT Region 36..48
 FT /label= VH_FR2
 FT Region 50..65
 FT /label= VH_CDR2
 FT Region 67..97
 FT /label= VH_FR3
 FT
 FT Misc-difference 86
 FT /note= "Encoded by GTG"
 FT Region 99..102
 FT /label= VH_CDR3
 FT Region 103..113
 FT /label= VH_FR4
 FT Region 114..128
 FT /label= Linker
 FT Region 129..150
 FT /label= VL_FR1
 FT Region 151..163
 FT /label= VL_CDR1
 FT Region 164..177
 FT /label= VL_FR2
 FT Region 179..185
 FT /label= VL_CDR2
 FT Region 186..219
 FT /label= VL_FR3
 FT Region 220..227
 FT /label= VL_CDR3
 FT Region 229..238
 FT /label= VL_FR4
 WO2003048337-A2.
 12-JUN-2003.
 04-DEC-2002; 2002WO-US038849.
 04-DEC-2001; 2001US-0337294P.
 (DAND) DANA FARBER CANCER INST INC.
 Marasco WA, Gennari F;
 WPI; 2003-482710/45.
 N-FSDB; ACC84105.
 Novel antibody to extracellular epitopes of Epstein Barr Virus latent
 membrane protein, useful for prevention and treatment of diseases caused
 by Epstein-Barr Virus, e.g. malignancies and lymphoproliferative
 diseases.
 Disclosure; Page 22; 52pp; English.
 The present sequence is the protein sequence of anti-Epstein-Barr virus
 (EBV) latent membrane protein (LMP) scFv FG-47. The scFv was isolated
 from a human antibody phage display library. It comprises a DP-10/hv1051
 VH germline and 6a.366E5/VL-22 VL germline. It is an example of
 antibodies of the invention directed against EBV LMP proteins (LMP1,
 LMP2A or LMP2B). Claimed methods of generating an immune reaction
 comprise administering an antibody with specificity for an EBV LMP, or an
 immune cell endowed with antibody specificity for an EBV LMP by
 transformation, to an individual having an EBV-associated disease such as
 malignancy, Hodgkin's disease, chronic EBV syndrome or oral hairy cell
 leukoplakia. The malignancy is especially Burkitt's lymphoma.

CC lymphoproliferative disease, B-lymphoproliferative disease, non-Hodgkin's
 CC lymphoma (NHL), T-NHL, NK-NHL, lymphonopharyngeal carcinoma or gastric
 CC carcinoma. Alternatively, the lymphocytes of an individual having an EBV
 CC associated malignancy are transformed with a chimeric gene encoding e.g.
 CC a single chain antibody as a means of treatment
 XX
 SQ Sequence 238 AA;

Query Match 91.9%; Score 57; DB 6; Length 238;
 Best Local Similarity 92.3%; Pred. No. 0.023;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||:||||
 Db 151 TRSSGSIASHYVQ 163

RESULT 12
 ABP45223
 ID ABP45223 standard; protein; 258 AA.
 XX
 AC ABP45223;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1234.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 1874-1875; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 258 AA;

Query Match 90.3%; Score 56; DB 5; Length 258;
 Best Local Similarity 92.3%; Pred. No. 0.038;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||:||||
 Db 170 TRSSGSIASNYVQ 182

RESULT 13
 ABP56513
 ID ABP56513 standard; protein; 112 AA.
 XX
 AC ABP56513;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE Human anti-Fc-epsilon-R1 alpha autoantibody light chain UG-alpha-8.
 XX
 KW Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;
 KW allergic disease; urticaria; late phase allergic reaction; malignancy;
 KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;
 KW conditional autoimmunity; IgE mediated disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200282085-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-EP003660.
 XX
 PR 04-APR-2001; 2001US-0281024P.
 XX
 PA (ZLBB-) ZLB BIOPLASMA AG.
 XX
 PI Miescher S;
 XX
 DR WPI; 2003-103348/09.
 XX
 PT Identifying and obtaining inhibitor of a pathological process for
 PT treating e.g. autoimmunity comprises determining if a compound is capable
 PT of modulating the binding of the Fc-epsilon-R1 receptor and an
 PT autoantibody against its alpha-chain.
 XX
 PS Claim 20; Page 22; 29pp; English.
 XX
 CC The present invention describes a method for identifying and obtaining an
 CC inhibitor of a pathological process. The method comprises determining if
 CC a compound is capable of modulating the binding of the Fc-epsilon-R1
 CC receptor alpha-chain and an autoantibody against its alpha-chain. Also
 CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor
 CC alpha-chain for identifying and obtaining an inhibitor of a pathological
 CC process; (2) use of the identified inhibitor for inhibiting activity of
 CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3)
 CC a compound identified by the method, which binds but does not activate
 CC the receptor; and (4) a polypeptide capable of specific binding to the Fc
 CC epsilon-R1 receptor alpha-chain. The method is useful for obtaining an
 CC inhibitor of a pathological process e.g. imbalance between cell-bound and
 CC free IgE e.g. allergic disease (urticaria, late phase allergic reactions,
 CC intrinsic asthma, drug intolerance and food intolerance), IgE mediated
 CC disease or malignancy. The compound is useful for treating a pathological
 CC process, particularly conditional autoimmunity. The present sequence
 CC represents a human recombinant anti-Fc-epsilon-R1 alpha autoantibody
 CC light chain protein sequence from the present invention

XX SQ Sequence 112 AA;
 Query Match 88.7%; Score 55; DB 6; Length 112;
 Best Local Similarity 92.3%; Pred. No. 0.022;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 Db 21 TRSSDSIASNYVQ 33
 |||||

RESULT 14
 ADD28298
 ID ADD28298 standard; protein; 161 AA.
 XX AC
 XX ADD28298;
 DT 15-JAN-2004 (first entry)
 DE Human heterodimeric antibody light chain lambda region SEQ ID NO:76.
 XX KW human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
 XX OS Synthetic.
 OS Homo sapiens.
 XX W02003076568-A2.
 XX 18-SEP-2003.
 XX 11-FEB-2003; 2003WO-US004206.
 XX 11-FEB-2002; 2002US-0356086P.
 PR 29-APR-2002; 2002US-0376408P.
 PR 27-SEP-2002; 2002US-0414053P.
 PR 25-NOV-2002; 2002US-0428807P.
 XX (ALEX-) ALEXION PHARM INC.
 XX Bowdish KS, Wild MA;
 PI WPI; 2003-722327/68.
 DR New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX Claim 10; SEQ ID NO 76; 67pp; English.
 PS The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virucide and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
 CC present sequence represents a human heterodimeric antibody light chain
 CC lambda region amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX SQ Sequence 161 AA;
 Query Match 87.1%; Score 54; DB 7; Length 161;
 Best Local Similarity 84.6%; Pred. No. 0.053;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 Db 25 TRSSGSIVGNVQ 37
 |||||

RESULT 15
 ADD28259
 ID ADD28259 standard; protein; 166 AA.
 XX AC
 XX ADD28259;
 DT 15-JAN-2004 (first entry)
 DE Human heterodimeric antibody light chain lambda region SEQ ID NO:37.
 XX KW human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
 XX OS Synthetic.
 OS Homo sapiens.
 XX W02003076568-A2.
 XX 18-SEP-2003.
 XX 11-FEB-2003; 2003WO-US004206.
 XX 11-FEB-2002; 2002US-0356086P.
 PR 29-APR-2002; 2002US-0376408P.
 PR 27-SEP-2002; 2002US-0414053P.
 PR 25-NOV-2002; 2002US-0428807P.
 XX (ALEX-) ALEXION PHARM INC.
 XX Bowdish KS, Wild MA;
 PI WPI; 2003-722327/68.
 DR New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX Claim 8; SEQ ID NO 37; 67pp; English.
 PS The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virucide and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
 CC present sequence represents a human heterodimeric antibody light chain
 CC lambda region amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX SQ Sequence 166 AA;
 Query Match 87.1%; Score 54; DB 7; Length 166;
 Best Local Similarity 84.6%; Pred. No. 0.055;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 |||||
 Db 25 TRSSGSIVGNVQ 37
 |||||

Search completed: June 8, 2004, 18:26:54
Job time : 60.1094 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 63.6562 Seconds
(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	80	100.0	14	4	AAB61295	Anti-TANG	
2	80	100.0	14	6	ABU11261	Human TAN	
3	52.5	65.6	267	5	AAU75503	Human s-a	
4	47	58.8	193	5	AAE15968	Fly CPl58	
5	47	58.8	325	4	ABB61108	Drosophil	
6	46	57.5	383	6	ABU02685	S. pneumo	
7	46	57.5	383	6	ABU02685	S. pneumo	
8	45	56.2	831	4	ABG08487	Streptoco	
9	44	55.0	169	2	AAW28034	Novel hum	
10	44	55.0	169	6	AAW28034	Amino aci	
11	44	55.0	354	4	ABM71535	Staphyloc	
12	44	55.0	354	4	ABE60901	Drosophil	
13	44	55.0	369	6	ABU71061	Human adi	
14	44	55.0	683	6	ABO52937	Human spl	
15	44	55.0	867	4	AAQ98887	E. coli g	
16	44	55.0	867	6	ABU14723	Protein e	
17	43	53.8	207	3	AAQ34190	Zea mays	
18	43	53.8	217	3	AAQ34189	Zea mays	
19	43	53.8	223	3	AAQ34188	Zea mays	
20	43	53.8	424	4	ABG29934	Novel hum	
21	43	53.8	866	6	ABU15381	Novel hum	
22	43	53.8	906	4	ABG18321	Novel hum	
23	43	53.8	1090	4	ABG17694	Novel hum	
24	42	52.5	71	4	AAO13076	Human pol	
25	42	52.5	243	5	ABP27382	Streptoco	

26	42	52.5	847	6	ABU31210	Protein e
27	41	51.2	172	4	AAU03641	Group B S
28	41	51.2	181	6	ABU42203	Protein e
29	41	51.2	205	4	AAU30764	Novel hum
30	41	51.2	245	5	ABP29803	Streptoco
31	41	51.2	249	5	ABP27381	Streptoco
32	41	51.2	312	3	AAE18153	Flasmodiu
33	41	51.2	323	6	ABU46346	Protein e
34	41	51.2	363	2	AAW10320	Soybean a
35	41	51.2	378	2	AAW70205	Alpha-gal
36	41	51.2	378	2	AAW00621	Coffee be
37	41	51.2	378	5	ABO09593	Coffea ca
38	41	51.2	378	5	ABO09592	Coffea ar
39	41	51.2	406	2	AAW26604	Senna alp
40	41	51.2	411	2	AAW70206	Alpha-gal
41	41	51.2	420	2	AAW71326	Coffee be
42	41	51.2	420	6	ABR42213	Coffee al
43	41	51.2	810	6	ADA35894	Acinetoba
44	41	51.2	829	6	ABU45589	Protein e
45	41	51.2	1846	4	ABB63163	Drosophil

ALIGNMENTS

RESULT 1
AAB61295
ID AAB61295 standard; peptide; 14 AA.
XX
AC AAB61295;
XX
DT 04-APR-2001 (first entry)
XX
DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 63.
XX
KW Human; antibody; scFv; CDR: complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
cancer.
XX
OS Homo sapiens.
XX
FN WO200100810-A1.
XX
PD 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US018152.
XX 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX (MILL-) MILLENNIUM PHARM INC.
PA Busfield SJ, Vilelale J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
XX WPI; 2001-080877/09.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
disorders.
XX Claim 31; Page 102; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 80; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFDV 14
 DB 1 DKWEAYITPGAFDV 14

RESULT 2
 ABU11261
 ID ABU11261 standard; peptide; 14 AA.

XX AC ABU1261;

XX DT 06-FEB-2003 (first entry)

XX DE Human TANGO 268 VHCDR3 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; Glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degradation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX OS Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Valleval J, Jandrot-perrus M, Vainchenker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis.

XX Claim 8; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 XX heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 XX or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 XX binding to a TANGO 268 (also referred as Glycoprotein VI (GPVI)) antigen.
 XX The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 80; DB 6; Length 14;

Best Local Similarity 100.0%; Pred. No. 7.5e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFDV 14

DB 1 DKWEAYITPGAFDV 14

RESULT 3

AAU75503

ID AAU75503 standard; protein; 267 AA.

XX AC AAU75503;

XX 23-APR-2002 (first entry)

XX Human s-acyl fatty acid synthase thioesterase-like enzyme #2.

XX S-acyl fatty acid synthase thioesterase-like; SFST-like; enzyme;
 KW cardiant; anorectic; vasotropic; extracellular matrix degradation;
 KW cardiovascular disease; hyperlipidaemia; obesity; anorexia; cachexia;
 KW wasting disorder; appetite suppression; appetite enhancement; bulimia;
 KW diabetes; congestive heart failure; myocardial infarction; human;
 KW ischaemic disease; atrial arrhythmia; ventricular arrhythmia;
 KW hypertensive vascular disease; peripheral vascular disease.

XX OS Homo sapiens.

XX WO200200855-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001WO-EP007297.

XX 26-JUN-2000; 2000US-0214012P.

XX 14-DEC-2000; 2000US-0255148P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI; 2002-130886/17.

XX New purified human s-acyl fatty acid synthase thioesterase-like enzyme,
 XX useful for identifying modulators of enzyme activity for treating
 XX cardiovascular disease, diabetes, obesity and hyperlipidemia.

XX PS Disclosure; Fig 4; 123pp; English.

XX CC The invention describes a purified human S-acyl fatty acid synthase

XX CC thioesterase (SFAST)-like enzyme (I). (I) is useful for screening for

XX CC agents which decrease or regulate the activity of an SFAST-like enzyme and

XX CC agents which decrease extracellular matrix degradation. The

XX CC polynucleotide (II) is useful for detecting a polynucleotide which

XX CC encodes (I) in a biological sample by formation of a hybridisation

XX CC complex. A reagent modulating the activity of SFAST-like enzyme or an

XX CC antibody can also be used to detect the polypeptide or polynucleotide in

XX CC a biological sample. A reagent modulating the activity of (I) or (II) is

XX CC also useful for treating a SFAST-like enzyme dysfunction related disease

XX CC condition such as cardiovascular disease, hyperlipidaemia, obesity,

XX CC anorexia, cachexia, wasting disorders, appetite suppression, appetite

XX CC enhancement, bulimia or diabetes. The cardiovascular diseases treated by

XX CC the above mentioned methods and reagents include congestive heart

XX CC failure, myocardial infarction, ischaemic diseases of the heart, atrial

XX CC and ventricular arrhythmia, hypertensive vascular diseases, and

XX CC peripheral vascular diseases. (II) is useful in diagnostic assays for

XX CC detecting diseases and abnormalities related to presence of mutations in

XX CC the nucleic acid sequences which encode the enzyme. This is the amino

XX CC acid sequence of a human S-acyl fatty acid synthase thioesterase-like

XX CC enzyme, described in the method of the invention

XX SQ Sequence 267 AA;

Query Match 65.6%; Score 52.5; DB 5; Length 267;

Best Local Similarity 71.4%; Pred. No. 1;

Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 DKWEAYITPGADV 14

Db 227 DRWREY-TPGADV 239

RESULT 4

AAE15968

ID AAE15968 standard; protein; 193 AA.

XX AC AAE15968;

XX DT 26-MAR-2002 (first entry)

XX DE Fly CPl5828/84-303 protein, member of Brainiac family.

XX KW Fringe protein; Brainiac protein; glycosyltransferase; EGF; mannose;

XX KW N-acetylglucosamine; fucose; epidermal growth factor; T cell leukaemia;

XX KW breast cancer; stroke; dementia; leucoencephalopathy; Alagille syndrome;

XX KW notch protein; EGF-module containing protein; fly.

XX OS Drosophila sp.

XX PN WO200187321-A2.

XX PD 22-NOV-2001.

XX PF 21-MAY-2001; 2001WO-IB001033.

XX PR 19-MAY-2000; 2000GB-00012216.

XX PS (EUMO-) EURO MOLECULAR BIOLOGY LAB.

XX PA Cohen S, Brueckner K, Clausen H, Keck B;

XX PI WPI; 2002-082940/11.

XX DR Use of Fringe protein or Brainiac protein as glycosyltransferase and

XX PT treatment of disease caused by epidermal growth factor-like module

XX PT containing protein, such as T cell leukemia, breast cancer, stroke and

XX PT dementia.

XX PS Claim 7; Fig 1; 52pp; English.

XX CC The invention relates to the use of a Fringe protein or a Brainiac

XX CC protein or a fragment or functional equivalent of a Fringe or a Brainiac

XX CC protein, as glycosyltransferase. Fringe and Brainiac proteins have been

XX CC found to possess glycosyltransferase activity in transferring sugar

XX CC residues onto certain proteins of biological interest, so affecting the

XX CC binding of effector molecules to these proteins. Particularly they are

XX CC useful for transferring a N-acetylglucosamine moiety onto a fucose or a

XX CC mannose substrate, whether free or attached to a lipid, carbohydrate or

XX CC protein. They act as glycosyltransferase on notch protein (EGF-module

XX CC containing protein) family. They are useful in treatment of a disease

XX CC caused by epidermal growth factor (EGF)-like module containing protein,

XX CC such as T cell leukemia, breast cancer, stroke, dementia, cerebral

XX CC autosomal dominant arteriopathy with subcortical infarcts,

XX CC leucoencephalopathy and Alagille syndrome. Fringe and Brainiac proteins

XX CC are also useful for screening ligands capable of modulating the activity

XX CC of the protein. The present sequence is fly protein which is a member of

XX CC Brainiac protein family

XX SQ Sequence 193 AA;

Query Match 58.8%; Score 47; DB 5; Length 193;

Best Local Similarity 58.3%; Pred. No. 6.5;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAP 12

Db 146 DRWPPYVTAGAP 157

RESULT 5

ABB61108

ID ABB61108 standard; protein; 325 AA.

XX AC ABB61108;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 10116.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL05211.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more

XX PT genes from Drosophila and for elucidating cell signaling and cell-cell

XX PT interactions.

XX PS Disclosure; SEQ ID NO 10116; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from Drosophila. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 325 AA;

Query Match 58.8%; Score 47; DB 4; Length 325;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAF 12
|:|:|:|:|:
Db 229 DRWPPYVTAGAF 240

RESULT 6
ABU02685
ID ABU02685 standard; protein; 383 AA.
XX
AC ABU02685;
XX
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
XX S. pneumoniae type 4 strain protein from coding region #2264.
XX
XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KW gene therapy; vaccine.
XX
XX Streptococcus pneumoniae; type 4 strain.
XX
XX WO200277021-A2.
XX
XX 03-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-IB002163.
XX
XX 27-MAR-2001; 2001GB-00007658.
XX
XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Masignani V, Tettelin H, Fraser C;
XX
XX WPI; 2003-040579/03.
XX N-PSDB; ABX07976.
XX
XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
XX useful as medicaments for treating or preventing a disease or infection
XX due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
XX ear infection.
XX
XX Claim 1; SEQ ID NO 4528; 56pp; English.
XX
XX The invention relates to a protein comprising or having at least 50%
XX identity to any of the 2469 amino acid sequences, identified in the
XX specification (available on a computer readable format), or its fragment,
XX expressed from 2469 of 2489 identified DNA coding regions from the
XX Streptococcus pneumoniae type 4 strain genomic sequence appearing as
XX ABB56454. Also included are an antibody which binds one of the proteins,
XX treating a patient by administering the protein, DNA or antibody (in a
XX composition), a kit comprising first and second primers, which are the
XX nucleic acid cited above or fragments between nucleotides 8-100 of a
XX sequence not defined in the specification, for amplifying a target
XX sequence contained within a Streptococcus nucleic acid sequence, where
XX the first primer is substantially complementary to the target sequence
XX and the second primer is substantially complementary to the complement of
XX the target sequence, and where the parts of the primers having
XX substantial complementarity define the termini of the target sequence to
XX be amplified, assay comprising contacting a test compound with the
XX protein, and determining whether the test compound binds to the protein

CC and a Streptococcus pneumoniae bacterium, where one or more genes
CC encoding the proteins has been rendered inactive. The proteins, nucleic
CC acid molecules, antibody and compositions are useful as medicaments for
CC treating or preventing a disease or infection due to streptococcus
CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
CC media or ear infection. They are also useful in developing vaccines,
CC immunodominant proteins. The methods are useful for identifying
CC CC expressed by the identified coding regions from the genomic sequence.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
XX CC standardise OS field)
XX
SQ Sequence 383 AA;

Query Match 57.5%; Score 46; DB 6; Length 383;
Best Local Similarity 72.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 EAYITPGAFDV 14
|:|:|:|:|:
Db 199 EALVTPGAYDV 209

RESULT 7
ABP81494
ID ABP81494 standard; protein; 383 AA.
XX
AC ABP81494;
XX
XX 04-MAR-2003 (first entry)
XX
XX Streptococcus pneumoniae polypeptide SEQ ID NO 411.
XX
XX Streptococcus pneumoniae; infection; otitis media; antibacterial;
KW diagnosis; gene therapy.
XX
XX Streptococcus pneumoniae.
XX
XX WO200283855-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US011524.
XX
XX 16-APR-2001; 2001US-0283948P.
XX 18-APR-2001; 2001US-0284443P.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP;
XX Wothers JI;
XX
XX WPI; 2003-093010/08.
XX N-PSDB; ABZ42342.
XX
XX New Streptococcus pneumoniae polynucleotides, useful for treating or
XX preventing S. pneumoniae infections, or non-systemic diseases, e.g.
XX otitis media, which are induced or exacerbated by S. pneumoniae.
XX
XX Claim 42; Page 680-682; 1091pp; English.
XX
XX The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of
XX a Streptococcus pneumoniae genomic sequence, a fragment or degenerate
XX variant of the polynucleotide or a nucleic acid sequence 95% identical to
XX one of the polynucleotides. The S. pneumoniae polynucleotides and encoded
XX polypeptides (ABP81299-ABP81674) are useful for treating or preventing S.
XX pneumoniae infections or non-systemic diseases, e.g. otitis media, which
XX are induced or exacerbated by S. pneumoniae. These are also useful for
XX detecting S. pneumoniae in a biological sample or diagnosing S.
XX pneumoniae infection in a subject. The polynucleotides have antibacterial
XX activity and are useful in gene therapy

XX SQ Sequence 383 AA;

Query Match 57.5%; Score 46; DB 6; Length 383;
 Best Local Similarity 72.7%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAYITPGAFDV 14
 |||||:|:|
 Db 199 EALVTPGAYDV 209

RESULT 8
 ABG08487
 ID ABG08487 standard; protein; 831 AA.
 XX AC ABG08487;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #8478.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WC200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX DR N-PSDB; AAS72674.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PS Claim 20; SEQ ID NO 38846; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 831 AA;

Query Match 56.2%; Score 45; DB 4; Length 831;
 Best Local Similarity 63.6%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KWEAYTPGAF 12
 |||||:|:|
 Db 72 KWEASVPPGSF 82

RESULT 9
 AAW28034
 ID AAW28034 standard; protein; 169 AA.
 XX AC AAW28034;
 XX DT 27-AUG-1998 (first entry)
 XX DE Amino acid sequence of the deoxyuridine 5' triphosphatase homologue.
 XX KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
 KW Staphylococcal gene; regulatory element; bacterial gene expression;
 KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
 KW toxic shock syndrome.
 XX OS Staphylococcus aureus.
 XX PN WO9730070-A1.
 XX PD 21-AUG-1997.
 XX PF 19-FEB-1997; 97WO-US002318.
 XX PR 20-FEB-1996; 96US-0011888P.
 XX PA (SMIX) SMITHKLINE BEECHAM CORP.
 XX PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
 PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;
 XX WPI; 1997-424969/39.
 XX DR N-PSDB; AAT83988.
 XX PT Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to
 PT isolate antimicrobial compounds, and in vaccines against S. aureus
 PT infection.
 XX PS Claim 6; Page 421; 989pp; English.

The present sequence represents a Staphylococcus aureus protein, which is believed to be a deoxyuridine 5' triphosphatase homologue. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome

SQ Sequence 169 AA;

Query Match 55.0%; Score 44; DB 2; Length 169;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YITPGAFDV 14
 |||||:|:|
 Db 102 YITPGVDFI 110

RESULT 10
ABW71535
ID ABW71535 standard; protein; 169 AA.
XX AC ABW71535;
XX AC
XX AC
DT 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #775.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002WO-1B002637.
XX
XX 27-MAR-2001; 2001GB-00007661.
XX (CHIR-) CHIRON SPA.
XX Masignani V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX N-PSDB; ACF73095.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 1550; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
XX Sequence 169 AA;
Query Match 55.0%; Score 44; DB 6; Length 169;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 6 YITPGAFDV 14
DB 102 YITPGVEDI 110
|||||
RESULT 11
ABB60901
ID ABB60901 standard; protein; 354 AA.
XX
XX ABB60901;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 9495.
DE
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX

PN WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI N-PSDB; ABL05004.
XX
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 9495; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 354 AA;
Query Match 55.0%; Score 44; DB 4; Length 354;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 KWEAVITPGAF 12
DB 31 KWELYMTFND 41
|||||
RESULT 12
ABU71061
ID ABU71061 standard; protein; 369 AA.
XX
XX AC ABU71061;
XX
XX 10-JUN-2003 (first entry)
DT
XX
XX Human adipocyte Selected Interacting domain, SID, #692.
DE
XX
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
KW antidiabetic; protein-protein interaction; diabetes;
KW yeast 2-hybrid assay; metabolic disorder; obesity.
XX
XX Homo sapiens.
OS
XX
XX WO200286122-A2.
PN
XX
XX 31-OCT-2002.
XX
XX 14-MAR-2002; 2002WO-EP003768.
XX
XX 14-MAR-2001; 2001US-0275734P.
PR
XX (HYBR-) HYBRIGENICS.
XX
XX Legrain P, Daviet L;
XX
XX WPI; 2003-103412/09.
XX
XX

DR N-PSDB; ACA57605.

XX New complex between two interacting proteins in adipocyte cells, useful

PT for identifying selected interacting domains that modulate protein

PT interactions, or for preventing or treating metabolic disorders such as

XX obesity or diabetes.

XX Claim 6; Page 346; 382pp; English.

XX The invention relates to a complex between two interacting proteins in

CC adipocyte cells, given in the specification. The proteins are identified

CC by selecting a bait protein from a known adipocyte marker and then

CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by

CC members of an adipocyte cDNA library. The proteins are designated SID

CC (RTM) (selected interacting domains) proteins. Also included are a

CC polynucleotide encoding a polypeptide in the adipocyte cells, a

CC recombinant host cell expressing at least one of the interacting

CC polypeptides of the complex, selecting a modulating compound in adipocyte

CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid

CC sequences given in the specification (including its fragment or variant),

CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences

CC given in the specification (including its fragment or variant), a vector

CC comprising the SID (RTM) polynucleotide, a recombinant host cell

CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.

CC The complex, polypeptides, polynucleotides and compounds are useful for

CC preventing or treating metabolic disorders such as obesity or diabetes.

CC The polynucleotides are useful as probes or primers. The complex is

CC particularly useful for identifying selected interacting domains (SID

CC (RTM)) for screening drugs that modulate the protein interaction, thus

CC exhibiting the therapeutic effect. The present sequence represents a SID

CC (prey) protein of the invention

XX Sequence 369 AA;

XX Query Match 55.0%; Score 44; DB 6; Length 369;

XX Best Local Similarity 50.0%; Pred. No. 43;

XX Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14

DB 237 WDSYIIPNGFDL 248

RESULT 13

ID ABO52937 standard; protein; 683 AA.

AC ABO52937;

DT 09-OCT-2003 (first entry)

DE Human spliceosome associated protein (SAP) #33.

XX Human; SAP; spliceosome associated protein; ribonucleoprotein;

KW RNP complex; RNA affinity substrate; RNP assembly sequence;

KW spliceosomal complex; hnRNP complex; mRNA export complex;

KW mRNA localisation complex; RNA editing complex; intron complex;

KW H complex; telomerase complex; fragile X protein complex;

KW reverse transcriptase complex; gene splicing complex.

OS Homo sapiens.

XX US2003068803-A1.

PN 10-APR-2003.

XX 14-JAN-2002; 2002US-00047991.

PF 12-JAN-2001; 2001US-0261521P.

PR (REED/) REED R.

PA (ZHOU/) ZHOU Z.

XX N-PSDB; ACA57605.

XX New complex between two interacting proteins in adipocyte cells, useful

PT for identifying selected interacting domains that modulate protein

PT interactions, or for preventing or treating metabolic disorders such as

XX obesity or diabetes.

XX Claim 6; Page 346; 382pp; English.

XX The invention relates to a complex between two interacting proteins in

CC adipocyte cells, given in the specification. The proteins are identified

CC by selecting a bait protein from a known adipocyte marker and then

CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by

CC members of an adipocyte cDNA library. The proteins are designated SID

CC (RTM) (selected interacting domains) proteins. Also included are a

CC polynucleotide encoding a polypeptide in the adipocyte cells, a

CC recombinant host cell expressing at least one of the interacting

CC polypeptides of the complex, selecting a modulating compound in adipocyte

CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid

CC sequences given in the specification (including its fragment or variant),

CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences

CC given in the specification (including its fragment or variant), a vector

CC comprising the SID (RTM) polynucleotide, a recombinant host cell

CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.

CC The complex, polypeptides, polynucleotides and compounds are useful for

CC preventing or treating metabolic disorders such as obesity or diabetes.

CC The polynucleotides are useful as probes or primers. The complex is

CC particularly useful for identifying selected interacting domains (SID

CC (RTM)) for screening drugs that modulate the protein interaction, thus

CC exhibiting the therapeutic effect. The present sequence represents a SID

CC (prey) protein of the invention

XX Sequence 369 AA;

XX Query Match 55.0%; Score 44; DB 6; Length 369;

XX Best Local Similarity 50.0%; Pred. No. 43;

XX Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14

DB 237 WDSYIIPNGFDL 248

RESULT 13

ID ABO52937 standard; protein; 683 AA.

AC ABO52937;

DT 09-OCT-2003 (first entry)

DE Human spliceosome associated protein (SAP) #33.

XX Human; SAP; spliceosome associated protein; ribonucleoprotein;

KW RNP complex; RNA affinity substrate; RNP assembly sequence;

KW spliceosomal complex; hnRNP complex; mRNA export complex;

KW mRNA localisation complex; RNA editing complex; intron complex;

KW H complex; telomerase complex; fragile X protein complex;

KW reverse transcriptase complex; gene splicing complex.

OS Homo sapiens.

XX US2003068803-A1.

PN 10-APR-2003.

XX 14-JAN-2002; 2002US-00047991.

PF 12-JAN-2001; 2001US-0261521P.

PR (REED/) REED R.

PA (ZHOU/) ZHOU Z.

XX Reed R, Zhou Z;

XX WPI; 2003-540885/51.

XX Isolating ribonucleoprotein complex, by contacting RNA affinity substrate

PT having ribonucleoprotein assembly sequence and affinity tag, with protein

PT mixture, subjecting complex formed to chromatography, affinity selection.

XX Claim 24; Page; 39pp; English.

XX The invention relates to forming (M1) an isolated ribonucleoprotein (RNP)

CC complex (C), involves contacting an RNA affinity substrate (S) comprising

CC an RNP assembly sequence (AS) and an affinity tag, with a protein mixture

CC to permit formation of (C) on AS, subjecting (C) to chromatographic

CC separation, and subjecting (C) to affinity selection, where the affinity

CC tag (e.g. bacteriophage MS2 coat protein in a fusion protein with E. coli

CC maltose binding protein) binds to an affinity matrix. Also included are

CC an isolated spliceosome preparation (isolated by (M1)), a RNA comprising

CC an RNP complex binding site and at least one phage coat protein

CC recognition site, a nucleic acid encoding the RNA, and treating (M2) a

CC subject having a disorder associated with abnormal RNP complexes (by

CC obtaining a sample of cells from a subject, purifying RNP complexes from

CC the cells of the subject by (M1), determining the presence in the

CC purified RNP complexes of one or more proteins, and normalising the

CC amount of RNPs in the subject. (M1) is useful for forming an isolated RNP

CC complex selected from a spliceosomal complex (selected from E, A, B and C

CC complex), an hnRNP complex, an mRNA export complex, an mRNA localisation

CC complex, an RNA editing complex, an intron complex, or an H complex. (M1)

CC is useful in a diagnostic assay for determining whether a subject has a

CC abnormal RNP complexes, (M2) is useful for treating a subject having a

CC disorder associated with abnormal RNP complexes. (M1) is useful for

CC forming an isolated RNP complex such as a telomerase complex, a fragile X

CC protein complex, a reverse transcriptase complex or a gene splicing

CC complex. The present sequence represents a known human spliceosome

CC associated protein (SAP) isolated by the methods of the invention. Note:

CC The present sequence is not shown in the specification but was obtained

CC from Genbank or Swissprot using the information provided in table 1 of

CC the specification

XX Sequence 683 AA;

XX Query Match 55.0%; Score 44; DB 6; Length 683;

XX Best Local Similarity 50.0%; Pred. No. 84;

XX Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14

DB 390 WDSYIIPNGFDL 401

RESULT 14

ID AAG98887 standard; protein; 867 AA.

XX AAG98887;

XX 26-SEP-2001 (first entry)

DE E. coli growth and proliferation related protein sequence SEQ ID NO:357.

XX Escherichia coli; growth; proliferation; microbial; antimicrobial;

KW bacterial infection; microorganism.

OS Escherichia coli.

XX WO200134810-A2.

PN 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030950.

PF 09-NOV-1999; 99US-0164415P.

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 46.5938 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	80	100.0	14	9	US-09-832-312-63	Sequence 63, Appl
2	80	100.0	14	11	US-09-829-495-63	Sequence 63, Appl
3	47	58.8	323	9	US-09-972-912-3	Sequence 3, Appl
4	47	58.8	324	14	US-10-344-440-3	Sequence 3, Appl
5	47	58.8	325	9	US-09-804-357-10	Sequence 10, Appl
6	47	58.8	325	9	US-09-739-451-5	Sequence 5, Appl
7	47	58.8	325	9	US-09-804-006-10	Sequence 10, Appl
8	47	58.8	325	10	US-09-284-320-90	Sequence 90, Appl
9	47	58.8	325	12	US-10-459-311-5	Sequence 5, Appl
10	44	55.0	473	12	US-10-424-599-227005	Sequence 227005, A
11	44	55.0	867	12	US-10-282-122A-42847	Sequence 42847, A
12	44	55.0	867	14	US-10-287-274-357	Sequence 357, App
13	43	53.8	213	12	US-10-425-114-41064	Sequence 41064, A
14	43	53.8	213	12	US-10-425-114-64240	Sequence 64240, A
15	43	53.8	333	15	US-10-369-493-18135	Sequence 18135, A

16	43	53.8	866	12	US-10-282-122A-43305	Sequence 43305, A
17	42	52.5	104	12	US-10-424-599-247362	Sequence 247362, A
18	42	52.5	847	12	US-10-282-122A-59134	Sequence 59134, A
19	41	51.2	162	12	US-10-424-599-271679	Sequence 271679, A
20	41	51.2	172	14	US-10-091-007-82	Sequence 82, Appl
21	41	51.2	181	12	US-10-282-122A-70127	Sequence 70127, A
22	41	51.2	323	12	US-10-282-122A-74270	Sequence 74270, A
23	41	51.2	426	12	US-10-424-599-271677	Sequence 271677, A
24	41	51.2	829	12	US-10-282-122A-73513	Sequence 73513, A
25	40	50.0	97	12	US-10-424-599-223520	Sequence 223520, A
26	40	50.0	180	9	US-09-847-519A-17	Sequence 17, Appl
27	40	50.0	206	12	US-10-424-599-219923	Sequence 219923, A
28	40	50.0	220	9	US-09-847-519A-2	Sequence 2, Appl
29	40	50.0	220	12	US-10-168-506-17	Sequence 17, Appl
30	40	50.0	220	16	US-10-444-795B-787	Sequence 787, App
31	40	50.0	220	16	US-10-470-992-5	Sequence 5, Appl
32	40	50.0	263	16	US-10-470-992-2	Sequence 2, Appl
33	40	50.0	360	12	US-10-282-122A-53708	Sequence 53708, A
34	40	50.0	370	12	US-10-072-012-625	Sequence 625, App
35	40	50.0	370	12	US-10-072-012-674	Sequence 674, App
36	40	50.0	663	12	US-10-425-114-65041	Sequence 65041, A
37	40	50.0	868	15	US-10-369-493-3985	Sequence 3985, App
38	40	50.0	870	12	US-10-282-122A-74962	Sequence 74962, A
39	40	50.0	1444	12	US-10-282-122A-60977	Sequence 60977, A
40	39	48.8	77	12	US-10-424-599-147349	Sequence 147349, A
41	39	48.8	141	9	US-09-847-539A-5	Sequence 5, Appl
42	39	48.8	143	12	US-10-424-599-222313	Sequence 222313, A
43	39	48.8	155	9	US-09-847-539A-9	Sequence 9, Appl
44	39	48.8	159	9	US-09-847-539A-6	Sequence 6, Appl
45	39	48.8	167	9	US-09-847-539A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-832-312-63
; Sequence 63, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-63

Query Match 100.0%; Score 80; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAFDV 14

Db 1 DKWEAYITPGAFDV 14

RESULT 2

US-09-829-495-63
; Sequence 63, Application US/09829495

Publication No. US20040001826A1
GENERAL INFORMATION:
APPLICANT: Busfield SJ
APPLICANT: Villeval J
APPLICANT: Jandrot-Perrus M
APPLICANT: Vainchenker W
APPLICANT: Gill DS
APPLICANT: Qian MD
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/829,495
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-829-495-63

Query Match 100.0%; Score 80; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAFDV 14
Db 1 DKWEAYITPGAFDV 14

RESULT 3
US-09-972-912-3
Sequence 3, Application US/09972912
Patent No. US20020110867A1
GENERAL INFORMATION:
APPLICANT: SOPPET, DANIEL R.
RUBEN, STEVEN M.
TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,912
FILING DATE: 10-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/049,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0620001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3;

SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020110867A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-972-912-3
Query Match 58.8%; Score 47; DB 9; Length 323;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DKWEAYITPGAF 12
Db 228 DRWPPYVTAGAF 239
RESULT 4
US-10-344-440-3
Sequence 3, Application US/10344440
Publication No. US20030131378A1
GENERAL INFORMATION:
APPLICANT: Aroian, Raffi
TITLE OF INVENTION: METHODS FOR BLOCKING RESISTANCE TO Bt TOXINS IN INSECTS AND NEMATODES
FILE REFERENCE: 6627-PA1023
CURRENT APPLICATION NUMBER: US/10/344,440
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/224,941
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US01/41687
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 324
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-344-440-3

Query Match 58.8%; Score 47; DB 14; Length 324;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAF 12
Db 229 DRWPPYVTAGAF 240

RESULT 5
US-09-804-357-10
Sequence 10, Application US/09804357
Patent No. US20010024808A1
GENERAL INFORMATION:
APPLICANT: White, David
APPLICANT: Zhou, Jianghong
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: LEPTIN INDUCED GENES
FILE REFERENCE: 07334/109001
CURRENT APPLICATION NUMBER: US/09/804,357
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/195,896
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: US 60/108,379
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 09/150,857
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 325
TYPE: PRT
ORGANISM: Drosophila melanogaster

US-09-804-357-10

Query Match 58.8%; Score 47; DB 9; Length 325;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:|
DB 229 DRWPPYVTAGAF 240

RESULT 6

US-09-739-451-5
; Sequence 5, Application US/09739451
; Patent No. US20010024813A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Dendriac and Brainiac-3
; FILE REFERENCE: PF464
; CURRENT APPLICATION NUMBER: US/09/739,451
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/213,364
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/108,928
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-451-5

Query Match 58.8%; Score 47; DB 9; Length 325;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:|
DB 229 DRWPPYVTAGAF 240

RESULT 7

US-09-804-006-10
; Sequence 10, Application US/09804006
; Patent No. US20020119517A1
; GENERAL INFORMATION:
; APPLICANT: White, David
; APPLICANT: Zhou, Jianghong
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: LEPTIN INDUCED GENES
; FILE REFERENCE: 07334/126001
; CURRENT APPLICATION NUMBER: US/09/804,006
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US/09/292,228
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US/60/108,379
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: US/09/150,857
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-804-006-10

Query Match 58.8%; Score 47; DB 9; Length 325;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:|
DB 229 DRWPPYVTAGAF 240

RESULT 8

US-09-284-320-90
; Sequence 90, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-09-284-320-90

Query Match 58.8%; Score 47; DB 10; Length 325;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:|
DB 229 DRWPPYVTAGAF 240

RESULT 9

US-10-459-311-5
; Sequence 5, Application US/10459311
; Publication No. US2003020396A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
; Corley, Neil C.
; Shah, Purvi
; Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/459,311
; FILING DATE: 10-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/373,902
; FILING DATE: 12-Aug-1999
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.

```
;
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1150971
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-459-311-5
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Query Match 58.8%; Score 47; DB 12; Length 325;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 1 DKWEAYITPGAF 12
Db 229 DRWPPYVTAGAF 240
||:|:|:|:|
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RESULT 10

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US-10-424-599-227005
; Sequence 227005, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
```

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; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227005
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(473)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_47015C.1.pep
US-10-424-599-227005
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Query Match 55.0%; Score 44; DB 12; Length 473;
Best Local Similarity 53.8%; Pred. No. 67;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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QY 1 DKWEAYITPGAFD 13
Db 299 DKWAAYAGPGWN 311
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RESULT 11

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US-10-282-122A-42647
; Sequence 42647, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
```

```
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42647
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-42647
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Query Match 55.0%; Score 44; DB 12; Length 867;
Best Local Similarity 41.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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QY 3 WEAYITPGAFDV 14
Db 309 YQSVVSPGAPEI 320
:::|:|:|:|:|
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RESULT 12

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US-10-287-274-357
; Sequence 357, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
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; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
; FILE REFERENCE: ELITRA.008DV1
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-357
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Query Match 55.0%; Score 44; DB 14; Length 867;
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Best Local Similarity 41.7%; Pred.No.1.2e+02;
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      3 WEAYITPGAFDV 14
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Db     309 YQSYVSPGAFEI 320

RESULT 13
US-10-425-114-41064
; Sequence 41064, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41064
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-012-C8_FLI.pep
US-10-425-114-41064

Query Match          53.8%; Score 43; DB 12; Length 213;
Best Local Similarity 42.9%; Pred.No.45;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DKWEAYITPGAFDV 14
       :|||:|||::
Db     89 EWEAILTPQFNI 102

RESULT 14
US-10-425-114-64240
; Sequence 64240, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64240
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-014-C8_FLI.pep
US-10-425-114-64240

Query Match          53.8%; Score 43; DB 12; Length 213;
Best Local Similarity 42.9%; Pred.No.45;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DKWEAYITPGAFDV 14
       :|||:|||::

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 18.1562 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80
Sequence: 1 DKWEAYTPGAFDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	58.8	325	2	US-09-055-097-5
2	47	58.8	325	4	US-09-373-902-5
3	44	55.0	867	4	US-09-711-164-357
4	42	52.5	838	4	US-09-489-039A-9864
5	42	52.5	869	4	US-09-489-039A-8561
6	41	51.2	363	1	US-08-488-961-4
7	41	51.2	363	3	US-08-973-297-4
8	41	51.2	363	4	US-09-632-957-4
9	41	51.2	363	5	PCT-US96-06511-4
10	41	51.2	411	3	US-09-070-356-6
11	41	51.2	420	4	US-08-113-890-2
12	41	51.2	810	4	US-09-328-352-7181
13	40	50.0	117	1	US-07-942-245-32
14	40	50.0	117	1	US-07-942-245-36
15	40	50.0	117	1	US-07-942-245-38
16	40	50.0	221	4	US-09-976-594-664
17	39	48.8	310	4	US-09-252-991A-25177
18	39	48.8	546	4	US-09-252-991A-31673
19	39	48.8	596	1	US-08-565-386-11
20	39	48.8	855	4	US-09-543-681A-7287
21	39	48.8	1045	1	US-08-452-083-2
22	38	47.5	114	4	US-09-344-587-10
23	38	47.5	117	2	US-08-822-028-2
24	38	47.5	117	3	US-08-479-285-2
25	38	47.5	117	4	US-08-961-309-45
26	38	47.5	117	4	US-09-503-653A-2
27	38	47.5	133	2	US-08-822-028-6

Sequence 30, Appli
Sequence 6, Appli
Sequence 30, Appli
Sequence 48, Appli
Sequence 6, Appli
Sequence 30, Appli
Patent No. 5219986
Sequence 10, Appli
Sequence 10, Appli
Sequence 49, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 10620, A
Sequence 4, Appli
Sequence 4737, Ap
Sequence 10682, A
Sequence 2, Appli
Sequence 2, Appli

28 38 47.5 133 2 US-08-822-028-30
29 38 47.5 133 3 US-08-479-285-6
30 38 47.5 133 3 US-08-479-285-30
31 38 47.5 133 4 US-08-961-309-48
32 38 47.5 133 4 US-09-503-653A-6
33 38 47.5 133 4 US-09-503-653A-30
34 38 47.5 133 6 5219986-17
35 38 47.5 134 2 US-08-822-028-10
36 38 47.5 134 3 US-08-479-285-10
37 38 47.5 134 4 US-08-961-309-49
38 47.5 134 4 US-09-503-653A-10
39 38 47.5 150 2 US-08-400-115-2
40 38 47.5 188 4 US-09-489-039A-10620
41 38 47.5 271 2 US-08-400-115-4
42 38 47.5 271 4 US-09-328-352-4737
43 38 47.5 286 4 US-09-489-039A-10682
44 38 47.5 288 3 US-08-995-280C-2
45 38 47.5 288 3 US-09-215-042-2

ALIGNMENTS

RESULT 1
US-09-055-097-5
; Sequence 5, Application US/09055097
; Patent No. 5955282
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto ,
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1150971
US-09-055-097-5
Query Match 58.8%; Score 47; DB 2; Length 325;

Best Local Similarity 58.3%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:
Db 229 DRWPPYVTAGAF 240

RESULT 2

US-09-373-902-5
; Sequence 5, Application US/09373902
; Patent No. 6649737
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
; Corley, Neil C.
; Shah, Purvi
; Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/373,902
; FILING DATE: 12-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1150971
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-373-902-5

Query Match 58.8%; Score 47; DB 4; Length 325;
Best Local Similarity 58.3%; Pred. No. 4.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
|:| |:| |:| |:
Db 229 DRWPPYVTAGAF 240

RESULT 3

US-09-711-164-357
; Sequence 357, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn

; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERE
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-357

Query Match 55.0%; Score 44; DB 4; Length 867;
Best Local Similarity 41.7%; Pred. No. 40;
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14
::|:|:|:|:|:
Db 309 QSYVSPGAFEI 320

RESULT 4

US-09-489-039A-9864
; Sequence 9864, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9864
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9864

Query Match 52.5%; Score 42; DB 4; Length 838;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WEAYITPGAF 12
::|:|:|:|:|:
Db 304 QTYVTGAF 313

RESULT 5

US-09-489-039A-8561
; Sequence 8561, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8561
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8561

Query Match 52.5%; Score 42; DB 4; Length 869;
 Best Local Similarity 41.7%; Pred. No. 84;
 Matches 5; Conservative 0; Gaps 0; Indels 2; Mismatches 5;

QY 3 WEAYITPGAFDV 14
 Db 333 YQTVVAPGAFEI 344

RESULT 6
 US-08-488-961-4
 ; Sequence 4, Application US/08488961
 ; Patent No. 5606042
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Daniel S.
 ; APPLICANT: Walker, John C.
 ; TITLE OF INVENTION: Glycine and Phaseolus
 ; TITLE OF INVENTION: alpha-D-Galactosidases
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reising, Bthington, Barnard & Perry
 ; STREET: P.O. Box 4390
 ; CITY: Troy
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48099-4390
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,961
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: P-320 (UMC)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 689-3500
 ; TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-488-961-4

Query Match 51.2%; Score 41; DB 1; Length 363;
 Best Local Similarity 46.2%; Pred. No. 50;
 Matches 6; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

QY 1 DKWEAYITPGAFD 13
 Db 201 DKWASYAGPGGWN 213

RESULT 7
 US-08-973-297-4
 ; Sequence 4, Application US/08973297
 ; Patent No. 6184017
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Daniel S.
 ; APPLICANT: Walker, John C.
 ; TITLE OF INVENTION: Glycine and Phaseolus
 ; TITLE OF INVENTION: alpha-D-Galactosidases
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6184017thwestern Hwy., Suite 410

; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/973,297
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: 0994.00050
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 539-5050
 ; TELEFAX: (810) 539-5055
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-973-297-4

Query Match 51.2%; Score 41; DB 3; Length 363;
 Best Local Similarity 46.2%; Pred. No. 50;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFD 13
 Db 201 DKWASYAGPGGWN 213

RESULT 8
 US-09-632-957-4
 ; Sequence 4, Application US/09632957
 ; Patent No. 6630339
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Daniel S.
 ; APPLICANT: Walker, John C.
 ; TITLE OF INVENTION: Glycine and Phaseolus
 ; TITLE OF INVENTION: alpha-D-Galactosidases
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6630339thwestern Hwy., Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/632,957
 ; FILING DATE: 04-Aug-2000
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: 0994.00050
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 539-5050
 ; TELEFAX: (810) 539-5055
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-632-957-4
Query Match 51.2%; Score 41; DB 4; Length 363;
Best local Similarity 46.2%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAFD 13
Db 201 DKWASYAGPGGN 213

RESULT 9
PCT-US96-06511-4
; Sequence 4, Application PC/TUS9606511
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-Galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 Northwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06511
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 0994.00050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-06511-4
Query Match 51.2%; Score 41; DB 5; Length 363;
Best local Similarity 46.2%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DKWEAYITPGAFD 13
Db 201 DKWASYAGPGGN 213

RESULT 10
US-09-070-356-6
; Sequence 6, Application US/09070356
; Patent No. 6228631
; GENERAL INFORMATION:
; APPLICANT: Alex Zhu
; APPLICANT: Jack Goldstein
; TITLE OF INVENTION: Recombinant a-N-
; TITLE OF INVENTION: Acetyl galactosaminidase
; TITLE OF INVENTION: Enzyme and cDNA Encoding
; TITLE OF INVENTION: Said Enzyme
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amster, Rothstein & Ebenstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,356
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,248
; FILING DATE: March 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: 63475/12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELETYPE: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: guar plant Cyamopsis tetragonoloba
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE: library
; POSITION IN GENOME: unknown
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; NAME/KEY: guar a-galactosidase
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Overbeek et al
; TITLE: Cloning and Nucleotide Sequence of
; Patent No. 6228631
; TITLE: the a-Galactosidase cDNA from
; JOURNAL: Plant Molecular Biology
; VOLUME: 13
; PAGES: 541-550
; DATE: 1989
; DOCUMENT NUMBER:
; FILING DATE:
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;
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-09-070-356-6

Query Match      51.2%; Score 41; DB 3; Length 411;
Best Local Similarity 46.2%; Pred. No. 57;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFD 13
Db 248 DKWASYAGPGGN 260

RESULT 11
US-08-113-890-2
; Sequence 2, Application US/08113890
; Patent No. 6329191
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: CLEMENTS, DAVID E.
; TITLE OF INVENTION: RECOMBINANT COFFEE BEAN
; TITLE OF INVENTION: ALPHA-GALACTOSIDASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/113,890
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0002.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-113-890-2

Query Match      51.2%; Score 41; DB 4; Length 420;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFD 13
Db 258 DKWASYAGPGGN 270

RESULT 12
US-09-328-352-7181
; Sequence 7181, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
```

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;
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7181
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7181

Query Match      51.2%; Score 41; DB 4; Length 810;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 AYITPGAFD 13
Db 160 SYATPGAFD 168

RESULT 13
US-07-942-245-32
; Sequence 32, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-32

Query Match      50.0%; Score 40; DB 1; Length 117;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KWEAYITPGAFDV 14
Db 46 EWVAYISSGFTI 58

RESULT 14
US-07-942-245-36
; Sequence 36, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
```

; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-942-245-36

Query Match 50.0%; Score 40; DB 1; Length 117;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KWEAYITPGADV 14
Db 46 EWYATISSGSFTI 58

RESULT 15

US-07-942-245-38
; Sequence 38, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-942-245-38

Query Match 50.0%; Score 40; DB 1; Length 117;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KWEAYITPGADV 14
Db 46 EWYATISSGSFTI 58

Search completed: June 8, 2004, 18:31:50
Job time : 19.1562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 12.7969 Seconds
(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	83.9	112	1 L6HU48	Ig lambda chain V-
2	52	83.9	131	1 L6HUEB	Ig lambda chain pr
3	51	82.3	111	1 L6HULT	Ig lambda chain V-
4	43	69.4	111	1 L6HUST	Ig lambda chain V-
5	40	64.5	778	2 T39047	hypothetical prote
6	38	61.3	112	1 L6HUAR	Ig lambda chain V-
7	38	61.3	505	1 TVHUHC	protein-tyrosine k
8	38	61.3	556	2 B82379	conserved hypotet
9	38	61.3	606	2 T27072	hypothetical prote
10	38	61.3	726	2 A90771	hypothetical prote
11	38	61.3	726	2 E85633	hypothetical prote
12	38	61.3	726	2 C64839	probable Arpase yc
13	37	59.7	108	2 PS0073	Ig kappa chain V r
14	37	59.7	236	2 E59098	hypothetical prote
15	37	59.7	1181	2 T30578	myosin IC - slime
16	36	58.1	140	2 H86292	F7H2.18 protein -
17	36	58.1	308	2 G90504	2-keto-3-deoxy glu
18	36	58.1	352	2 T27677	hypothetical prote
19	36	58.1	522	2 JC1204	hypothetical prote
20	36	58.1	539	2 B49114	vga protein - Stap
21	36	58.1	549	2 S61706	protein-tyrosine k
22	36	58.1	997	2 T15243	RNA 5'-triphosphat
23	35	56.5	131	2 S24321	hypothetical prote
24	35	56.5	278	2 T39517	Ig lambda chain pr
25	35	56.5	402	2 C69110	dual-specificity M
26	35	56.5	503	1 JQ1321	glutamate N-acetyl
27	35	56.5	503	1 TVMSHC	protein-tyrosine k
28	35	56.5	512	1 TVHULY	protein-tyrosine k
29	35	56.5	537	2 I51592	protein-tyrosine k

30 35 56.5 541 2 S31645 protein-tyrosine k
31 35 56.5 574 2 T40213 hypothetical prote
32 35 56.5 788 2 AC2767 formate dehydrogen
33 35 56.5 788 2 F97547 probable oxidoredu
34 35 56.5 859 2 AE2217 hypothetical prote
35 35 56.5 1007 2 H81670 conserved hypotet
36 35 56.5 1167 2 T06146 disease resistance
37 34 54.8 47 2 B30607 Ig kappa chain V-I
38 34 54.8 55 2 PQ0829 E2/NS1 protein (cD
39 34 54.8 72 2 I37232 calcitonin gene-re
40 34 54.8 97 2 D89792 conserved hypotet
41 34 54.8 98 2 S36048 Ig lambda chain -
42 34 54.8 124 2 C48234 hypothetical prote
43 34 54.8 127 2 A25864 calcitonin gene-re
44 34 54.8 129 2 S78058 Ig lambda chain pr
45 34 54.8 130 2 S78057 Ig lambda chain pr

ALIGNMENTS

RESULT 1

L6HU48

Ig lambda chain V-VI region (Nig-48) - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1980 #sequence_revision 28-Feb-1980 #text_change 02-Sep-1997

C:Accession: A01991

R:Takahashi, N.; Takayasu, T.; Isobe, T.; Shinoda, T.; Okuyama, T.; Shimizu, A.

J. Biochem. 86, 1523-1535, 1979

A:Title: Comparative study on the structure of the light chains of human immunoglobulins

A:Reference number: A01991; MUID:80094390; PMID:118171

A:Accession: A01991

A:Molecule type: protein

A:Residues: 1-112 <TAK>

A:Note: this is the first sequenced V region of lambda chain subgroup VI

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGLV@

A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:15-93/Domain: immunoglobulin homology <IMM>

F:22-91/Disulfide bonds: #status predicted

Query Match 83.9%; Score 52; DB 1; Length 112;

Best Local Similarity 84.6%; Pred. No. 0.016;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13

||:|||||

Db 23 TFTSDSIASNYVQ 35

RESULT 2

L6HUEB

Ig lambda chain precursor V-VI region (EB4) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997

C:Accession: A01990

R:Anderson, M.L.M.; Brown, L.; McKenzie, E.; Kellow, J.E.; Young, B.D.

Nucleic Acids Res. 13, 2931-2941, 1985

A:Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in the

A:Reference number: A01990; MUID:85215660; PMID:3923440

A:Accession: A01990

A:Molecule type: mRNA

A:Residues: 1-131 <AND>

C:Genetics:

A:Gene: GDB:IGLV@

A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C;Superfamily: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-131/Product: Ig lambda chain V-VI region (BB4) #status predicted <MAT>

F;20-41/Region: framework 1

F;24-112/Domain: immunoglobulin homology <IMM>

F;42-54/Region: complementarity-determining 1

F;55-69/Region: framework 2

F;70-76/Region: complementarity-determining 2

F;77-110/Region: framework 3

F;111-118/Region: complementarity-determining 3

F;119-131/Region: framework 4

F;41-110/Disulfide bonds: #status predicted

Query Match 83.9%; Score 52; DB 1; Length 131;
Best Local Similarity 84.6%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| : ||||| |||||
Db 42 TGSIGSIASNYVQ 54

RESULT 3

L6HUST

Ig lambda chain V-VI region (WLT) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997

C;Accession: A01989

R;Dwulet, F.E.; Strako, K.; Benson, M.D.

Scand. J. Immunol. 22, 653-660, 1985

A;Title: Amino acid sequence of a lambda VI primary (AL) amyloid protein (WLT).

A;Reference number: A01989; PMID:86122667; PMID:4089539

A;Accession: A01989

A;Molecule type: protein

A;Residues: 1-111 <DWU>

C;Genetics:

A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C;Superfamily: heterotetramer; immunoglobulin

F;1-22/Region: framework 1

F;15-93/Domain: immunoglobulin homology <IMM>

F;23-35/Region: complementarity-determining 1

F;36-50/Region: framework 2

F;51-57/Region: complementarity-determining 2

F;58-91/Region: framework 3

F;92-101/Region: complementarity-determining 3

F;102-111/Region: framework 4

F;22-91/Disulfide bonds: #status predicted

Query Match 82.3%; Score 51; DB 1; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| : ||||| |||||
Db 23 TGSIGSIASNYVQ 35

RESULT 4

L6HUST

Ig lambda chain V-VI region (SUT) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997

C;Accession: A01988

R;Solomon, A.; Kyle, R.A.; Frangione, B.

in Amyloidosis, Glenner, G.G.; Osserman, E.F.; Benditt, E.P.; Calkins, E.; Cohn, A.S., a

A;Title: Light chain variable region subgroups of monoclonal immunoglobulins in amyloid

A;Reference number: A01988

A;Accession: A01988

A;Molecule type: protein

A;Residues: 1-111 <SOL>

C;Genetics:

A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C;Superfamily: heterotetramer; immunoglobulin

F;1-22/Region: framework 1

F;15-93/Domain: immunoglobulin homology <IMM>

F;23-35/Region: complementarity-determining 1

F;36-50/Region: framework 2

F;51-57/Region: complementarity-determining 2

F;58-91/Region: framework 3

F;92-100/Region: complementarity-determining 3

F;101-111/Region: framework 4

F;22-91/Disulfide bonds: #status predicted

Query Match 69.4%; Score 43; DB 1; Length 111;
Best Local Similarity 69.2%; Pred. No. 0.81;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
| : ||||| |||||
Db 23 TRSDGTIAGYIVQ 35

RESULT 5

T39047

hypothetical protein SPAC6F6.13c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000

C;Accession: T39047

R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21797

A;Accession: T39047

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-778 <GEN>

A;Cross-references: EMBL:Z98981; PIDN:CAB11736.1; GSPDB:GN00066; SPDB:SPAC6F6.13c

A;Experimental source: strain 972h-; cosmid c6F6

C;Genetics:

A;Gene: SPDB:SPAC6F6.13c

A;Map position: 1

C;Superfamily: Candida albicans conserved hypothetical protein PI09050.2

Query Match 64.5%; Score 40; DB 2; Length 778;
Best Local Similarity 72.7%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 SSGSIASNYVQ 13
| : ||||| |||||
Db 39 SKGSIATENYVQ 49

RESULT 6

L6HUST

Ig lambda chain V-VI region (AR) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000

C;Accession: A01987

R;Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.

Biochem. J. 195, 561-572, 1981

A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-chain

A;Reference number: A01987; PMID:82091000; PMID:6797401

A;Contents: amyloid protein AR

A;Accession: A01987

A:Molecule type: protein
A:Residues: 1-112 <SE>
A>Note: about half of the lambda chain C region is missing from this protein
C:Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMW>
F:22-91/Disulfide bonds: #status predicted

Query Match 61.3%; Score 38; DB 1; Length 112;
Best Local Similarity 61.5%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSGSIASNYVQ 13
Db 23 TSGSGSIADSFVQ 35

RESULT 7
TVHUHC
protein-tyrosine kinase (EC 2.7.1.112) hck - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C:Accession: A27811; A27812; JCI149; C38268; S31103
R:Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; DiMol. Cell. Biol. 7, 2267-2275, 1987
A:Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and encodes a protein-tyrosine kinase and
A:Reference number: A27811; MUID:87257942; PMID:3496523
A:Accession: A27811
A:Molecule type: mRNA
A:Residues: 1-505 <QUI>
A:Cross-references: GB:M16591
A>Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
R:Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
Mol. Cell. Biol. 7, 2276-2285, 1987
A:Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin
A:Reference number: A27812; MUID:87257943; PMID:3453117
A:Accession: A27812
A:Molecule type: mRNA
A:Residues: 1-505 <ZIE>
A:Cross-references: GB:M16592; NID:9183913; PIDN:AAA52644.1; PID:G306833
R:Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A:Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase
A:Reference number: JCI149; MUID:92241680; PMID:1572549
A:Accession: JCI149
A:Molecule type: DNA
A:Residues: 157-505 <HRA>
A:Cross-references: EMBL:X59741
R:Partanen, J.; Maekela, T.P.; Alitalo, R.; Leivaeslahti, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; MUID:91062389; PMID:2247464
A:Accession: C38268
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 362-417 <PAR>
C:Genetics:
A:Gene: GDB:HCK
A:Cross-references: GDB:119303; OMIM:142370
A:Map position: 20q11-20q12
A:Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphatase
F:2-505/Product: protein-tyrosine kinase hck #status predicted <MAI>

F:64-112/Domain: SH3 homology <SH3>
F:123-220/Domain: SH2 homology <SH2>
F:239-497/Domain: protein kinase homology <KIN>
F:247-255/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Binding site: palmitate (Cys) (covalent) #status predicted
F:269/Active site: Lys #status predicted
F:390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 61.3%; Score 38; DB 1; Length 505;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRSGSGSIASNYV 12
Db 101 TRKEGVIPSNV 112

RESULT 8
B82379
conserved hypothetical protein VCA1085 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82379
R:Reidberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82379
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-556 <HEI>
A:Cross-references: GB:AE004434; GB:AE003853; NID:9658531; PIDN:BAF96978.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA1085
A:Map position: 2

Query Match 61.3%; Score 38; DB 2; Length 556;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RSSGSIASNYVQ 13
Db 343 KSGGSIRANYAQ 354

RESULT 9
T27072
hypothetical protein Y51A2D.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T27072
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20307
A:Accession: T27072
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-606 <WIL>
A:Cross-references: EMBL:AL021497; PIDN:CAA16400.1; GSPDB:GN00023; CESP:Y51A2D.4
A:Experimental source: clone Y51A2D
C:Genetics:
A:Gene: CESP:Y51A2D.4
A:Map position: 5
A:Introns: 4/3; 76/1; 144/1; 226/3; 400/2; 446/1; 562/3
C:Superfamily: glucose transport protein

Query Match 61.3%; Score 38; DB 2; Length 606;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSGSSTASNY 11
| :|||||:
Db 442 TNSNGSIANNF 452

RESULT 10

A90771
hypothetical protein ECs1137 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A90771
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasakura, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA834560.1; PID:g13360597; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 050952
C:Genetics:
A:Gene: ECs1137

Query Match 61.3%; Score 38; DB 2; Length 726;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSSTASNYVQ 13
||| :|||:
Db 243 TRILNSIANNYLQ 255

RESULT 11

E85633
hypothetical protein yccC [imported] - Escherichia coli (strain O157:H7, substrain EDL933
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85633
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <STO>
A:Cross-references: GB:AB005174; NID:g12514246; PIDN:AAG55529.1; GSPDB:GN00145; UWGP:Z13
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yccC

Query Match 61.3%; Score 38; DB 2; Length 726;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSSTASNYVQ 13
||| :|||:
Db 243 TRILNSIANNYLQ 255

RESULT 12

C64839
probable ATPase yccC - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: C64839
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C64839
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-726 <BIAT>
A:Cross-references: GB:AB000200; GB:U00096; NID:g2367111; PIDN:AAC74066.1; PID:g1787216
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yccC
C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F:34-50/Domain: transmembrane #status predicted <TM1>
F:428-444/Domain: transmembrane #status predicted <TM2>
F:539-546/Region: nucleotide-binding motif A (P-loop)

Query Match 61.3%; Score 38; DB 2; Length 726;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSSTASNYVQ 13
||| :|||:
Db 243 TRILNSIANNYLQ 255

RESULT 13

PS0073
Ig kappa chain V region (38C13.V2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0073
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangem
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0073
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMV>

Query Match 59.7%; Score 37; DB 2; Length 108;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSSGSIASNYV 12
| :||| :|||:
Db 24 RASSISSNYL 34

RESULT 14

E59098
hypothetical protein pX01-61 - Bacillus anthracis virulence plasmid pX01
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 16-Feb-2001
C:Accession: E59098
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harbor
A:Reference number: A59091; MUID:99445483; PMID:10515943
A:Accession: E59098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-236 <OKI>
A:Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32365.1; PID:g4894277
A:Experimental source: strain Sterne
C:Genetics:
A:Gene: pX01-61
A:Genome: plasmid
C:Superfamily: hypothetical protein pX01-61

Query Match 59.7%; Score 37; DB 2; Length 236;

Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RSSGSIASNYVQ 13
: |||: |||:
Db 25 KDSGLLTNYVE 36

RESULT 15

T30578
myosin IC - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 08-Sep-2000
C:Accession: T30578
R:Peterson, M.D.; Novak, K.D.; Reedy, M.C.; Ruman, J.I.; Titus, M.A.
J. Cell Sci. 108, 1093-1103, 1995
A:Title: Molecular genetic analysis of myoC, a Dictyostelium myosin I.
A:Reference number: Z20872; MUID:95348228; PMID:7622596
A:Accession: T30578
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1181 <PET>
A:Cross-references: EMBL:L35323; NID:g532123; PID:g532124; PIDN:AAC37427.1
C:Genetics:
A:Gene: myoC
A:Introns: 307/1
C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo
F18-685/Domain: myosin motor domain homology <MMO>

Query Match 59.7%; Score 37; DB 2; Length 1181;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
: | : |||
Db 1167 TRQIGMLPSNYVQ 1179

Search completed: June 8, 2004, 18:54:13
Job time : 13.7969 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 7.3125 seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-64
Perfect score: 62
Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	83.9	112	1 LV6E HUMAN	P01722 homo sapien
2	52	83.9	131	1 LV6E HUMAN	P06319 homo sapien
3	51	82.3	111	1 LV6D HUMAN	P06318 homo sapien
4	43	69.4	111	1 LV6C HUMAN	P06317 homo sapien
5	42	67.7	517	1 SR42 DROME	Q9v9j3 drosophila
6	38	61.3	112	1 LV6A HUMAN	P01721 homo sapien
7	38	61.3	503	1 HCK MACFA	Q95m30 macaca fasc
8	38	61.3	525	1 HCK HUMAN	P08631 homo sapien
9	38	61.3	726	1 ETK ECO27	P58764 escherichia
10	38	61.3	726	1 ETK ECO57	Q8xc28 escherichia
11	38	61.3	726	1 ETK ECOLI	P38134 escherichia
12	38	61.3	1399	1 Z291 HUMAN	Q9by12 homo sapien
13	37	59.7	1181	1 MYSC DICDI	P42522 dictyosteli
14	36	58.1	308	1 OM40 ARATH	Q9lbe5 arabidopsis
15	36	58.1	352	1 GAE7 CAEL	Q27536 caenorhabdi
16	36	58.1	416	1 PXN1 XENLA	P49263 xenopus lae
17	36	58.1	549	1 CET1 YEAST	O13297 saccharomyc
18	35	56.5	278	1 PMPI SCHPO	O13453 schizosacch
19	35	56.5	402	1 ARGJ METTH	O26284 m arginine
20	35	56.5	489	1 ATR2 HUMAN	P58335 homo sapien
21	35	56.5	502	1 HCK RAT	P50545 rattus norv
22	35	56.5	511	1 LYN HUMAN	P07948 homo sapien
23	35	56.5	523	1 HCK MOUSE	P08103 mus musculu
24	35	56.5	536	1 FYN XIPIE	P27446 xiphophorus
25	35	56.5	541	1 YES MOUSE	Q04736 mus musculu
26	35	56.5	574	1 YB2A SCHPO	P87311 schizosacch
27	35	56.5	1007	1 Y741 CHLMU	Q9pjtc6 chlamydia m
28	34	54.8	37	1 CALI_PIG	P10092 sus scrofa
29	34	54.8	127	1 CAL2 HUMAN	P03880 homo sapien
30	34	54.8	294	1 TSX ECOLI	P22786 escherichia
31	34	54.8	367	1 SS81 YEAST	P40073 saccharomyc
32	34	54.8	409	1 IVD ARATH	Q9swg0 arabidopsis
33	34	54.8	740	1 GAG_SMRVH	P21411 squirrel mo

34	34	54.8	1556	1 GLTS SYNY3	P55038 synchocyst
35	33	53.2	37	1 CALI SHEEP	P30881 ovis aries
36	33	53.2	129	1 CAL2 HORSE	Q9n0t3 equus caball
37	33	53.2	178	1 FBOH BOWMA	Q99050 bombyx mand
38	33	53.2	182	1 YMBA ECOLI	P75866 escherichia
39	33	53.2	186	1 PEBP BOVIN	P13696 bos taurus
40	33	53.2	186	1 PEBP HUMAN	P30086 homo sapien
41	33	53.2	186	1 PEBP MACFA	P48737 macaca fasc
42	33	53.2	186	1 PEBP MOUSE	P70296 mus musculu
43	33	53.2	271	1 CRK DROME	Q9xym0 drosophila
44	33	53.2	325	1 Y230 ARATH	O80934 arabidopsis
45	33	53.2	336	1 ACT2_LYCES	Q96483 lycopersico

ALIGNMENTS

```
RESULT 1
LV6E_HUMAN          STANDARD;          PRT;   112 AA.
ID   LV6E_HUMAN
AC   P01722;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region NIG-48.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80094390; PubMed=118171;
RA   Takahashi N., Takayasu T., Isobe T., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative study on the structure of the light chains of human
RT   immunoglobulins. II. Assignment of a new subgroup.";
RL   J. Biochem. 86:1523-1535(1979).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01991; L6HU48.
DR   HSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN 1 107
FT   NON TER 112 112
SQ   SEQUENCE 112 AA; 12152 MW; CFBB307BC527A384 CRC64;
Query Match      83.9%; Score 52; DB 1; Length 112;
Best Local Similarity 84.6%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY   1 TRSSGSIASNYVQ 13
Db    23 TRTSDSIASNYVQ 35
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RESULT 2
LV6E_HUMAN          STANDARD;          PRT;   131 AA.
ID   LV6E_HUMAN
AC   P06319;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region EB4 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85215660; PubMed=3923440;
 RA Anderson M.L.M.; Brown L.; McKenzie E.; Kellow J.E.; Young B.D.;
 RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
 expressed in the Burkitt's lymphoma cell line EB4.";
 RL Nucleic Acids Res. 13:2931-2941(1985).
 DR PIR; A01990; L6HUEB.
 DR HSSP; P01709; 2MCG.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
 FT DOMAIN 20 41 FRAMEWORK-1.
 FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 110 FRAMEWORK-3.
 FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 131 FRAMEWORK-4.
 FT DISULFID 41 110 BY SIMILARITY.
 FT NON TER 131
 SQ SEQUENCE 131 AA; 14147 MW; 02A9179C805C2CD CRC64;

Query Match 83.9%; Score 52; DB 1; Length 131;
 Best Local Similarity 84.6%; Pred. No. 0.0035;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 Db 42 TGNSSGSIASNYVQ 54

RESULT 3
 LV6D HUMAN
 ID LV6D_HUMAN STANDARD; PRT; 111 AA.
 AC P06318;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-VI region WLT.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86122667; PubMed=4089539;
 RA Dwulet F.E.; Strako K.; Benson M.D.;
 RT "Amino acid sequence of a lambda Vi primary (AL) amyloid protein
 (WLT).";
 RL Scand. J. Immunol. 22:653-660(1985).
 DR PIR; A01989; L6HULT.
 DR HSSP; P01709; 2MCG.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 22 FRAMEWORK-1.

FT DOMAIN 23 35 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 36 50 FRAMEWORK-2.
 FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 58 91 FRAMEWORK-3.
 FT DOMAIN 92 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 22 91 BY SIMILARITY.
 FT NON TER 111
 SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 82.3%; Score 51; DB 1; Length 111;
 Best Local Similarity 84.6%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 Db 23 TGNSSGSIASNYVQ 35

RESULT 4
 LV6C HUMAN
 ID LV6C_HUMAN STANDARD; PRT; 111 AA.
 AC P06317;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-VI region SUT.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA Solomon A.; Kyle R.A.; Frangione B.;
 RT "Light chain variable region subgroups of monoclonal immunoglobulins
 in amyloidosis AL.";
 RL (In) Glenner G.G.; Osseman E.F.; Benditt E.P.; Calkins E.,
 RL Cohen A.S.; Zucker-Franklin D. (eds.);
 RL Amyloidosis, pp.449-462, Plenum Press, New York (1986).
 DR PIR; A01988; L6HUST.
 DR PDB; 1CD0; 06-MAR-00.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT DOMAIN 1 22 FRAMEWORK-1.
 FT DOMAIN 23 35 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 36 50 FRAMEWORK-2.
 FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 58 91 FRAMEWORK-3.
 FT DOMAIN 92 100 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 101 111 FRAMEWORK-4.
 FT DISULFID 22 91 BY SIMILARITY.
 FT NON TER 111
 SQ SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;

Query Match 69.4%; Score 43; DB 1; Length 111;
 Best Local Similarity 69.2%; Pred. No. 0.18;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
 Db 23 TRSDGTIAGYVQ 35

RESULT 5
 SR42 DROME
 ID SR42 DROME STANDARD; PRT; 517 AA.
 AC Q9V9J3; O18369; Q26297; Q94879;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase Src42A [EC 2.7.1.112] (Derc41).
 GN SRC42A OR SRC41 OR TK5 OR CG7873.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
 RP STAGE.
 RC STRAIN=Canton-S; TISSUE=Pupae;
 RX MEDLINE=96268448; PubMed=8692295;
 RA Takahashi F., Endo S., Kojima T., Saigo K.;
 RT "Regulation of cell-cell contacts in developing Drosophila eyes by
 RT Derc41, a new, close relative of vertebrate c-src.";
 RL Genes Dev. 10:1645-1656(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Berkely;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champ M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Brokstein P., Brottier P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Lasko P., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosnere A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Berkely; TISSUE=Embryo;
 RC MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarini H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [4]
 RP SEQUENCE OF 374-428 FROM N.A.
 RX MEDLINE=92008631; PubMed=1915852;
 RA Shishido E., Emori Y., Saigo K.;
 RT "Identification of seven novel protein-tyrosine kinase genes of

RT Drosophila by the polymerase chain reaction.";
 RL FEBS Lett. 289:235-238(1991).
 RN [5]
 RP SEQUENCE OF 376-427 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA.";
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -!- FUNCTION: Essential for correct eye morphogenesis (ommatidial R7
 CC neuron formation), this requires the Ras1/MAPK signal transduction
 CC pathway. May be involved in the regulation of cytoskeleton
 CC organization and cell-cell contacts in developing ommatidia.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- TISSUE SPECIFICITY: Ubiquitous in early embryos, in stages 13-16
 CC expression is seen in visceral mesoderm, hindgut, brain, anal pads
 CC and ventral ganglions. In larvae, expression is in CNS, wing disk,
 CC leg disk and photoreceptor precursors in the eye-antenna disks
 CC posterior to the morphogenetic furrow.
 CC -!- DEVELOPMENTAL STAGE: In early embryos expression is very low,
 CC expression increases during embryogenesis. Also expressed in
 CC larvae and pupae.
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 DR EMBL; D42125; BAA07705.1; -
 DR EMBL; AF003784; AAM68337.1; -
 DR EMBL; AY058652; AAL13881.1; -
 DR EMBL; S55977; AAB19907.1; -
 DR EMBL; AJ002911; CAA05746.1; -
 DR HSSP; P00523; 1SRLL.
 DR Flybase; FBgn004603; Src42A.
 DR GO; GO:0005912; C:adherens junction; IDA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; NAS.
 DR GO; GO:0007154; P:cell communication; IDA.
 DR GO; GO:0007456; P:eye morphogenesis (sensu Drosophila); IMP.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IGI.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; Developmental protein;
 KW ATP-binding; SH2 domain; SH3 domain.
 FT DOMAIN 63 124 SH2.
 FT DOMAIN 130 222 SH2.
 FT DOMAIN 248 504 PROTEIN KINASE.

DB 99 TRKEGIPSNV 110

RESULT 8

ID HCK_HUMAN STANDARD; PRT: 525 AA.
 AC P08631; Q96CC0; Q9H5Y5; Q9NUA4; Q9UMJ5;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK/p60-HCK)
 DE (Hemopoietic cell kinase).
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 21-525 FROM N.A.
 RX MEDLINE=87257942; PubMed=3496523;
 RA Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J.,
 RA le Beau M.M., Diaz M.O., Rowley J.D.;
 RT "Identification of a human gene (HCK) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells.";
 RL Mol. Cell. Biol. 7:2267-2275 (1987).
 RN [2]
 RP SEQUENCE OF 21-525 FROM N.A.
 RX MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., Marth J.D., Lewis D.B., Perlmuter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hematopoietic origin.";
 RL Mol. Cell. Biol. 7:2276-2285 (1987).
 RN [3]
 RP SEQUENCE OF 21-525 FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=22388237; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerbahn B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 21-525 FROM N.A.
 RC TISSUE=ileal mucosa;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakaajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Isogai T., Sugano S.;
 RT "NEO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
 RA LeHaevaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [6]
 RP SEQUENCE OF 178-525 FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=92241680; PubMed=1572549;
 RA Hradetzky D., Streibhardt K., Ruesamen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
 RT exon-intron structure among human PTKs of the scr family.";
 RL Gene 113:275-280 (1992).
 RN [7]
 RP SEQUENCE OF 1-21 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370 (1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-525.
 RX MEDLINE=97177106; PubMed=9024658;
 RA Sicheiri F., Moarefi I., Kurlyan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609 (1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 80-136.
 RX MEDLINE=98453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 RA Ladbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691 (1998).
 RN [10]
 RP STRUCTURE BY NMR OF 77-137.
 RX MEDLINE=98239731; PubMed=9571048;
 RA Horita D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 RA Gmeiner W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265 (1998).
 RN [11]
 RP STRUCTURE BY NMR OF 138-244.
 RX MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Gmeiner W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett. 406:131-135 (1997).
 CC -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
 CC receptor to the activation of the respiratory burst. May also
 CC contribute to neutrophil migration and may regulate the
 CC degranulation process of neutrophils.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Isoform p60-HCK and isoform p59-HCK are
 CC associated with membranes. Isoform p60-HCK is also cytoplasmic (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, p60-HCK (shown here) and p59-HCK, are
 CC produced by alternative initiation;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in cells of the
 CC myeloid and b-lymphoid lineages.
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC
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 CC
 CC -----
 CC EMBL; M16591; AAA52643.1; -.
 CC EMBL; M16592; AAA52644.1; -.
 CC EMBL; BC014435; AAH14435.1; -.
 CC EMBL; AK026432; BAB15482.1; -.
 CC EMBL; AL049539; CAB75606.1; -.
 CC EMBL; X58741; CAA41565.2; -.
 CC EMBL; X58742; CAA41565.2; JOINED.
 CC EMBL; X58743; CAA41565.2; JOINED.
 CC PIR; A27811; TVHUHC.
 CC PDB; 2HCK; 20-AUG-97.
 CC PDB; 3HCK; 15-OCT-97.
 CC PDB; 4HCK; 17-JUN-98.
 CC PDB; 5HCK; 17-JUN-98.
 CC PDB; 1AD5; 15-MAY-97.
 CC PDB; 1BU1; 11-NOV-98.
 CC PDB; 1OCF; 08-JUN-99.
 CC Genew; HGNC:4840; HCK.
 CC MIM; 142370; -.
 CC GO; GO:0004713; P:protein-tyrosine kinase activity; TAS.
 CC GO; GO:0007498; P:mesoderm development; TAS.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001452; SH3.
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR008266; Tyr_kinase_AS.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF00018; SH3; 1.
 CC PRINTS; PR00401; SH2DOMAIN.
 CC PRINTS; PR00452; SH3DOMAIN.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC ProDom; PD000093; SH2; 1.
 CC ProDom; PD000066; SH3; 1.
 CC
 CC Query Match 61.3%; Score 38; DB 1; Length 525;
 CC Best Local Similarity 66.7%; Pred. No. 10;
 CC Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 TRSSGSIASNYV 12
 CC DB 121 TRKEGYIPSNYV 132
 CC
 CC RESULT 9
 CC ETK_ECO27
 CC ID ETK_ECO27 STANDARD; PRT; 726 AA.
 CC AC P58764;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase etk (EC 2.7.1.112)
 GN ETK.
 OS Escherichia coli O127:H6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=168807;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 1-17, AND CHARACTERIZATION.
 RC STRAIN=O127:H6 / E2348/69;
 RX MEDLINE=99298177; PubMed=10369665;
 RA Ilan O.A., Bloch Y., Frankel G., Ullrich H., Geider K., Rosenshine I.;
 RT "Protein tyrosine kinases in bacterial pathogens are associated with
 RT virulence and production of exopolysaccharide.";
 RL EMBL J. 18:3241-3248(1999).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Inner membrane.
 CC -!- PTM: Autophosphorylated. Dephosphorylated by etp (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
 CC
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 CC
 CC -----
 CC EMBL; AJ238695; CAB43868.1; -.
 CC InterPro; IPR003856; LPS_Wzz_MPA.
 CC Pfam; PF02706; wzz; 1.
 CC Transferase; Tyrosine-protein kinase; Phosphorylation; Transmembrane;
 CC Inner membrane.
 CC TRANSMEM 33 53 POTENTIAL.
 CC TRANSMEM 425 445 POTENTIAL.
 CC SEQUENCE 726 AA; 81082 MW; 91F97DF8AD8BE302 CRC64;
 CC
 CC Query Match 61.3%; Score 38; DB 1; Length 726;
 CC Best Local Similarity 61.5%; Pred. No. 14;
 CC Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1 TRSSGSIASNYVQ 13
 CC DB 243 TRILSIANNYLQ 255
 CC
 CC RESULT 10
 CC ETK_ECO57
 CC ID ETK_ECO57 STANDARD; PRT; 726 AA.
 CC AC Q8XC28;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DE Tyrosine-protein kinase etk (EC 2.7.1.112).
 CC GN ETK OR Z1398 OR ECS1137.
 CC OS Escherichia coli O157:H7.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC OX NCBI_TaxID=83334;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 CC RX MEDLINE=21074935; PubMed=11206551;
 CC RA Perna N.T., Plunkett G., Evans P.S., Gregor J., Kirkpatrick H.A.,
 CC Rose D.J., Mayhew G.F., Boutin A., Shao Y., Miller L.,
 CC Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 CC Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
 CC Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 CC Welch R.A., Blattner F.R.;
 CC "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


```

RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Inner membrane (By similarity).
CC -!- PTM: Autophosphorylated. Dephosphorylated by etp (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
CC -----
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CC -----
DR EMBL; AB005292; AG55529.1; -.
DR EMBL; AF002554; BAB34560.1; -.
DR PIR; A90771; A90771.
DR PIR; E85633; E85633.
DR InterPro; IPR003856; LPS_WZZ_MPA.
DR Pfam; PF02706; wzz; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 425 445 POTENTIAL.
SQ SEQUENCE 726 AA; 81259 MW; 7EEA1912097118DC CRC64;

Query Match 61.3%; Score 38; DB 1; Length 726;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
Db 243 TRILSIANNYIQ 255

RESULT 11
ETK_ECOLI STANDARD; PRT; 726 AA.
AC P38134; P75879;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase etk (EC 2.7.1.112).
GN ETK OR B0981.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;

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RX MEDLINE=97061202; PubMed=8905232;
RA Oehlma T., Aiba H., Baba T., Fujita K., Hayaashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Naahimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [3]
RP SEQUENCE OF 628-726 FROM N.A.
RX MEDLINE=90368616; PubMed=2168385;
RA Dassa J., Marck C., Boquet P.L.;
RT "The complete nucleotide sequence of the Escherichia coli gene appA
RT reveals significant homology between pH 2.5 acid phosphatase and
RT glucose-1-phosphatase."
RL J. Bacteriol. 172:5497-5500(1990).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome."
RL Nucleic Acids Res. 22:4756-4767(1994).
RN [5]
RP CHARACTERIZATION.
RC STRAIN=K12 / JM109;
RX MEDLINE=20545593; PubMed=11090276;
RA Vincent C., Duclos B., Grangeasse C., Vaganay E., Riberty M.,
RA Cozzone A.J., Doublet P.;
RT "Relationship between exopolysaccharide production and protein-
RT tyrosine phosphorylation in Gram-negative bacteria."
RL J. Mol. Biol. 304:311-321(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Inner membrane (By similarity).
CC -!- PTM: Autophosphorylated. Dephosphorylated by etp.
CC -!- SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
CC -!- CAUTION: Seems to be expressed only in enteropathogenic E.coli
CC strains.
CC -----
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CC -----
DR EMBL; AB000200; AAC74066.1; -.
DR EMBL; D90735; BAA35746.1; -.
DR EMBL; M58708; -. NOT_ANNOTATED_CDS.
DR PIR; C64839; C64839.
DR PhosSite; P38134; -.
DR Ecogene; EGI1826; etk.
DR InterPro; IPR003856; LPS_WZZ_MPA.
DR Pfam; PF02706; wzz; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 425 445 POTENTIAL.
FT CONFLICT 726 726 E -> EEN (IN REF. 2).
SQ SEQUENCE 726 AA; 81241 MW; BAA060F59680DA22 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 726;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSSGSIASNYVQ 13
Db 243 TRILSIANNYIQ 255

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RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.,
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846(2003).
 RN [3]
 RP SEQUENCE OF 1-15; 21-42; 63-80; 207-219 AND 245-258.
 RC STRAIN=cv. Columbia;
 RX PubMed=11161051;
 RA Werhahn W., Niemeyer A., Jaensch L., Kruff V., Schmitz U.K.,
 RA Braun H.-P.;
 RT "Purification and characterization of the preprotein translocase of
 RT the outer mitochondrial membrane from Arabidopsis thaliana.
 RT Identification of multiple forms of TOM20.";
 RL Plant Physiol. 125:943-954(2001).
 RN [4]
 RP SEQUENCE OF 1-15 AND 246-258, AND SUBCELLULAR LOCATION.
 RC TISSUE=leaf, and Stem;
 RX MEDLINE=21608403; PubMed=11743114;
 RA Kruff V., Eubel H., Jaensch L., Werhahn W., Braun H.-P.;
 RT "Proteomic approach to identify novel mitochondrial proteins in
 RT Arabidopsis.";
 RL Plant Physiol. 127:1694-1710(2001).
 CC -!- FUNCTION: Central component of the receptor complex responsible
 CC for the recognition and translocation of cytosolically synthesized
 CC mitochondrial preproteins. Together with TOM22 functions as the
 CC transit peptide receptor at the surface of the mitochondrion outer
 CC membrane and facilitates the movement of preproteins into the
 CC translocation pore. Directly involved in the pore formation.
 CC -!- SUBUNIT: Forms part of mitochondrial receptor complex.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC outer membrane.
 CC -!- SIMILARITY: Belongs to the Tom40 family.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC
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 CC
 CC EMBL; AF02050; BAB03165.1; ALT_SEQ.
 DR EMBL; AY050925; AAK93602.1; --.
 DR InterPro; IPR001925; Porin_Ruk.
 DR Pfam; PF01459; Eukporin; 1.
 KW Transport; Protein transport; Outer membrane; Mitochondrion;
 KW Transmembrane.
 FT INIT MET 0 0 INTERMEMBRANE (POTENTIAL).
 FT DOMAIN 1 70 POTENTIAL.
 FT TRANSMEM 71 86 POTENTIAL.
 FT DOMAIN 87 187 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 308 AA; 34119 MW; A013F8798BAAA720 CRC64;
 Query Match 58.1%; Score 36; DB 1; Length 308;
 Best Local Similarity 54.5%; Pred. No. 14;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SSGSIASNYVQ 13
 DB 216 STGVVNYVQ 226

RESULT 15

GA7 CAEEL STANDARD; PRT; 352 AA.
 AC Q27536;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Probable galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
 DE (Gal-1-P uridylyltransferase) (UDP-glucose-hexose-1-phosphate
 DE uridylyltransferase).
 GN ZK1058.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Mortimore B.J.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate =
 CC alpha-D-glucose 1-phosphate + UDP-galactose.
 CC -!- COFACTOR: Binds 1 zinc and 1 iron ion per subunit (Potential).
 CC -!- PATHWAY: Galactose metabolism; second step.
 CC -!- SIMILARITY: Belongs to the galactose-1-phosphate
 CC uridylyltransferase family 1.
 CC
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 CC
 CC EMBL; Z35604; CAA84679.1; --.
 DR PIR; T27677; T27677.
 DR HSSP; P09148; 1HXQ.
 DR WormPep; ZK1058.3; CE01103.
 DR InterPro; IPR001937; Galp_UDPtransf1.
 DR InterPro; IPR005851; Galp_Utransf1.
 DR InterPro; IPR005850; Galp_Utransf1.
 DR InterPro; IPR005849; Galp_Utransf1.
 DR Pfam; PF02744; Galp_UDP_tf_C; 1.
 DR Pfam; PF01087; Galp_UDPtransf1.
 DR ProDom; PD005051; Galp_UDPtransf1; 1.
 DR TIGRFAMs; TIGR00209; gal1_1.
 DR PROSITE; PS00117; GAL_P_UDP_TRANSF_I; 1.
 KW Transferase; Nucleotidytransferase; Galactose metabolism; Zinc; Iron;
 KW Metal-binding.
 FT ACT SITE 167 167 NUCLEOPHILE (BY SIMILARITY).
 FT METAL 165 165 ZINC (POTENTIAL).
 FT METAL 300 300 IRON (POTENTIAL).
 SQ SEQUENCE 352 AA; 41042 MW; F1B433A926C47C4C CRC64;
 Query Match 58.1%; Score 36; DB 1; Length 352;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYV 12
 DB 59 TRSSGSIASNYV 70

Search completed: June 8, 2004, 18:56:15

Job time : 8.3125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 37.5781 Seconds
(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	112	4 Q96JD1	Q96JD1 homo sapien
2	52	83.9	116	4 Q96JD0	Q96JD0 homo sapien
3	44	71.0	3567	4 Q86UP3	Q86UP3 homo sapien
4	41	66.1	112	4 Q96UD2	Q96UD2 homo sapien
5	40	64.5	474	16 Q89Y07	Q89Y07 bradyrhizob
6	40	64.5	778	3 Q14244	Q14244 schizosacch
7	39	62.9	945	3 Q8XIV8	Q8XIV8 aspergillus
8	38	61.3	121	4 Q9H4Y2	Q9H4Y2 homo sapien
9	38	61.3	371	5 Q8MKV0	Q8MKV0 drosophila
10	38	61.3	423	16 Q89D22	Q89D22 bradyrhizob
11	38	61.3	498	15 Q8AC27	Q8AC27 human immun
12	38	61.3	519	3 Q13420	Q13420 trametes sp
13	38	61.3	556	16 Q9KKL8	Q9KKL8 vibrio chol
14	38	61.3	606	5 Q9XXR3	Q9XXR3 caenorhabdi
15	38	61.3	648	16 Q83LL7	Q83LL7 shigella fl
16	38	61.3	762	5 Q9V5B0	Q9V5B0 drosophila

17	38	61.3	1041	5 Q8MNE4	Q8MNE4 dictyosteli
18	38	61.3	1153	4 Q9H3D8	Q9H3D8 homo sapien
19	38	61.3	1265	4 Q9P274	Q9P274 homo sapien
20	38	61.3	1433	15 Q8ADE1	Q8ADE1 human immun
21	37	59.7	229	2 Q8KYN9	Q8KYN9 bacillus an
22	37	59.7	236	2 Q9X331	Q9X331 bacillus an
23	37	59.7	287	16 Q8XKS7	Q8XKS7 clostridium
24	37	59.7	417	16 Q7UVZ8	Q7UVZ8 rhodopirell
25	37	59.7	522	8 Q9B8W0	Q9B8W0 taenia cras
26	36	58.1	80	16 Q8FEB3	Q8FEB3 escherichia
27	36	58.1	140	10 Q9LMQ0	Q9LMQ0 arabidopsis
28	36	58.1	234	1 Q54288	Q54288 sulfolobus
29	36	58.1	308	17 Q97U28	Q97U28 sulfolobus
30	36	58.1	317	2 Q9F5B5	Q9F5B5 agrobacteri
31	36	58.1	468	10 Q84KZ1	Q84KZ1 nicotiana t
32	36	58.1	522	2 Q53784	Q53784 staphylococ
33	36	58.1	870	16 Q83AC6	Q83AC6 coxiella bu
34	36	58.1	938	5 Q7YYA2	Q7YYA2 cryptospori
35	36	58.1	997	5 Q01858	Q01858 caenorhabdi
36	36	58.1	1453	16 Q89SM7	Q89SM7 bradyrhizob
37	35	56.5	76	5 Q7YV11	Q7YV11 trypanosoma
38	35	56.5	124	15 Q8J3Y0	Q8J3Y0 human immun
39	35	56.5	132	15 Q97686	Q97686 human immun
40	35	56.5	132	15 Q97687	Q97687 human immun
41	35	56.5	144	15 Q99IE9	Q99IE9 human immun
42	35	56.5	175	10 Q7X7P7	Q7X7P7 oryza sativ
43	35	56.5	287	10 Q9FVG5	Q9FVG5 zea mays [m
44	35	56.5	319	16 Q7WEE3	Q7WEE3 bordetella
45	35	56.5	319	16 Q7VS37	Q7VS37 bordetella

ALIGNMENTS

RESULT 1
Q96JD1 PRELIMINARY; PRT; 112 AA.
ID Q96JD1
AC Q96JDI;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Amyloid lambda 6 light chain variable region PIP (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perletti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region PIP."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267874; AAK58586.1; -.
DR PIR; A30323; A30323.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 100.0%; Score 62; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0

QY 1 TRSSGSIASNYVQ 13
|||
Db 23 TRSSGSIASNYVQ 35

RESULT 2

Q96JD0 Q96JD0 PRELIMINARY; PRT; 116 AA.
AC Q96JD0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid lambda 6 light chain variable region SAR (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perifetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region SAR."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267875; AAK58587.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 83.9%; Score 52; DB 4; Length 116;
Best Local Similarity 84.6%; Pred. No. 0.026;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TRSGSGSIASNYVQ 13
Db 23 TGSSGSIATNYVQ 35

RESULT 3
Q86UP3 Q86UP3 PRELIMINARY; PRT; 3567 AA.
AC Q86UP3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Zinc finger homeodomain 4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shan Y.X., Huang C.Q., Dang Y.J., Yu L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY260762; AAP20225.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001400; Somatotropin.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR003604; Znf_U1.
DR Pfam; PF00046; homeobox; 4.
DR Pfam; PF00096; zf-C2H2; 18.
DR ProDom; PD000010; Homeobox; 4.
DR SMART; SM00389; HOX; 4.
DR SMART; SM00355; Znf_C2H2; 23.
DR SMART; SM00451; Znf_U1; 7.
DR PROSITE; PS00455; AMP_BINDING; 1.

DR PROSITE; PS00027; HOMEBOX 1; 2.
DR PROSITE; PS00071; HOMEBOX 2; 4.
DR PROSITE; PS00338; SOMATOTROPIN 2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 7.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 3567 AA; 393727 MW; 99DE9E581F477EFB CRC64;

Query Match 71.0%; Score 44; DB 4; Length 3567;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RSSGSIASNY 11
Db 543 RASGSVASNY 552

RESULT 4
Q96JD2 Q96JD2 PRELIMINARY; PRT; 112 AA.
AC Q96JD2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region NEG."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK58585.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11908 MW; 080B4E37E2360B06 CRC64;

Query Match 66.1%; Score 41; DB 4; Length 112;
Best Local Similarity 76.9%; Pred. No. 3.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TRSGSGSIASNYVQ 13
Db 23 TGSSGSIASNSVQ 35

RESULT 5
Q89Y07 Q89Y07 PRELIMINARY; PRT; 474 AA.
AC Q89Y07;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MFS permease.
GN BL0148.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideawa K., Iriguchi M., Kawashima K.,

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RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RL DNA Res. 9:189-197(2002).
RL EMBL; AF005935; BAC45413.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0008524; F-ATP binding; IEA.
DR GO; GO:0004672; F-protein kinase activity; IEA.
DR GO; GO:0005215; F-transporter activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR000425; MIP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR ProDom; PD000295; MIP family; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR Complete proteome.
SQ SEQUENCE 474 AA; 50619 MW; 7C5629D1B10B1201 CRC64;

Query Match 64.5%; Score 40; DB 16; Length 474;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSSGSIASNVQ 13
DB 395 QSSGAIASNFQ 406

RESULT 6
O14244 PRELIMINARY; PRT; 778 AA.
AC O14244;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical protein.
GN SPAC6F6.13C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Genties S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98981; CAB11736.1; -.
DR PIR; T39047; T39047.
DR GeneDB Spombe; SPAC6F6.13C; -.
DR GO; GO:0003824; F:atcatalytic activity; IEA.
DR InterPro; IPR007941; DUF726.
DR InterPro; IPR008262; Lipase_AS.
DR Pfam; PF05277; DUF726; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR Hypothetical protein.
SQ SEQUENCE 778 AA; 86129 MW; 0B052AC3885D1796 CRC64;

Query Match 64.5%; Score 40; DB 3; Length 778;
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 SSGSIASNVQ 13
DB 39 SKGSIENYVQ 49

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RESULT 7
Q8XIV8 PRELIMINARY; PRT; 945 AA.
AC Q8XIV8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exo-beta-1,3-glucanase (EC 3.2.1.58).
GN EXGS.
OS Aspergillus saitoi (Aspergillus phoenicis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurtiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=186681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC14332;
RA Oda K., Abe K., Kasahara S., Nakajima T.;
RT "Cloning and nucleotide sequencing of the exo- beta-1,3-glucanase gene
RT (exgs) from Aspergillus saitoi.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB070739; BAB83607.1; -.
DR GO; GO:0004338; F:glucan 1,3-beta-glucosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006162; Ppantne_S.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
DR Hydrolase; Glycosidase.
SQ SEQUENCE 945 AA; 99332 MW; 58D0CC3D84853BC0 CRC64;

Query Match 62.9%; Score 39; DB 3; Length 945;
Best Local Similarity 77.8%; Pred. No. 11e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GSIASNVQ 13
DB 355 GSVSNVYQ 363

RESULT 8
Q9H4Y2 PRELIMINARY; PRT; 121 AA.
AC Q9H4Y2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DJ180113.1 (Hemopoietic cell kinase) (Fragment).
GN HCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Almeida J.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC !- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL353092; CAC08002.1; -.
DR HSSP; P08631; 1AD5.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR00108; Neu_cyt_fact_2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00499; P67PHOX.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR Kinase; SH3 domain.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; AA20F3132FBA1D9C CRC64;

Query Match 61.3%; Score 38; DB 4; Length 121;
Best Local Similarity 66.7%; Pred. No. 17;

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Matches      8;  Conservative      0;  Mismatches      4;  Indels      0;  Gaps      0;

Qy      1 TRSSGSIASNVV 12
Db      101 TRKEGYIPSNV 112

RESULT 9
O8MKV0      SEQUENCE FROM N.A.
ID      O8MKV0      PRELIMINARY;      PRT;      371 AA.
AC      O8MKV0;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      CG30004-PA.
DE      CG30004
GN      CG30004
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Berkely;
RX      MEDLINE=20196006; PubMed=10731132;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA      Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng X., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA      Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster.";
RL      Science 287:2185-2195(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA      Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA      Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA      Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA      Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA      Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA      Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA      Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

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RA      McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA      Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA      Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA      Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA      Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT      "Sequencing of Drosophila melanogaster genome.";
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA      Hradscky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA      Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA      Clamp M., Drysdale R., Emmert D., Frise E., Ge Grey A., Harris N.,
RA      Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA      Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA      Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT      "Annotation of Drosophila melanogaster genome.";
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RA      FlyBase;
RL      Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE003832; AAM68791.1; -
DR      FlyBase; FBgn050004; CG30004.
SQ      SEQUENCE      371 AA; 39670 MW; 6055C345D2EFA270 CRC64;

Query Match      61.3%; Score 38; DB 5; Length 371;
Best Local Similarity      58.3%; Pred. No. 60;
Matches      7; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 TRSSGSIASNVV 12
Db      217 TRSNTSSNYI 228

RESULT 10
O89D22      ID      O89D22      PRELIMINARY;      PRT;      423 AA.
AC      O89D22;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Blt7623 protein.
GN      Blt7623.
OS      Bradyrhizobium japonicum.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Bradyrhizobiaceae; Bradyrhizobium.
OX      NCBI_TaxID=375;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=USDA 110;
RX      MEDLINE=22484998; PubMed=12597275;
RA      Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA      Sasamoto S., Watanabe A., Idesawa K., Itiguchi M., Kawashima K.,
RA      Kohara M., Matsumoto M., Shimpso S., Tsuruoka H., Wada T., Yamada M.,
RA      Tabata S.;
RT      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RL      Bradyrhizobium japonicum USDA110.";
RL      DNA Res. 9:189-197(2002).
DR      EMBL; AP005962; BAC52888.1; -
DR      InterPro; IPR001828; ANF_receptor.
DR      Pfam; PF01094; ANF_receptor; 1.
KW      Complete proteome.
SQ      SEQUENCE      423 AA; 46818 MW; F9DBE60427A3E1C4 CRC64;

Query Match      61.3%; Score 38; DB 16; Length 423;
Best Local Similarity      58.3%; Pred. No. 69;
Matches      7; Conservative      2; Mismatches      3; Indels      0; Gaps      0;

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QY      2 RSSGSIASNYVQ 13
Db      171 RSEGRYANYIQ 182

RESULT 11
Q8AC27 PRELIMINARY; PRT; 498 AA.
AC Q8AC27;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag polyprotein precursor (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UG57143;
RX MEDLINE=20564795; PubMed=11112486;
RA Salminen M.O., Ehrenberg P.K., Mascola J.R., Dayhoff D.E., Merling R.,
RA Blake B., Louder M., Hegerich S., Polonis V.R., Birx D.L., Robb M.L.,
RA McCutchan F.E., Michael N.L.;
RA "Construction and biological characterization of infectious molecular
RT clones of HIV-1 subtypes B and E (CRF01_AE) generated by the
RT polymerase chain reaction.";
RL Virology 278:103-110(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=98UG57143;
RX MEDLINE=22375625; PubMed=12487816;
RA Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA Kigozi G., Kiwanuka N., Phillips J.B., Meehan M., Lutalo T.,
RA Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA McCutchan F.E.;
RA "Among 46 Near Full Length HIV Type 1 Genome Sequences from Rakai
RT District, Uganda, Subtype D and AD Recombinants Predominate.";
RL AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
DR EMBL; AF484514; AAN73764.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR000071; Retrovir_p17.
DR InterPro; IPR008916; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; zf-CCHC; 2.
DR PRINTS; PR00939; C2HCCZNFINGER.
DR PRINTS; PR00234; HIV1MATRIX.
DR SMART; SM00343; Znf_C2HC; 2.
DR PROSITE; PS00158; ZF_CCHC; 2.
KW Polyprotein.
FT NON TER.
SQ SEQUENCE 498 AA; 55308 MW; FFC0A709464CA6D7 CRC64;

Query Match 61.3%; Score 38; DB 15; Length 498;
Best Local Similarity 54.5%; Pred.No. 83;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 TRSSGSIASNY 11
Db      120 TRNSGQVSQNY 130

RESULT 12
O13420 PRELIMINARY; PRT; 519 AA.
AC O13420
AC O13420;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenoloxidase (EC 1.10.3.2).
GN POX1.
OS Trametes sp. I-62.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=51095;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 20197;
RX MEDLINE=97355933; PubMed=9212414;
RA Mansur M., Suarez T., Fernandez-Larrea J.B., Brizuela M.A.,
RA Gonzalez A.E.;
RA "Identification of a laccase gene family in the new lignin-degrading
RT basidiomycete CECT 20197.";
RL Appl. Environ. Microbiol. 63:2637-2646(1997).
DR EMBL; U65399; AAB63443.1; -
DR HSSP; P37064; LAOZ.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0008471; F:laccase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 519 AA; 55665 MW; CD226C498770DDE4 CRC64;

Query Match 61.3%; Score 38; DB 3; Length 519;
Best Local Similarity 72.7%; Pred.No. 87;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RSSGSIASNYV 12
Db      428 RSAGSTAYNYV 438

RESULT 13
Q9KKL8 PRELIMINARY; PRT; 556 AA.
AC Q9KKL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VCA1085.
GN VCA1085.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettlin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bas S., Olin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.K., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004434; AAF96978.1; -
DR FIR; B82379; B82379.
DR TIGR; VCA1085; -
DR InterPro; IPR005646; DUF342.
DR Pfam; PF03961; DUF342; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 556 AA; 60476 MW; 8565B105B6F2E2DF CRC64;
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Query Match          61.3%; Score 38; DB 16; Length 556;
Best Local Similarity 58.3%; Pred. No. 94;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 RSSGSIASNYVQ 13
DB      343 KSGGSIRANYAQ 354

RESULT 14
Q9XXR3      PRELIMINARY;      PRT;      606 AA.
AC Q9XXR3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Y51A2D.4 protein.
GN Y51A2D.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
DR EMBL; AL021497; CAA16400.1; -.
DR PIR; T27072; T27072.
DR WormPep; Y51A2D.4; CE19201.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008643; P:carbohydrate transport; IEA.
DR InterPro; IPR000777; GPI20.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR003663; Sugar_transpt.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR TIGRFAMs; TIGR00879; SP; 1.
DR PROSITE; PS0850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Sugar transport; Transmembrane; Transport.
SQ SEQUENCE 606 AA; 66658 MW; 5A217A21AF87B501 CRC64;

Query Match          61.3%; Score 38; DB 5; Length 606;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 TRSSGSIASNY 11
DB      442 TNSNGSIANNF 452

RESULT 15
Q83LL7      PRELIMINARY;      PRT;      648 AA.
AC Q83LL7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf, conserved hypothetical protein.

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GN YCCC OR SF0983.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AB015127; AAM42611.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR InterPro; IPR003856; LPS_Wzz_MPA.
DR Pfam; PF02706; wzz; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 648 AA; 72757 MW; 777AF881C96B85CA CRC64;

Query Match          61.3%; Score 38; DB 16; Length 648;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 TRSSGSIASNYVQ 13
DB      165 TRILNSIANNYLQ 177

Search completed: June 8, 2004, 18:30:08
Job time : 39.5781 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 40.4688 Seconds

(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAPDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.25:*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	65.0	167	16 Q98D81	Q98d81 rhizobium 1
2	47	58.8	244	5 Q8SZS9	Q8szs9 drosophila
3	47	58.8	325	5 Q9W4N0	Q9w4n0 drosophila
4	47	58.8	325	5 Q24157	Q24157 drosophila
5	46	57.5	383	16 Q97N98	Q97n98 streptococc
6	46	57.5	383	16 Q8DN25	Q8dn25 streptococc
7	45	56.2	428	10 Q84VQ7	Q84vq7 helianthus
8	45	56.2	765	16 P74599	P74599 synechocyst
9	44	55.0	169	9 Q8SDV3	Q8sdv3 bacterioph
10	44	55.0	175	9 Q80091	Q80091 staphylococ
11	44	55.0	257	16 Q9SUM3	Q9sum3 bradyrhizob
12	44	55.0	354	5 Q9VCT5	Q9vct5 drosophila
13	44	55.0	869	16 Q8XCT4	Q8xct4 escherichia
14	43	53.8	229	16 Q7U3M1	Q7u3m1 synechococc
15	43	53.8	653	16 Q8XDDL1	Q8xddl escherichia
16	43	53.8	799	10 Q94GF8	Q94gf8 oryza sativ

17	43	53.8	851	16 Q83RY1	Q83ry1 shigella fl
18	43	53.8	866	16 Q7UD22	Q7ud22 shigella fl
19	43	53.8	1087	10 Q8SAX4	Q8sax4 oryza sativ
20	42	52.5	80	2 Q8KLB0	Q8klb0 rhizobium e
21	42	52.5	238	17 Q981B6	Q981b6 sulfolobus
22	42	52.5	243	16 Q99ZB9	Q99zb9 streptococc
23	42	52.5	317	16 Q9A3U0	Q9a3u0 caulobacter
24	42	52.5	705	17 Q8U121	Q8u121 pyrococcus
25	42	52.5	873	2 Q8GC99	Q8gc99 citrobacter
26	42	52.5	908	5 Q86JH7	Q86jh7 dictyosteli
27	42	52.5	1522	10 Q942K3	Q942k3 oryza sativ
28	41	51.2	181	16 Q884P2	Q884p2 pseudomonas
29	41	51.2	245	16 Q8P0G8	Q8p0g8 streptococc
30	41	51.2	245	16 Q8E6F3	Q8e6f3 streptococc
31	41	51.2	245	16 Q8E0T5	Q8e0t5 streptococc
32	41	51.2	295	17 Q8U371	Q8u371 pyrococcus
33	41	51.2	312	5 Q96116	Q96116 plasmodium
34	41	51.2	329	16 Q8K717	Q8k717 streptococc
35	41	51.2	380	16 Q8RSY1	Q8rsyl deinococcus
36	41	51.2	383	11 Q9CUL6	Q9cul6 mus musculu
37	41	51.2	395	10 Q8S2Q4	Q8s2q4 oryza sativ
38	41	51.2	422	10 Q39811	Q39811 glycine max
39	41	51.2	446	16 Q9RIU8	Q9riu8 streptomyce
40	41	51.2	604	16 Q8VWY1	Q8vwy1 anabaena sp
41	41	51.2	684	16 Q9KU70	Q9ku70 vibrio chol
42	41	51.2	696	5 Q9SST9	Q9sst9 drosophila
43	41	51.2	741	10 Q9FJD2	Q9fjd2 arabidopsis
44	41	51.2	948	6 Q9TTD7	Q9tttd7 trichosurus
45	41	51.2	2030	5 Q9VWN8	Q9vwn8 drosophila

ALIGNMENTS

RESULT 1

Q98D81	PRELIMINARY;	PRT;	167 AA.
ID Q98D81			
AC Q98D81;			
DT 01-OCT-2001 (TREMBLrel. 18, Created)			
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Transcription regulator.			
GN MLL4820.			
OS Rhizobium loti (Mesorhizobium loti).			
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC Phyllobacteriaceae; Mesorhizobium.			
OX NCBI_TaxID=381;			
RN [1]_TaxID=381;			
RP SEQUENCE FROM N.A.			
RC STRAIN=MAFF303099;			
RX MEDLINE=21082930; PubMed=11214968;			
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,			
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,			
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,			
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,			
RA Takeuchi C., Yamada M., Tabata S.;			
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium			
RT Mesorhizobium loti."			
RL DNA Res. 7:331-338(2000).			
DR EMBL; AP003005; BAB51390.1; --			
DR InterPro; IPR002579; DUF25.			
DR InterPro; IPR006311; Tat.			
DR Pfam; PF01641; SelR; 1.			
DR ProDom; PD004057; DUF25; 1.			
DR TIGRPFAMg; TIGR01409; TAT signal_seq; 1.			
DR TIGRPFAMg; TIGR00357; TIGR00357; 1.			
KW Complete proteome.			
SQ SEQUENCE 167 AA; 17876 MW; 1E0F7327BE2646CC CRC64;			

Query Match 65.0%; Score 52; DB 16; Length 167;
Best Local Similarity 57.1%; Pred. No. 0.46;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 DKWEAYITPGAFDV 14
Db 45 DEWKALISPRAFDV 58

RESULT 2
Q8SZS9 PRELIMINARY; PRT; 244 AA.
AC Q8SZS9
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE LD10479p.
GN BRN OR EG:EG0007.6 OR CG4934.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY070536; AAL48007.1; -.
DR FlyBase; FBgn0000221; brn.
DR GO; GO:0008375; F:acetylglucosaminyltransferase activity; IDA.
DR GO; GO:0007292; P:female gamete generation; NAS.
DR GO; GO:0008314; P:guanine receptor signaling pathway; NAS.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
SQ SEQUENCE 244 AA; 28448 MW; FF78A628F12C3C6B CRC64;

Query Match 58.8%; Score 47; DB 5; Length 244;
Best Local Similarity 58.3%; Pred. No. 5.2;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
Db 148 DRWPPYVTAGAF 159

RESULT 3
Q9W4N0 PRELIMINARY; PRT; 325 AA.
AC Q9W4N0
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE BRN OR protein.
GN BRN OR EG:EG0007.6 OR CG4934.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003430; AAF45918.1; -.
DR FlyBase; FBgn0000221; brn.
DR GO; GO:0008375; F:acetylglucosaminyltransferase activity; IDA.
DR GO; GO:0007292; P:female gamete generation; NAS.
DR GO; GO:0008314; P:guanine receptor signaling pathway; NAS.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
SQ SEQUENCE 325 AA; 37619 MW; 0DF89B720F43657B CRC64;

Query Match 58.8%; Score 47; DB 5; Length 325;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAF 12
Db 229 DRWPPYVTAGAF 240

RESULT 4
Q24157 PRELIMINARY; PRT; 325 AA.
AC Q24157
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Neurogenic secreted signaling protein precursor (Brainiac
DE protein).
GN BRN OR EG:EG0007.6.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97164700; PubMed=9012507;
RA Goode S., Melnick M., Chou T.-B., Perrimon N.;
RT "The neurogenic genes egghead and brainiac define a novel signaling
RT pathway essential for epithelial morphogenesis during Drosophila
RT oogenesis.";
RL Development 122:3863-3879(1996).
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN=OREGON-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Bartell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert P., Borkova D.,
 RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 RA Modolell J., Peter G., Schoettler P., Werner M., Mourikioti F.,
 RA Beilstein N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamsou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster.";
 RL Science 287:2220-2222 (2000).
 CC -!- FUNCTION: NEUROGENIC PROTEIN ESSENTIAL FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF EPITHELIAL STRUCTURE. REQUIRED IN THE GERMLINE FOR
 CC ESTABLISHING THE FOLLICULAR EPITHELIUM AND FOR DETERMINING THE
 CC DORSAL-VENTRAL POLARITY. COLLABORATES WITH NOTCH ON THE APICAL
 CC SURFACE OF FOLLICLE CELLS TO MEDIATE GERMLINE-FOLLICLE CELL
 CC ADHESION. BRN HAS A ROLE IN CHORION FORMATION.
 DR EMBL; U41449; AA85211.1; -;
 DR EMBL; AL033125; CAA21833.1; -;
 DR FlyBase; FBgn000221; brn.
 DR GO; GO:0008375; F:acetylglucosaminyltransferase activity; IDA.
 DR GO; GO:0007292; P:female gamete generation; NAS.
 DR GO; GO:0008314; P:gurken receptor signaling pathway; NAS.
 DR InterPro; IPR002659; Glyco trans _1.
 DR Pfam; PF01762; Galactosyl T; 1.
 DR Developmental protein; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 325 NEUROGENIC SECRETED SIGNALING PROTEIN.
 FT CONFLICT 142 142 D -> E (IN REF. 2).
 FT CONFLICT 163 163 E -> D (IN REF. 2).
 SQ SEQUENCE 325 AA; 37619 MW; BDA96F2DE04D7ECB CRC64;

Query Match 58.8%; Score 47; DB 5; Length 325;
 Best Local Similarity 58.3%; Pred. No. 7.2;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DKWEAVITPGAF 12
 D 229 DRWPVVTAGAF 240
 |||:|||||
 |||:|||||

RESULT 5
 Q97N98
 ID Q97N98 PRELIMINARY; PRT; 383 AA.
 AC Q97N98;
 DT 01-OCT-2001 (TREMELrel. 18, Created)
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Alcohol dehydrogenase, iron-containing.
 GN SP2157.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC BAA-334 / TIGR4;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., White M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., Gwinn O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzaple E., Khouiri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickson T.J., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506 (2001).

DR EMBL; AE007504; AAK76211.1; -;
 DR PIR; B95252; B95252.
 DR TIGR; SP2157; -;
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001670; Fe-ADH.
 DR Pfam; PF00465; Fe-ADH; 1.
 DR PROSITE; PS00913; ADH_IRON_1; 1.
 DR PROSITE; PS00060; ADH_IRON_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 41224 MW; E65A0C14E951B7BF CRC64;

Query Match 57.5%; Score 46; DB 16; Length 383;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAYITPGAFDV 14
 D 199 EALVTPGAYDV 209
 |||:|||||
 |||:|||||

RESULT 6
 Q8DN25
 ID Q8DN25 PRELIMINARY; PRT; 383 AA.
 AC Q8DN25;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Probable alcohol dehydrogenase (EC 1.1.1.1).
 GN ADH2 OR SPRL963.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Alborn W.B. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAhren S.W., McHenry M., McLeaster K., Mundy C.W., Niclas T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
 RA Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717 (2001).
 DR EMBL; AE008560; AAL00765.1; -;
 DR PIR; H98116; H98116.
 DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001670; Fe-ADH.
 DR Pfam; PF00465; Fe-ADH; 1.
 DR PROSITE; PS00913; ADH_IRON_1; 1.
 DR PROSITE; PS00060; ADH_IRON_2; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 383 AA; 41154 MW; 8E181FCD5A168B4B CRC64;

Query Match 57.5%; Score 46; DB 16; Length 383;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAYITPGAFDV 14
 D 199 EALVTPGAYDV 209
 |||:|||||
 |||:|||||

RESULT 7

Q84VQ7 ID Q84VQ7 PRELIMINARY; PRT; 428 AA.
 AC Q84VQ7
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Alpha-galactosidase.
 GN GLA
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Asterioideae; Heliantheae;
 OC Helianthus.
 OC NCBI_TaxID=4232;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Kim W., Kaneko S., Park G., Tanaka H., Kusakabe I., Kobayashi H.;
 RT "Purification and characterization of a-galactosidase from sunflower
 RT seeds.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092594; BAC66445.1; -
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR002241; Glyco_hydro_27.
 DR InterPro; IPR000111; Glyco_hydro_GHD.
 DR Pfam; PF02065; Melibiase; I
 DR PRINTS; PR00740; GLYDRIASE27.
 DR PRODOM; PD002572; Glyco_hydro_GHD; 1.
 DR PROSITE; PS00512; ALPHA GALACTOSIDASE; 1.
 SQ SEQUENCE 428 AA; 47120 MW; 0D59FE7A0F20B902 CRC64;

Query Match 56.2%; Score 45; DB 10; Length 428;
 Best Local Similarity 53.8%; Pred. No. 22;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY

1 DKWEAYITPGAFD 13

|||||

266 DKMAAYAKPGGWN 278

RESULT 8

P74599 ID P74599 PRELIMINARY; PRT; 765 AA.
 AC P74599
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hypothetical protein slr1567.
 GN SLR1567.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90916; BAA18707.1; -
 DR PIR; S76795; S76795.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 765 AA; 85407 MW; 97F8DBE3D4800902 CRC64;

Query Match 56.2%; Score 45; DB 16; Length 765;
 Best Local Similarity 63.6%; Pred. No. 41;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKWEAYITPGA 11

|||||

160 DGMQIFITPGA 170

RESULT 9

Q8SDV3 ID Q8SDV3 PRELIMINARY; PRT; 169 AA.
 AC Q8SDV3
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE DUTPase.
 OS Bacteriophage phi-11.
 OC Viruses.
 OC NCBI_TaxID=12360;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Iandolo J.J., Worrell V., Roe B., Qian Y., Dorman A., Tian R., Lin S.,
 RA Jia H.;
 RT "Comparative analysis of the genomes of the temperate bacteriophages
 RT #11, #12 and #13 of Staphylococcus aureus 8325.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF424781; AAL82253.1; -
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0046080; P:dutp metabolism; IEA.
 DR InterPro; IPR008180; DecoyUTPase.
 DR InterPro; IPR008181; dUTPase_1.
 DR InterPro; IPR008182; dUTPase_2.
 DR Pfam; PF00692; dUTPase; 1.
 DR PRODOM; PD000946; dUTPase; 1.
 DR TIGRFAMs; TIGR00576; dut; 1.
 SQ SEQUENCE 169 AA; 18369 MW; 294A86E24F333DAF CRC64;

Query Match 55.0%; Score 44; DB 9; Length 169;
 Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YITPGAFDV 14

|||||

102 YITPGVFDD 110

RESULT 10

O80091 ID O80091 PRELIMINARY; PRT; 175 AA.
 AC O80091
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE DUTPase.
 OS Staphylococcus aureus bacteriophage PVL.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OC NCBI_TaxID=71366;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Kaneko J., Muramoto K., Kamio Y.;
 RT "Gene of LukP-PV-like component of Panton-Valentine leukocidin in
 RT Staphylococcus aureus P83 is linked with lukM.";
 RL Biosci. Biotechnol. Biochem. 61:1960-1962(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98332719; PubMed=9666077;
 RA Kaneko J., Kimura T., Narita S., Tomita T., Kamio Y.;
 RT "Complete nucleotide sequence and molecular characterization of the
 RT temperate staphylococcal bacteriophage phi PVL carrying Panton-
 RT Valentine leukocidin genes.";
 RL Gene 215:57-67(1998).
 DR EMBL; AB009866; BAA31926.1; -
 DR PIR; T00186; T00186.
 DR HSSP; P16088; 1DUT.

```

DR GO: GO:0016787; F-hydrolase activity; IEA.
DR GO: GO:0046080; P-dutp metabolism; IEA.
DR InterPro: IPR008180; DeoxyUTPase.
DR InterPro: IPR008181; dUTPase 1.
DR InterPro: IPR008182; dUTPase 2.
DR Pfam: PF00692; dUTPase; 1.
DR ProDom: PD000946; dUTPase_2; 1.
DR TIGRFAMs: TIGR00576; dut; 1.
SQ SEQUENCE 175 AA; 19081 MW; B93B547104EC9BA0 CRC64;

Query Match 55.0%; Score 44; DB 9; Length 175;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YITPGAFDV 14
Db 108 YITPGVFDI 116
|||||

RESULT 11
Q89UM3 PRELIMINARY; PRT; 257 AA.
ID Q89UM3;
AC Q89UM3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51).
GN PLSC OR BLR1393.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=USDA 110;
RC MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Teurukoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL: AF005940; BAC4658.1; -.
DR GO: GO:0003841; F:1-acylglycerol-3-phosphate O-acyltransferase activity; IEA.
DR GO: GO:0008415; F:acyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002123; Acyltransferase.
DR InterPro: IPR000219; RhogEF.
DR Pfam: PF01553; Acyltransferase; 1.
KW Acyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 257 AA; 28789 MW; 3C1BA53D5DAA0268 CRC64;

Query Match 55.0%; Score 44; DB 16; Length 257;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEAYITPGAFD 13
Db 83 WETFVLPGFFD 93
|||||

RESULT 12
Q9VCT5 PRELIMINARY; PRT; 354 AA.
ID Q9VCT5;
AC Q9VCT5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG4704 protein.
DE CG4704.
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svikas R., Tector C., Turner R., Weinstock G.M., Weissbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003740; AAF56070.1; -.
DR FlyBase: FBgn0039029; CG4704.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; efhand; 2.
DR PROSITE: PS00018; EF HAND; 2.
KW Calcium; Calcium-binding.
SQ SEQUENCE 354 AA; 41790 MW; 9B00F103E6EC66B1 CRC64;

Query Match 55.0%; Score 44; DB 5; Length 354;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KWEAYITPCAF 12
Db 31 KWELYMTNDF 41
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RESULT 13
Q8XCT4 PRELIMINARY; PRT; 869 AA.
ID Q8XCT4;
AC Q8XCT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative outer membrane protein, export function.
DE SFMD OR Z0689 OR ECS0594.
GN

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 22.0469 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDSEKYYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	82	92.1	98	1	US-07-942-245-37
2	82	92.1	117	3	US-08-545-809A-95
3	82	92.1	312	4	US-09-079-029-10
4	69	77.5	116	3	US-08-545-809A-134
5	67	75.3	117	3	US-09-240-274-141
6	65	73.0	17	4	US-09-383-667-11
7	65	73.0	114	3	US-08-545-809A-124
8	65	73.0	126	1	US-08-478-039-95
9	65	73.0	126	1	US-08-476-349A-95
10	64	71.9	17	4	US-09-383-667-16
11	64	71.9	17	4	US-09-383-667-18
12	64	71.9	98	1	US-08-211-202-118
13	64	71.9	116	1	US-08-211-202-141
14	64	71.9	117	3	US-08-545-809A-115
15	64	71.9	119	1	US-08-331-398A-46
16	64	71.9	119	2	US-08-331-397B-46
17	64	71.9	119	2	US-08-759-804A-46
18	64	71.9	119	3	US-09-227-693-46
19	64	71.9	120	1	US-08-211-202-135
20	64	71.9	120	1	US-07-942-245-35
21	64	71.9	123	3	US-08-983-607-38
22	64	71.9	125	1	US-08-276-852-72
23	64	71.9	125	1	US-08-276-852-73
24	64	71.9	125	1	US-08-276-852-74
25	64	71.9	125	1	US-08-276-852-75
26	64	71.9	125	1	US-08-276-852-76
27	64	71.9	125	1	US-08-276-852-77

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28      64      71.9      125      1      US-08-899-575-72      Sequence 72, Appl
29      64      71.9      125      1      US-08-899-575-73      Sequence 73, Appl
30      64      71.9      125      1      US-08-899-575-74      Sequence 74, Appl
31      64      71.9      125      1      US-08-899-575-75      Sequence 75, Appl
32      64      71.9      125      1      US-08-899-575-76      Sequence 76, Appl
33      64      71.9      125      1      US-08-899-575-77      Sequence 77, Appl
34      64      71.9      125      1      US-08-899-575-72      Sequence 72, Appl
35      64      71.9      125      1      US-08-899-575-73      Sequence 73, Appl
36      64      71.9      125      1      US-08-899-575-74      Sequence 74, Appl
37      64      71.9      125      1      US-08-899-575-75      Sequence 75, Appl
38      64      71.9      125      1      US-08-899-575-76      Sequence 76, Appl
39      64      71.9      125      1      US-08-899-575-77      Sequence 77, Appl
40      64      71.9      125      5      PCT-US95-08743-72      Sequence 72, Appl
41      64      71.9      125      5      PCT-US95-08743-73      Sequence 73, Appl
42      64      71.9      125      5      PCT-US95-08743-74      Sequence 74, Appl
43      64      71.9      125      5      PCT-US95-08743-75      Sequence 75, Appl
44      64      71.9      125      5      PCT-US95-08743-76      Sequence 76, Appl
45      64      71.9      125      5      PCT-US95-08743-77      Sequence 77, Appl

```

ALIGNMENTS

```

RESULT 1
US-07-942-245-37
; Sequence 37, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sugrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-37

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Query Match 92.1%; Score 82; DB 1; Length 98;
Best Local Similarity 88.2%; Pred.No. 5.8e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
DB 50 NIKQDSEKYYVDVK 66

```
RESULT 2
US-08-545-809A-95
; Sequence 95, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-95

Query Match 92.1%; Score 82; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDQSEKYYVDSVRG 17
Db 69 NIKDQSEKYYVDSVKG 85

RESULT 3
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match 92.1%; Score 82; DB 4; Length 312;
Best Local Similarity 88.2%; Pred. No. 2.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDQSEKYYVDSVRG 17
Db 89 NIKDQSEKYYVDSVKG 105

RESULT 4
US-08-545-809A-134
; Sequence 134, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-134
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Query Match 77.5%; Score 69; DB 3; Length 116;
Best Local Similarity 76.5%; Pred. No. 0.00013;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 68 DIKQDSEKYYVDSVKG 84

RESULT 5
US-09-240-274-141
; Sequence 141, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 141
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH17
US-09-240-274-141

Query Match 75.3%; Score 67; DB 3; Length 117;
Best Local Similarity 76.5%; Pred. No. 0.00029;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 50 NIKQDGSKNYVDSVKG 66

RESULT 6
US-09-383-667-11
; Sequence 11, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-11

Query Match 73.0%; Score 65; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.2e-05;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IKQDSEKYYADSVRG 17
Db 2 ISYDGSKKYYADSVKG 17

RESULT 7
US-08-545-809A-124
; Sequence 124, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-124

Query Match 73.0%; Score 65; DB 3; Length 114;
Best Local Similarity 70.6%; Pred. No. 0.00062;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 68 HIWNDGSQYYADSVKG 84

RESULT 8
US-08-478-039-95
; Sequence 95, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.

; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ1
; US-08-478-039-95

Query Match 73.0%; Score 65; DB 1; Length 126;
Best Local Similarity 75.0%; Pred. No. 0.00069;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKQDGSSEKYADSVRG 17
| ||| |||||:|
Db 51 ISDDGSNKYADSVKG 66

RESULT 9
US-08-476-349A-95
; Sequence 95, Application US/08/476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ1
; US-08-476-349A-95

Query Match 73.0%; Score 65; DB 1; Length 126;
Best Local Similarity 75.0%; Pred. No. 0.00069;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKQDGSSEKYADSVRG 17
| ||| |||||:|
Db 51 ISDDGSNKYADSVKG 66

RESULT 10
US-09-383-667-16
; Sequence 16, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-383-667-16

Query Match 71.9%; Score 64; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.00011;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
| ||| ||||| :
Db 2 ISYDGSNKYYADSVKG 17

RESULT 11

US-09-383-667-18
; Sequence 18, Application US/09383667
; Patent No. 6624295

; GENERAL INFORMATION:

; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies

; FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383,667

; CURRENT FILING DATE: 1999-08-26

; EARLIER APPLICATION NUMBER: US 60/098,233

; EARLIER FILING DATE: 1998-08-28

; EARLIER APPLICATION NUMBER: US 60/122,767

; EARLIER FILING DATE: 1999-03-03

; NUMBER OF SEQ ID NOS: 32

; SEQ ID NO 18

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-383-667-18

Query Match 71.9%; Score 64; DB 4; Length 17;

Best Local Similarity 75.0%; Pred. No. 0.00011;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
| ||| ||||| :
Db 2 ISYDGSNKYYADSVKG 17

RESULT 12

US-08-211-202-118

; Sequence 118, Application US/08211202

; Patent No. 5565332

; GENERAL INFORMATION:

; APPLICANT: HOOGENDOORN, Hendricus Renerus Jacobus Matteus

; APPLICANT: BAIER, Michael

; APPLICANT: JESPERS, Laurent Stephane Anne Therese

; APPLICANT: WINTER, Gregory Paul

; TITLE OF INVENTION: Production of chimeric antibodies - a

; TITLE OF INVENTION: combinatorial approach

; NUMBER OF SEQUENCES: 144

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/211,202

; FILING DATE: 23-SEP-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-118

Query Match 71.9%; Score 64; DB 1; Length 98;

Best Local Similarity 75.0%; Pred. No. 0.00078;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDGEKYYADSVRG 17
| ||| ||||| :
Db 51 ISYDGSNKYYADSVKG 66

RESULT 13

US-08-211-202-141

; Sequence 141, Application US/08211202

; Patent No. 5565332

; GENERAL INFORMATION:

; APPLICANT: HOOGENDOORN, Hendricus Renerus Jacobus Matteus

; APPLICANT: BAIER, Michael

; APPLICANT: JESPERS, Laurent Stephane Anne Therese

; APPLICANT: WINTER, Gregory Paul

; TITLE OF INVENTION: Production of chimeric antibodies - a

; TITLE OF INVENTION: combinatorial approach

; NUMBER OF SEQUENCES: 144

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/211,202

; FILING DATE: 23-SEP-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9120252.3

; FILING DATE: 23-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9120377.8

```
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-141

Query Match 71.9%; Score 64; DB 1; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.00094;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKQDSEKYYADSVRG 17
Db 51 ISYDGSNKYYADSVKG 66

RESULT 14
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 71.9%; Score 64; DB 3; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00095;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKQDSEKYYADSVRG 17
Db 70 ISYDGSNKYYADSVKG 85

RESULT 15
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Human fetal immunoglobulin
; OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 71.9%; Score 64; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00097;
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Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17

Db 51 ISYDGSNKYYADSVKG 66

Search completed: June 8, 2004, 18:31:49
Job time : 22.0469 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 13.7812 Seconds
(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	57.5	383	2 B95252	alcohol dehydrogen
2	46	57.5	383	2 H98116	probable alcohol d
3	46	57.5	484	2 T38463	probable aminotran
4	45	56.2	765	2 S76795	hypothetical prote
5	44	55.0	175	2 T00186	dutp diphosphatase
6	44	55.0	682	2 T50840	U4/U6-associated R
7	44	55.0	683	2 T50839	U4/U6 small nuclea
8	44	55.0	867	1 C64785	outer membrane ush
9	44	55.0	869	2 B90703	probable outer mem
10	44	55.0	869	2 B85553	hypothetical prote
11	43	53.8	653	2 F85620	partial fimbrial u
12	43	53.8	653	2 H90756	partial fimbrial u
13	43	53.8	866	1 C64834	probable outer mem
14	42	52.5	108	2 PH1015	Ig heavy chain v r
15	42	52.5	238	2 E90142	conserved hypotet
16	42	52.5	317	2 F87634	conserved hypotet
17	41	51.2	293	2 AF0475	LysR-family transc
18	41	51.2	312	2 E71624	rifin PFB0055c - m
19	41	51.2	378	2 T50781	alpha-galactosidas
20	41	51.2	380	2 A75328	PhoF-related prote
21	41	51.2	411	2 S07472	alpha-galactosidas
22	41	51.2	422	2 T06388	alpha-galactosidas
23	41	51.2	604	2 AB1989	hypothetical prote
24	41	51.2	684	2 H82296	c-di-GMP phosphodi
25	41	51.2	796	2 T23238	hypothetical prote
26	40	50.0	721	2 C71014	hypothetical prote
27	40	50.0	1444	2 AD1602	DNA polymerase III
28	40	50.0	1444	2 AH1239	DNA polymerase III
29	40	50.0	3158	2 T17483	peptide synthetase

ALIGNMENTS

RESULT 1

B95252

alcohol dehydrogenase, iron-containing [imported] - Streptococcus pneumoniae (strain TIG

C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: B95252

R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: B95252

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-383 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK76211.1; PID:gl4973668; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP2157

C;Superfamily: lactaldehyde reductase; lactaldehyde reductase homology

Query Match 57.5%; Score 46; DB 2; Length 383;

Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAYITPGAFDV 14

DB 199 EALVTPGAYDV 209

RESULT 2

H98116

probable alcohol dehydrogenase (EC 1.1.1.1) [imported] - Streptococcus pneumoniae (strai

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C;Accession: H98116

R;Hoekings, J.A.; Alborn Jr., M.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E

y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: H98116

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-383 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00765.1; PID:gl5459663; GSPDB:GN00174

C;Genetics:

A;Gene: adh2

C;Superfamily: lactaldehyde reductase; lactaldehyde reductase homology
C;Keywords: oxidoreductase; NAD

Query Match 57.5%; Score 46; DB 2; Length 383;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAVITPGAFDV 14
||:||||:|
Db 199 EALVTPGADV 209

RESULT 3

T38463 Probable aminotransferase (EC 2.6.1.-) - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T38463

R;Harris, D.; McDonald, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A;Reference number: Z21794

A;Accession: T38463

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-484 <HAR>

A;Cross-references: EMBL:Z69368; PIDN:CAA93294.1; GSPDB:GNO00666; SPDB:SPAC27F1.05c

A;Experimental source: strain 972h-; cosmid c27F1

C;Genetics:

A;Gene: SPDB:SPAC27F1.05c

A;Map position: 1

C;Superfamily: beta-alanine-pyruvate transaminase

C;Keywords: aminotransferase

Query Match 57.5%; Score 46; DB 2; Length 484;
Best Local Similarity 50.0%; Pred. No. 4.8;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFDV 14
||:||||:|
Db 204 EKWQIOPAPFDV 217

RESULT 4

S76795 hypothetical protein - Synecocystis sp. (strain PCC 6803)

C;Species: Synecocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S76795

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76795

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-765 <KAN>

A;Cross-references: EMBL:D90916; GB:AB001339; NID:G1653715; PIDN:BAAL8707.1; PID:d101944

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 56.2%; Score 45; DB 2; Length 765;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKWEAYITPGA 11
||:||||:|
Db 160 DGWQIFITPGA 170

RESULT 5

T00186

dUTP diphosphatase (EC 3.6.1.23) - Staphylococcus aureus phage phi PVL

N;Alternate names: dUTPase

C;Species: Staphylococcus aureus phage phi PVL

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Sep-2003

C;Accession: T00186

R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.

Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997

A;Title: Pantone-Valentine leukocidin genes in a phage-like particle isolated from mitom

A;Reference number: Z14119; MUID:98067870; PMID:9404084

A;Accession: T00186

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-175 <KAN>

A;Cross-references: EMBL:AB009866; NID:G3341907; PIDN:BAAS1926.1; PID:G3341960

C;Function:

A;Description: catalyzes the hydrolysis of dUTP to dUMP

C;Superfamily: dUTP diphosphatase

C;Keywords: hydrolase; nucleotide metabolism

Query Match 55.0%; Score 44; DB 2; Length 175;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YITPGAFDV 14
||:||||:|
Db 108 YITPGVFDI 116

RESULT 6

T50840

U4/U6-associated RNA splicing factor [imported] - human

C;Species: Homo sapiens (man)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C;Accession: T50840

R;Wang, A.; Forman-Kay, J.; Luo, Y.; Luo, M.; Chow, Y.H.; Plumb, J.; Friesen, J.D.; Tsu

Hum. Mol. Genet. 6, 2117-2126, 1997

A;Title: Identification and characterization of human genes encoding Hrp3p and Hrp4p,

A;Reference number: Z12232

A;Accession: T50840

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-682 <WAN>

A;Cross-references: EMBL:AF001947; PIDN:AAC09069.1

C;Genetics:

A;Gene: PRP3

Query Match 55.0%; Score 44; DB 2; Length 682;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14
||:||||:|
Db 390 WDSYIIPNGFDL 401

RESULT 7

T50839

U4/U6 small nuclear ribonucleoprotein hPrp3 [imported] - human

C;Species: Homo sapiens (man)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C;Accession: T50839

R;Horowitz, D.S.; Kobayashi, R.; Krainer, A.R.

RNA 3, 1374-1387, 1997

A;Title: A new cyclophilin and the human homologues of yeast Prp3 and Prp4 form a compl

A;Reference number: Z12233

A;Accession: T50839

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-683 <HOR>

A;Cross-references: EMBL:AF016370; PIDN:AAC51926.1

C;Genetics:

A;Gene: hPrp3

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 7.875 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	57.5	484	1 YAV5_SCHPO	Q10174 schizosacch
2	44	55.0	669	1 PPLB_STRCO	Q9ky04 streptomyce
3	44	55.0	683	1 PRP3_HUMAN	O43395 homo sapien
4	44	55.0	683	1 PRP3_MOUSE	Q922ul mus musculu
5	44	55.0	867	1 SFMD_ECOLI	P77468 escherichia
6	43	53.8	333	1 DCUP_THEAC	Q9h1b9 thermoplasma
7	43	53.8	866	1 YCBS_ECOLI	P75857 escherichia
8	41	51.2	293	1 HDPR_YERPE	Q8zaa7 versinia pe
9	41	51.2	378	1 AGAL_COPAR	Q42656 coffea arab
10	41	51.2	411	1 AGAL_CVATE	P14749 cyanopsis t
11	41	51.2	796	1 YRS7_CABEL	Q10003 caenorhabdi
12	40	50.0	870	1 FIMD_SALTY	P37924 salmonella
13	40	50.0	1444	1 DP03_LISIN	Q92c34 listeria in
14	40	50.0	1444	1 DP03_LISMO	Q8y7g1 listeria mo
15	39	48.8	283	1 PHLC_BACCE	P03598 bacillus ce
16	39	48.8	283	1 PHLD_BACCE	P33376 bacillus ce
17	39	48.8	366	1 QUBA_CAUCR	Q9a7y2 caulobacter
18	39	48.8	595	1 VPI_BPCHP	P19192 bacterioph
19	39	48.8	1041	1 SYI_MYCTU	Q10765 mycobacteri
20	38	47.5	66	1 RPON_SULTO	Q96yW4 sulfolobus
21	38	47.5	71	1 RPBX_SCHPO	O13877 schizosacch
22	38	47.5	109	1 Y030_MYCTU	P71600 mycobacteri
23	38	47.5	208	1 RS3A_SULSO	Q9uxd4 sulfolobus
24	38	47.5	258	1 SSRA_ARATH	P45434 arabidopsis
25	38	47.5	422	1 PYRC_HALNI	Q9hmb9 halobacteri
26	38	47.5	756	1 MAC1_SCHPO	P10268 schizosacch
27	37.5	46.9	599	1 RPPO_PEAUV	P29154 pea enation
28	37	46.2	66	1 RPON_SULSO	Q98028 sulfolobus
29	37	46.2	70	1 RPBX_YEAST	P22139 saccharomyc
30	37	46.2	225	1 MTRD_METKA	O32864 methanopyru
31	37	46.2	329	1 XYNA_THETA	P23360 thermococcus
32	37	46.2	341	1 QUBA_CLOPE	Q8xj15 clostridium
33	37	46.2	463	1 Y030_NPVAC	P41434 autographa

RESULT 1

ID	YAV5_SCHPO	STANDARD;	PRT;	484 AA.
AC	Q10174;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Probable aminotransferase C27F1.05c (EC 2.6.1.-).			
GN	SPAC27F1.05C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,			
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,			
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,			
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,			
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;			
RT	"The genome sequence of Schizosaccharomyces pombe.";			
RL	Nature 415:871-880(2002).			
CC	-!- COPACITOR: Pyridoxal phosphate (Potential).			
CC	-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent			
CC	aminotransferases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			

ALIGNMENTS

DR EMBL; Z69368; CAA93294.1; --
 DR PIR; T38463; T38463.
 DR HSP; P12995; IQJ3.
 DR GeneB SPombe; SPAC27F1.05c; --
 DR InterPro; IPR005814; Aminotrans_3.
 DR Pfam; PF00202; aminotran 3; 1.
 DR PROSITE; PS00600; AA_TRANSFER_CLASS 3; 1.
 KW Hypothetical protein; Transferase; Aminotransferase;
 KW Pyridoxal phosphate.
 FT BINDING 305 305 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 484 AA; 53190 MW; 5DB9A13BA33C497 CRC64;
 Query Match 57.5%; Score 46; DB 1; Length 484;
 Best Local Similarity 50.08; Pred. No. 3;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DKWEAYITPGAFDV 14
 Db 204 EKWKYQSPAPFDV 217
 RESULT 2
 PP1B STROCO
 ID PP1B STROCO STANDARD; PRT; 669 AA.
 AC Q9KY04; O70012;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative glucanohydrolase pepIB (EC 3.2.1.-).
 GN PEP1B OR PEP1II OR PEP1 OR SC07335 OR SC4G10.14C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OC NCBI_Taxid=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=20279210; PubMed=10821190;
 RA Schneider D., Bruton C.J., Chater K.F.;
 RT "Duplicated gene clusters suggest an interplay of glycogen and
 RT trehalose metabolism during sequential stages of aerial mycelium
 RT development in Streptomyces coelicolor A3(2).";
 RL Mol. Gen. Genet. 263:543-553(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M45;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,
 RA Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor J.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -!- FUNCTION: Could convert glycogen into units that may be
 CC subsequently converted into trehalose.
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases. GlGE
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ001206; CAA04606.1; --

DR EMBL; AL939131; CAB92881.1; --
 DR InterPro; IPR006047; Alpha amyl cat.
 DR Pfam; PF00128; alpha-amylase; 1-
 KW Hydrolase; Glycosidase; Complete proteome.
 FT CONFLICT 632 632 W -> R (IN REF. 1).
 SQ SEQUENCE 669 AA; 74143 MW; 5463E0134CD66518 CRC64;
 Query Match 55.0%; Score 44; DB 1; Length 669;
 Best Local Similarity 63.6%; Pred. No. 8.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 DKWEAYITPGCA 11
 Db 77 DRWGATVTPGA 87
 RESULT 3
 PRP3 HUMAN
 ID PRP3 HUMAN STANDARD; PRT; 683 AA.
 AC O43395; O43446;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE U4/U6 small nuclear ribonucleoprotein Prp3 (Pre-mRNA splicing factor
 DE 3) (U4/U6 snRNP 90 kDa protein) (hPrp3).
 GN PRP3 OR HPRP3 OR PRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH PRPF4 AND
 RP U4/U5/U6 SNRNPs.
 RX MEDLINE=97472464; PubMed=9328476;
 RA Wang A., Forman-Kay J., Luo Y., Luo M., Chow Y.-H., Plumb J.,
 RA Friesen J.D., Tsui L.-C., Heng H.H.Q., Woolford J.L. Jr., Hu J.;
 RT "Identification and characterization of human genes encoding Hprp3
 RT and Hprp4, interacting components of the spliceosome.";
 RL Hum. Mol. Genet. 6:2117-2126(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 93-101; 253-267; 351-361;
 RP 409-428 AND 560-576, AND INTERACTION WITH PPIH; PRPF4 AND U4/U6
 RP SNRNPs.
 RC TISSUE=Neuroepithelium;
 RX MEDLINE=98067393; PubMed=9404889;
 RA Horowitz D.S., Kobayashi R., Krainer A.R.;
 RT "A new cyclophilin and the human homologues of yeast Prp3 and Prp4
 RT form a complex associated with U4/U6 snRNPs.";
 RL RNA 3:1374-1387(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Eye, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez A., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]
 RP VARIANT RP18 MET-494, AND TISSUE SPECIFICITY.
 RX MEDLINE=21634624; PubMed=11773002;
 RA Chakarova C.F., Hims M.M., Bolz H., Abu-Safieh L., Patel R.J.,
 RA Papaioannou M.G., Inglehearn C.F., Keen T.J., Willis C., Moore A.T.,
 RA Rosenberg T., Webster A.R., Bird A.C., Gal A., Hunt D., Vithana E.N.,
 RA Bhattacharya S.S.;
 RT "Mutations in HRPp3, a third member of pre-mRNA splicing factor
 RT genes, implicated in autosomal dominant retinitis pigmentosa.";
 RL Hum. Mol. Genet. 11:87-92(2002).
 [5]
 RN VARIANT RP18 MET-494.
 RX MEDLINE=22600169; PubMed=12714658;
 RA Martinez-Glamo M., Gamundi M.J., Hernan I., Maseras M., Milla E.,
 RA Ayuso C., Garcia-Sandoval B., Beneyto M., Vilela C., Baiget M.,
 RA Antinolo G., Carballo M.;
 RT "Mutations in the pre-mRNA splicing-factor genes PRPF3, PRPF8, and
 RT PRPF31 in Spanish families with autosomal dominant retinitis
 RT pigmentosa";
 RL Invest. Ophthalmol. Vis. Sci. 44:2171-2177(2003).
 CC -!- FUNCTION: Participates in pre-mRNA splicing. May play a role in
 CC the assembly of the U4/U5/U6 tri-snRNP complex.
 CC -!- SUBUNIT: Interacts directly with snRNP4. Part of a heteromeric
 CC complex containing PRPF1, HRPp3 and PRPF4 that is stable in the
 CC absence of RNA. This complex interacts with the U4/U5/U6 tri-snRNP
 CC complex.
 CC -!- SUBCELLULAR LOCATION: Nuclear, in nuclear speckles. Co-localizes
 CC with spliceosomal snRNPs.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O43395-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O43395-2; Sequence=VSP_008326;
 CC -!- TISSUE SPECIFICITY: Highly expressed in retina, liver, kidney and
 CC blood. Detected at lower levels in heart and brain.
 CC -!- DISEASE: Defects in PRPF3 are a cause of retinitis pigmentosa 18
 CC (RP18) [MIM:601414]. RP18 is a form of autosomal dominant
 CC retinitis pigmentosa (adRP). This is the most common form of the
 CC inherited retinal dystrophies. It is characterized by a
 CC progressive degeneration of the peripheral retina, leading to
 CC night blindness and loss of peripheral visual field.
 CC -!- SIMILARITY: Contains 1 PVI domain.
 CC
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 CC
 CC EMBL; AF001947; AAC09069.1; -;
 CC EMBL; AF016370; AAC51926.1; -;
 CC EMBL; BC000184; AAH00184.1; -;
 CC EMBL; BC001954; AAH01954.1; -;
 CC PIR; T50839; T50839.
 CC PIR; T50840; T50840.
 CC MIM; 607301; -;
 CC MIM; 601414; -;
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0008248; F:pre-mRNA splicing factor activity; TAS.
 CC GO; GO:0006397; F:mRNA processing; TAS.
 CC GO; GO:0006371; F:mRNA splicing; TAS.
 CC InterPro; IPR002483; PVI.
 CC Pfam; PF01480; PVI; 1.
 CC SMART; SM00311; PVI; 1.
 CC Vision; mRNA processing; mRNA splicing; Nuclear protein; Spliceosome;
 CC Alternative splicing; Disease mutation; Retinitis pigmentosa.
 KW DOMAIN 8 79 PVI.
 FT DOMAIN 579 584 POLY-VAL.
 FT VARSPLIC 587 587 Missing (in isoform 2).
 FT /FTID=VSP_008326.

FT VARIANT 494 494 T -> M (in RP18).
 FT /FTID=VAR_016877.
 FT CONFLICT 142 142 I -> T (IN REF. 1).
 FT CONFLICT 273 274 EL -> SV (IN REF. 1).
 SQ SEQUENCE 683 AA; 77528 MW; 4AA6AA4C99110284 CRC64;
 Query Match 55.0%; Score 44; DB 1; Length 683;
 Best Local Similarity 50.0%; Pred. No. 9.1;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 3 WEAYITPGAFDV 14
 Db 390 WDSYIIPNGFDL 401
 ID PRP3 MOUSE STANDARD; PRT; 683 AA.
 AC Q922U1; Q9D6C6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE U4/U6 small nuclear ribonucleoprotein Prp3 (Pre-mRNA splicing factor
 DE 3).
 GN PRPF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOB; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bragdi T.A., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 CC -1- FUNCTION: Participates in pre-mRNA splicing. May play a role in
 CC the assembly of the U4/U5/U6 tri-snRNP complex (By similarity).
 CC -1- SUBUNIT: Interacts directly with PRPF4. Part of a heteromeric
 CC complex containing PRPH, HPRP3 and PRPF4 that is stable in the
 CC absence of RNA. This complex interacts with the U4/U5/U6 tri-snRNP
 CC complex (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear, in nuclear speckles. Co-localizes
 CC with spliceosomal snRNPs (By similarity).
 CC -1- SIMILARITY: Contains 1 PVI domain.
 CC
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 CC
 CC EMBL; AK014398; BAB29324.1; -;
 CC DR EMBL; AK088194; BAC40202.1; -;
 CC DR EMBL; BC006782; AAB06782.1; -;
 CC DR MGD; MGI:1918017; 3632413F13Rik.
 CC DR InterPro; IPR002483; PVI.
 CC DR Pfam; PF01480; PVI; 1.
 CC DR SMART; SM00311; PVI; 1.
 CC KW mRNA processing; mRNA splicing; Nuclear protein; Spliceosome.
 FT DOMAIN 8 79 PVI
 FT DOMAIN 579 584 POLY-VAL.
 FT CONFLICT 78 78 H -> L (IN REF. 1; BAB29324).
 SQ SEQUENCE 683 AA; 77454 MW; 988219CF88E0EC4A CRC64;
 Query Match 55.0%; Score 44; DB 1; Length 683;
 Best Local Similarity 50.0%; Pred. No. 9.1;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WEAYITPGAFDV 14
 Db 390 WDSYIENGFDL 401
 RESULT 5
 SFMD ECOLI
 ID SFMD ECOLI STANDARD; PRT; 867 AA.
 AC P77468; P77133;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 4L, Last annotation update)
 DE Outer membrane usher protein sfmd precursor.
 GN SFMD OR B0532.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OK NCBI_TaxID=562;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12 / MGI:655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Riegley J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

MAU B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
 RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RA "Sequence of minutes 4-25 of Escherichia coli.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF SFMA FIMBRIAL
 CC SUBUNITS ACROSS THE OUTER MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the fimbrial export usher family.
 CC
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 CC
 CC EMBL; AE000159; AAC73634.1; -;
 CC DR EMBL; U82598; AAB40730.1; -;
 CC DR EMBL; U82664; AAB40285.1; -;
 CC DR PIR; C64785; C64785.
 CC DR EcoGene; EGI3883; sfmd.
 CC DR InterPro; IPR000015; Fimb_usher.
 CC DR Pfam; PF00577; Usher; 1.
 CC DR PROSITE; PS01151; FIMBRIAL USHER; 1.
 CC KW Outer membrane; Transmembrane; Fimbria; Transport; Signal;
 KW Complete proteome.
 FT SIGNAL 1 35 POTENTIAL.
 FT CHAIN 36 867 OUTER MEMBRANE USHER PROTEIN SFMD.
 FT DISULFID 840 862 POTENTIAL.
 SQ SEQUENCE 867 AA; 95677 MW; DF8591D0E6C4205A CRC64;
 Query Match 55.0%; Score 44; DB 1; Length 867;
 Best Local Similarity 41.7%; Pred. No. 11;
 Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WEAYITPGAFDV 14
 Db 309 YQSYVSPGAFEI 320
 RESULT 6
 DCUP THEAC
 ID DCUP THEAC STANDARD; PRT; 333 AA.
 AC Q9HLB9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 4L, Last annotation update)
 DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
 GN HEME OR TA0310.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OK NCBI_TaxID=2303;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RA "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513 (2000).
 CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
 CC CO(2).
 CC -1- PATHWAY: Porphyrin biosynthesis.


```

CC CC      -!- SIMILARITY: Belongs to the fimbrial export usher family.
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CC CC      EMBL; AE000196; AAC74026.1; -.
CC CC      EMBL; D90732; BAA35695.1; -.
CC CC      PIR; C64834; C64834.
CC CC      EcoGene; EGI3711; ycbS.
CC CC      InterPro; IPR000015; Fimb_usher.
CC CC      Pfam; PF00577; Usher; 1.
CC CC      PROSITE; PS01151; FIMBRIAL USHER; 1.
CC CC      KW Hypothetical protein; Outer membrane; Transmembrane; Fimbria;
CC CC      KW Transport; Signal; Complete proteome.
CC CC      SIGNAL 1 35 POTENTIAL.
CC CC      CHAIN 36 866 HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN
CC CC      FT FT FT YCB.
CC CC      SO SEQUENCE 866 AA: 95241 MW: 0004DCSE9F1F5796 CRC64:

```

Query Match	53.8%;	Score 43;	DB 1;	Length 866;
Best Local Similarity	41.7%;	Pred. NO. 17;		
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			Indels	0;
			Gaps	0;

QY 3 WEAYITPGAFDV 14
: : : : : :
308 YOTYVSPGAFEI 319
Db

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RESULT 8
HDRF_YERPE
ID ID HDRF_YERPE STANDARD; PRT; 293 AA.
AC Q8ZAA7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DE HTH-type transcriptional regulator hdrf (H-NS-dependent flhdc
DE DE regulator).
DE DE Hdrf OR YP03904 OR Y0332.
OS Yersinia pestis.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=632;
[1]_
RN RN SEQUENCE FROM N.A.
RP STRAIN=CO-92 / Biovar Orientalis;
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague."
RT Nature 413:523-527(2001).
RL [2]
RN RN SEQUENCE FROM N.A.
RP STRAIN=KIM5 / Biovar Mediaevalis;
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Yersinia pestis KIM."
RT J. Bacteriol. 184:4601-4611(2002).
RL J. Bacteriol. 184:4601-4611(2002).
CC -!- FUNCTION: Negatively regulates the transcription of the flagellar
CC master operon flhdc by binding to the upstream region of the

```

```

CC operon (By similarity).
CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
CC -----
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CC -----
CC EMBL; AJ414159; CAC93370.1; -.
CC EMBL; AE013633; AAM83923.1; -.
CC PIR; AF0475; AF0475.
CC HAMAP; MF_01233; -.
CC InterPro; IPR000847; HTH_LysR.
CC InterPro; IPR005119; LysR_subst.
CC Pfam; PF00126; HTH_1; 1.
CC Pfam; PF03466; LysR_substrate; 1.
CC PRINTS; PR00039; HTHLYSR.
CC PROSITE; PS50931; HTH_LYSR; 1.
CC Transcription regulation; Repressor; DNA-binding; Complete proteome.
CC DOMAIN 1 58 HTH_LYSR-TYPE.
CC FT DNA BIND 18 37 H-T-H MOTIF (BY SIMILARITY).
CC SQ SEQUENCE 293 AA; 33932 MW; P5EC224D0D7E71EB CRC64;

Query Match 51.2%; Score 41; DB 1; Length 293;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WEAYITP 9
Db 100 WEAYITP 106

RESULT 9
AGAL COFAR STANDARD; PRT; 378 AA.
AC Q42656;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-galactosidase precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-
DE galactoside galactohydrolase).
OS Coffea arabica (Coffee).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Gentianales; Rubiaceae; Ixoroideae; Coffeae; Coffea.
OC NCBI_TaxID=13443;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-34; 215-231 AND 373-378.
RP TISSUE=Seed;
RC MEDLINE=94193002; PubMed=8144030;
RA Zhu A., Goldstein J.;
RT "Cloning and functional expression of a cDNA encoding coffee bean
RT alpha-galactosidase."
RL Gene 140:227-231(1994).
CC -1- FUNCTION: Preferentially cleaves alpha-1,3 and alpha-1,4 glycoside
CC linkages. Involved in the hydrolysis of the galactomannan, it
CC splits alpha-linked galactose moieties. It is particularly
CC suitable for the hydrolysis of guar gum to a gum with improved
CC gelling properties. Can cleave terminal alpha-1,3-linked galactose
CC residues responsible for blood group B specificity from the
CC surface of erythrocytes thereby converting these cells
CC serologically to group O.
CC -1- CATALYTIC ACTIVITY: Melibiose + H(2)O = galactose + glucose.
CC -1- SIMILARITY: Belongs to family 27 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L27992; AAA33022.1; -.
CC PIR; T50781; T50781.
CC InterPro; IPR002241; Glyco_hydro_27.
CC InterPro; IPR000111; Glyco_hydro_GHD.
CC Pfam; PF02065; Melibiase; 1.
CC PRINTS; PR00740; GLHYDRLASE27.
CC PRODOM; PD002572; Glyco_hydro_GHD; 1.
CC PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
CC KW Hydrolase; Glycosidase; Signal.
CC FT CHAIN 1 15
CC FT ACT SITE 16 378 ALPHA-GALACTOSIDASE.
CC FT ACT SITE 287 287 POTENTIAL.
CC SQ SEQUENCE 378 AA; 41310 MW; 9FC7610BFD760AE3 CRC64;

Query Match 51.2%; Score 41; DB 1; Length 378;
Best Local Similarity 46.2%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DKWEAYITRGAFD 13
Db 216 DKWEAYITRGAFD 228

RESULT 10
AGAL CYATE STANDARD; PRT; 411 AA.
AC P14749;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1997 (Rel. 35, Last annotation update)
DE Alpha-galactosidase precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-
DE galactoside galactohydrolase).
OS Cyamopsis tetragonoloba (Guar) (Cluster bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Indigoferae;
OC Cyamopsis.
OC NCBI_TaxID=3832;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Alleurone;
RC MEDLINE=91370836; PubMed=2577496;
RX Overbeek N., Fellinger A.J., Toonen M.Y., van Wassenaar D.,
RA Verrips C.T.;
RA "Cloning and nucleotide sequence of the alpha-galactosidase cDNA from
RA Cyamopsis tetragonoloba (guar).";
RT Plant Mol. Biol. 13:541-550(1989).
RN [2]
RP SEQUENCE OF 48-57 AND 172-178.
RP TISSUE=Seed;
RC Hughes S.G., Overbeek N., Robinson S., Pollock K., Smeets F.L.M.;
RA "Messenger RNA from isolated aleurone cells directs the synthesis of
RA an alpha-galactosidase found in the endosperm during germination of
RA guar (Cyamopsis tetragonoloba) seed."
RL Plant Mol. Biol. 11:783-789(1988).
CC -1- FUNCTION: Involved in the hydrolysis of the galactomannan, it
CC splits alpha-linked galactose moieties. It is particularly
CC suitable for the hydrolysis of guar gum to a gum with improved
CC gelling properties. Preferentially cleaves alpha-1,6 glycoside
CC linkages.
CC -1- CATALYTIC ACTIVITY: Melibiose + H(2)O = galactose + glucose.
CC -1- SIMILARITY: Belongs to family 27 of glycosyl hydrolases.
CC -----
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CC EMBL; X14619; CAA32772.1; -.
DR PIR; S07472; S07472.
DR InterPro; IPR002241; Glyco_hydro_27.
DR InterPro; IPR001111; Glyco_hydro_GHD.
DR Pfam; PF02065; Melibiase; 1.
DR PRINTS; PR00740; GLHYDLASE27.
DR PRODOM; PD002572; Glyco_hydro_GHD; 1.
DR PROSITE; PS00512; ALPHA GALACTOSIDASE; 1.
KW Hydrolase; Glycosidase; Signal; Glycoprotein.
FT SIGNAL 1 24
FT PROPEP 25 47
FT CHAIN 48 411
FT CARBOHYD 32 32
FT CARBOHYD 145 145
FT CARBOHYD 352 352
FT ACT SITE 319 319
FT SEQUENCE 411 AA; 51135 MW; 5B1715858D1AB11E CRC64;
SQ
Query Match 51.2%; Score 41; DB 1; Length 411;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFD 13
DB 248 DKWASYAGPGGWN 260

RESULT 11
YRS7 CAEEL
ID YRS7 CAEEL STANDARD; PRT; 796 AA.
AC Q10003;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hypothetical 90.8 kDa protein T05H10.7 in chromosome II.
GN T05H10.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Lightning J., Thomas K.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; 247811; CAA87788.1; -.
DR EMBL; 247812; CAA87788.1; JOINED.
DR EMBL; 247812; CAA87796.1; -.
DR EMBL; 247811; CAA87796.1; JOINED.
DR PIR; T23238; T23238.
DR WormPep; T05H10.7; CH03637.
DR InterPro; IPR002044; CHD 4.
DR InterPro; IPR004129; GDFD.
DR Pfam; PF03009; GDFD; 1.
KW Hypothetical protein.
FT DOMAIN 38 42
FT DOMAIN 67 70
FT DOMAIN 524 527
FT SEQUENCE 796 AA; 90831 MW; 7BDFF8E0A4D2AA9F1 CRC64;
SQ
Query Match 51.2%; Score 41; DB 1; Length 796;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CC EMBL; X14619; CAA32772.1; -.
DR PIR; S07472; S07472.
DR InterPro; IPR002241; Glyco_hydro_27.
DR InterPro; IPR001111; Glyco_hydro_GHD.
DR Pfam; PF02065; Melibiase; 1.
DR PRINTS; PR00740; GLHYDLASE27.
DR PRODOM; PD002572; Glyco_hydro_GHD; 1.
DR PROSITE; PS00512; ALPHA GALACTOSIDASE; 1.
KW Hydrolase; Glycosidase; Signal; Glycoprotein.
FT SIGNAL 1 24
FT PROPEP 25 47
FT CHAIN 48 411
FT CARBOHYD 32 32
FT CARBOHYD 145 145
FT CARBOHYD 352 352
FT ACT SITE 319 319
FT SEQUENCE 411 AA; 51135 MW; 5B1715858D1AB11E CRC64;
SQ
Query Match 51.2%; Score 41; DB 1; Length 411;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DKWEAYITPGAFD 13
DB 248 DKWASYAGPGGWN 260

RESULT 12
FIMD SALTY
ID FIMD SALTY STANDARD; PRT; 870 AA.
AC P37924;
DT 01-OCT-1994 (Rel. 30, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane usher protein fimd precursor.
GN FIMD OR STM0546.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]_TaxID=602;
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dente M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856 (2001).
CC
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF FIMA FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (BY similarity).
CC -!- SIMILARITY: Belongs to the fimbrial export usher family.
CC
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CC
CC EMBL; L19338; AAA75419.1; -.
DR EMBL; AE008721; AAL19500.1; -.
DR StyGene; SG10505; fimd.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW Outer membrane, Transmembrane, Fimbria; Transport; Signal;
KW Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 870
FT DISULFID 843 865
FT CONFLICT 265 265
FT CONFLICT 361 361
FT SEQUENCE 870 AA; 95127 MW; A6B00139F654A29 CRC64;
SQ
Query Match 50.0%; Score 40; DB 1; Length 870;
Best Local Similarity 41.7%; Pred. No. 55;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 WEAYITPGAFDV 14
DB 310 QQSYVSPGAFAL 321
```

Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DKWEAYITPG 10
|:|:|:|:|
Db 460 DKFEAFITPG 469

RESULT 14

ID DPO3_LISMO STANDARD; PRT; 1444 AA.
AC Q8Y7GI;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (POLIII).
GN POLC OR LMO1320.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
BA Quero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of *Listeria species*."
RL Science 294:849-852 (2001).
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-C family. PolC
CC subfamily.
CC
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CC
CC EMBL; AL591978; CAC99198.1; -.
DR PIR; AH1239; AH1239.
DR Listlist; LMO1320; -.
DR HAMAP; MF_00356; -; 1.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004013; PHP C.
DR InterPro; IPR003141; PHP N.
DR InterPro; IPR006308; PolC_gram_pos.
DR InterPro; IPR004365; trna_anti.
DR Pfam; PF00929; Exonuclease; 1.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR Pfam; PF01336; trna_anti; 1.
DR Pfam; PF01336; trna_anti; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIICAC; 1.
DR TIGRFAMS; TIGR00573; dnaq; 1.
DR TIGRFAMS; TIGR00573; dnaq; 1.
DR TIGRFAMS; TIGR01405; polC_gram_pos; 1.

RESULT 13

ID DPO3_LISIN STANDARD; PRT; 1444 AA.
AC Q2C34;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (POLIII).
GN POLC OR LIN1357.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
BA Quero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of *Listeria species*."
RL Science 294:849-852 (2001).
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-C family. PolC
CC subfamily.
CC
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CC
CC EMBL; AL596168; CAC96588.1; -.
DR PIR; AD1602; AD1602.
DR Listlist; LIN1357; -.
DR HAMAP; MF_00356; -; 1.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004013; PHP C.
DR InterPro; IPR003141; PHP N.
DR InterPro; IPR006308; PolC_gram_pos.
DR InterPro; IPR004365; trna_anti.
DR Pfam; PF00929; Exonuclease; 1.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR Pfam; PF01336; trna_anti; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIICAC; 1.
DR TIGRFAMS; TIGR00573; dnaq; 1.
DR TIGRFAMS; TIGR01405; polC_gram_pos; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Nuclease; Exonuclease; Complete protease.
FT DOMAIN 428 592 EXONUCLEASE.
SQ SEQUENCE 1444 AA; 162904 MW; D4E78BCA39D9AD95 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 1444;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKWEAYITP 9
||| | :||
Db 248 DKWRAEVTP 256

Search completed: June 8, 2004, 18:56:14
Job time : 9.875 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 56.5781 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89
Sequence: 1 NIKQDSEKYYADSVRG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues 1155919

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	17	9	US-09-832-312-62
2	89	100.0	17	11	US-09-829-495-62
3	82	92.1	17	15	US-10-173-551-16
4	82	92.1	98	12	US-10-453-638-55
5	82	92.1	98	12	US-10-029-926B-85
6	82	92.1	98	14	US-10-194-975-15
7	82	92.1	98	15	US-10-308-817-55
8	82	92.1	98	15	US-10-032-037B-85
9	82	92.1	98	15	US-10-029-988B-85
10	82	92.1	98	15	US-10-032-423A-85
11	82	92.1	118	15	US-10-173-551-14
12	82	92.1	120	10	US-09-995-529-8
13	82	92.1	120	12	US-09-995-529-8
14	82	92.1	134	9	US-09-811-737-3
15	82	92.1	241	10	US-09-880-748-1889

16	82	92.1	241	12	US-10-293-418-1889	Sequence 1889, Ap
17	82	92.1	247	10	US-09-880-748-1470	Sequence 1470, Ap
18	82	92.1	247	12	US-10-293-418-1470	Sequence 1470, Ap
19	82	92.1	247	14	US-10-322-673-48	Sequence 48, Appl
20	82	92.1	251	10	US-09-880-748-1594	Sequence 1594, Ap
21	82	92.1	251	12	US-10-293-418-1594	Sequence 1594, Ap
22	82	92.1	253	10	US-09-880-748-1003	Sequence 1003, Ap
23	82	92.1	253	10	US-09-880-748-1007	Sequence 1007, Ap
24	82	92.1	253	12	US-10-293-418-1003	Sequence 1003, Ap
25	82	92.1	253	12	US-10-293-418-1007	Sequence 1007, Ap
26	82	92.1	262	9	US-09-811-737-19	Sequence 19, Appl
27	82	92.1	312	13	US-10-052-798-10	Sequence 10, Appl
28	82	92.1	312	14	US-10-288-917-10	Sequence 10, Appl
29	82	92.1	312	15	US-10-423-448-10	Sequence 10, Appl
30	75	84.3	17	10	US-09-977-797A-98	Sequence 98, Appl
31	75	84.3	133	15	US-10-364-743-78	Sequence 78, Appl
32	75	84.3	250	10	US-09-880-748-1319	Sequence 1319, Ap
33	75	84.3	250	10	US-09-880-748-1486	Sequence 1486, Ap
34	75	84.3	250	12	US-10-293-418-1319	Sequence 1319, Ap
35	75	84.3	250	12	US-10-293-418-1486	Sequence 1486, Ap
36	75	84.3	251	12	US-10-293-418-3245	Sequence 3245, Ap
37	74	83.1	121	15	US-10-364-743-79	Sequence 79, Appl
38	74	83.1	254	10	US-09-880-748-1511	Sequence 1511, Ap
39	74	83.1	254	12	US-10-293-418-1511	Sequence 1511, Ap
40	73	82.0	17	10	US-09-977-797A-110	Sequence 110, App
41	73	82.0	254	10	US-09-880-748-1350	Sequence 1350, Ap
42	73	82.0	254	12	US-10-293-418-1350	Sequence 1350, Ap
43	70	78.7	17	15	US-10-338-366-16	Sequence 16, Appl
44	70	78.7	116	15	US-10-338-366-2	Sequence 2, Appli
45	69	77.5	124	14	US-10-010-729-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

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US-09-832-312-62
; Sequence 62, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USBS THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-62
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Query Match 100.0%; Score 89; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17

DB 1 NIKQDSEKYYADSVRG 17

RESULT 2

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US-09-829-495-62
; Sequence 62, Application US/09829495
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; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevial J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-829-495-62

Query Match      100.0%; Score 89; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NIKDGSSEKYYADSVRG 17
      |||||
Db      1 NIKDGSSEKYYADSVRG 17

RESULT 3
US-10-173-551-16
; Sequence 16, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855-2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-173-551-16

Query Match      92.1%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NIKDGSSEKYYADSVRG 17
      |||||
Db      1 NIKDGSSEKYYADSVRG 17

RESULT 4
US-10-453-698-55
; Sequence 55, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698

; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevial J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-829-495-62

Query Match      92.1%; Score 82; DB 12; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NIKDGSSEKYYADSVRG 17
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Db      50 NIKDGSSEKYYVDSVKG 66

RESULT 5
US-10-029-926B-85
; Sequence 85, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-926B-85

Query Match      92.1%; Score 82; DB 12; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NIKDGSSEKYYADSVRG 17
      |||||
Db      50 NIKDGSSEKYYVDSVKG 66

RESULT 6
US-10-194-975-15
; Sequence 15, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-194-975-15

Query Match      92.1%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NIKDGSSEKYYADSVRG 17
      |||||
Db      1 NIKDGSSEKYYVDSVKG 17
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Db 50 NIKQDSEKYYVDSVKG 66

RESULT 7

US-10-308-817-55

; Sequence 55, Application US/10308817

; Publication No. US20030219861A1

; GENERAL INFORMATION:

; APPLICANT: Rother, Russell

; TITLE OF INVENTION: HYBRID ANTIBODIES

; FILE REFERENCE: 1087-37

; CURRENT APPLICATION NUMBER: US/10/308,817

; CURRENT FILING DATE: 2002-12-03

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 55

; LENGTH: 98

; TYPE: PRT

; ORGANISM: human

US-10-308-817-55

Query Match 92.1%; Score 82; DB 15; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.1e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17

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Db 50 NIKQDSEKYYVDSVKG 66

RESULT 8

US-10-032-037B-85

; Sequence 85, Application US/10032037B

; Publication No. US20040001822A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE REFERENCE: 10793/44

; CURRENT APPLICATION NUMBER: US/10/032,037B

; CURRENT FILING DATE: 2001-12-31

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 85

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-037B-85

Query Match 92.1%; Score 82; DB 15; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.1e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17

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Db 50 NIKQDSEKYYVDSVKG 66

RESULT 9

US-10-029-988B-85

; Sequence 85, Application US/10029988B

; Publication No. US20040001839A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE REFERENCE: 10793/46

; CURRENT APPLICATION NUMBER: US/10/029,988B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

US-10-029-988B-85

Query Match 92.1%; Score 82; DB 15; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.1e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17

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Db 50 NIKQDSEKYYVDSVKG 66

RESULT 10

US-10-032-423A-85

; Sequence 85, Application US/10032423A

; Publication No. US20040002450A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE REFERENCE: 10793/45

; CURRENT APPLICATION NUMBER: US/10/032,423A

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; PRIOR FILING DATE: 12/29/2000

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 85

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-423A-85

Query Match 92.1%; Score 82; DB 15; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.1e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17

|||||

Db 50 NIKQDSEKYYVDSVKG 66

RESULT 11

US-10-173-551-14

; Sequence 14, Application US/10173551

; Publication No. US20030232387A1

; GENERAL INFORMATION:

; APPLICANT: Lu, Chafen

; TITLE OF INVENTION: Antibodies that bind alphaE Integrin

; FILE REFERENCE: 1855.2025-000

; CURRENT APPLICATION NUMBER: US/10/173,551

; CURRENT FILING DATE: 2002-06-14

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (31)...(35)

; OTHER INFORMATION: CDR1

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (50)...(66)

; OTHER INFORMATION: CDR2

; FEATURE:

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; NAME/KEY: SITE
; LOCATION: (99)...(107)
; OTHER INFORMATION: CDR3
US-10-173-551-14

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Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDGSSEKYYADSVRG 17
Db 50 NIKDGSSEKYYVDSVKG 66
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RESULT 12
US-09-995-529-8
; Sequence 8, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-529-8

Query Match          92.1%; Score 82; DB 10; Length 120;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDGSSEKYYADSVRG 17
Db 50 NIKDGSSEKYYVDSVKG 66
|||||
|

RESULT 13
US-09-995-529-8
; Sequence 8, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-529-8

Query Match          92.1%; Score 82; DB 12; Length 120;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDGSSEKYYADSVRG 17
Db 50 NIKDGSSEKYYVDSVKG 66
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RESULT 14
US-09-811-737-3
; Sequence 3, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Human FAP-alpha-specific antibodies
; FILE REFERENCE: 1-1129
; CURRENT APPLICATION NUMBER: US/09/811,737
; CURRENT FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-737-3

Query Match          92.1%; Score 82; DB 9; Length 134;
Best Local Similarity 88.2%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDGSSEKYYADSVRG 17
Db 50 NIKDGSSEKYYVDSVKG 66
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RESULT 15
US-09-880-748-1889
; Sequence 1889, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1889
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1889

Query Match          92.1%; Score 82; DB 10; Length 241;
Best Local Similarity 88.2%; Pred. No. 3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NIKDGSSEKYYADSVRG 17
Db 50 NIKDGSSEKYYVDSVKG 66
|||||
|

Search completed: June 8, 2004, 18:52:57
Job time : 56.5781 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 77.2969 Seconds
(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQGSSEKYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	89	100.0	17	6	ABU11260 Human TANG
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4	82	92.1	98	2	AAR52066 Heavy cha
5	82	92.1	98	2	AAR72074 DP54 VH r
6	82	92.1	98	3	AAB40138 Anti-hi11
7	82	92.1	98	3	AAB40140 Anti-hi11
8	82	92.1	98	5	ABG78210 Human FV
9	82	92.1	98	5	ABG91901 Human ant
10	82	92.1	98	6	ABO27082 Human ger
11	82	92.1	98	7	Add28039 Lymphoma
12	82	92.1	109	6	Abr55320 Amino aci
13	82	92.1	117	2	AAR56301 Human imm
14	82	92.1	120	7	Add94123 Human VHI
15	82	92.1	125	4	AAB62776 Human HIV
16	82	92.1	134	5	AAO14049 Human ant
17	82	92.1	241	5	ABP45878 Human Bly
18	82	92.1	247	5	ABP45459 Human Bly
19	82	92.1	247	6	AAO31142 Human CM0
20	82	92.1	251	5	ABP45583 Human Bly
21	82	92.1	253	5	ABP44996 Human Bly
22	82	92.1	253	5	ABP44992 Human Bly
23	82	92.1	262	5	AAO14058 Anti-FAPA
24	82	92.1	271	2	AAW90180 Human CLO
25	82	92.1	312	2	AAW83323 Single ch

26	82	92.1	312	5	ABB09604	Abb09604 Amino aci
27	82	92.1	312	6	ABG74385	Abg74385 Single ch
28	79	88.8	157	6	ABR55915	Abr55915 Human mAb
29	79	88.8	157	6	ABR55886	Abr55886 Human mAb
30	78	87.6	17	5	AAU75740	Aau75740 Anti-DMCP
31	78	87.6	122	5	AAU75737	Aau75737 AAV293 an
32	76	85.4	264	5	AAU75152	Aau75152 Protein f
33	76	85.4	265	5	AAU75154	Aau75154 Protein f
34	76	85.4	265	5	AAU75149	Aau75149 Amino aci
35	76	85.4	265	5	AAU75153	Aau75153 Protein f
36	75	84.3	17	2	AAU05049	Aay05049 Tumour an
37	75	84.3	17	7	ADC82816	Adc82816 CDR regio
38	75	84.3	133	7	ADD28300	Add28300 Human het
39	75	84.3	250	5	ABP45475	Abp45475 Human Bly
40	75	84.3	250	5	ABP45308	Abp45308 Human Bly
41	74	83.1	121	7	ADD28301	Add28301 Human het
42	74	83.1	122	5	AAU75745	Aau75745 AAV294 an
43	74	83.1	254	5	ABP45500	Abp45500 Human Bly
44	73	82.0	17	2	AAU05055	Aay05055 Tumour an
45	73	82.0	17	7	ADC82828	Adc82828 CDR regio

ALIGNMENTS

RESULT 1

AA61294	ID	AA61294	standard; peptide; 17 AA.
XX	XX	AA61294	
XX	XX	AA61294	
DT	04-APR-2001	(first entry)	
XX	XX	AA61294	
DE	Anti-TANGO 268 scFv CDR, SEQ ID NO: 62.		
XX	XX	AA61294	
KW	Human; antibody; scFv; CDR; complementarity determining region;		
KW	TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;		
KW	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;		
KW	platelet membrane glycoprotein receptor; bleeding disorder;		
KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;		
KW	ischaemia; cardiovascular disease; immunological disease; liver disorder;		
XX	XX	AA61294	
OS	Homo sapiens.		
XX	XX	AA61294	
PN	WO200100810-A1.		
XX	XX	AA61294	
PD	04-JAN-2001.		
XX	XX	AA61294	
PF	30-JUN-2000; 2000WO-US018152.		
XX	XX	AA61294	
PR	30-JUN-1999; 99US-00345468.		
PR	06-DEC-1999; 99US-00454824.		
PR	14-FEB-2000; 2000US-00503387.		
XX	XX	AA61294	
PA	(MILL-) MILLENNIUM PHARM INC.		
XX	XX	AA61294	
PI	Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;		
PI	Gill DS, Qian MD, Kingsbury G;		
XX	XX	AA61294	
DR	WPI; 2001-080877/09.		
XX	XX	AA61294	
PT	New genes encoding human platelet-expressed collagen receptor,		
PT	glycoprotein VI, and its modulators, useful for preventing, treating and		
PT	diagnosing hemorrhagic disorders, thrombotic diseases and immunological		
XX	XX	AA61294	
PS	Claim 31; Page 102; 227pp; English.		
XX	XX	AA61294	
CC	The present sequence is given in a specification relating to an isolated		
CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor		
CC	glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides		
CC	and polypeptides and their modulators, e.g. antisense nucleic acids,		

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver

XX Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NIKQDSEKYYADSVRG 17

RESULT 2
 ABU11260
 ID ABU11260 standard; peptide; 17 AA.

XX
 AC ABU11260;

XX 06-FEB-2003 (first entry)

XX Human TANGO 268 VHCDR2 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchenker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Claim 7; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, venous
 CC disorders, liver disorders, cerebral vascular diseases, embryonic
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention

XX Sequence 17 AA;

Query Match 100.0%; Score 89; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIKQDSEKYYADSVRG 17
 |||||
 Db 1 NIKQDSEKYYADSVRG 17

RESULT 3

AAO17611

ID AAO17611 standard; peptide; 17 AA.

XX AAO17611;

XX 08-AUG-2002 (first entry)

XX Human FAPalpha specific VL region from VH50 CDR2 peptide.

XX Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
 KW gene therapy; cancer; wound healing; inflammation; cytostatic.

XX Homo sapiens.

XX WO200168708-A2.

XX 20-SEP-2001.

XX 16-MAR-2001; 2001WO-EP004716.

XX 17-MAR-2000; 2000DE-01013286.

XX 11-SEP-2000; 2000GB-00022216.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
 PI Schmidt A;

XX WPI; 2002-041180/05.

XX N-PSDB; AAL46556.

XX New human humanized antibody that specifically binds to fibroblasts
 PT activating protein alpha, useful for treating cancer or tumor, and for
 PT imaging tumors associated with activated stromal fibroblasts, e.g. lung
 XX or breast cancer.

PS Disclosure; Fig 6C; 109pp; English.


```
XX SQ Sequence 98 AA;
Query Match 92.1%; Score 82; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKDGSSEKYYADSVRG 17
   |||||
Db 50 NIKDGSSEKYYVDSVKG 66

RESULT 6
AAB40138
ID AAB40138 standard; protein; 98 AA.
XX AC AAB40138;
XX DT 05-FEB-2001 (first entry)
XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 664.
XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
XX KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis.
XX OS Homo sapiens.
XX PN WO200056772-A1.
XX PD 28-SEP-2000.
XX PF 24-MAR-2000; 2000WO-US007946.
XX PR 25-MAR-1999; 99US-0126603P.
XX PA (BADI ) BASF AG.
XX PA (GEMY ) GENETICS INST INC.
XX PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX PI Kaymakalan Z, Iabkovsky B, Sakorafas P, Friedrich S, Myles A;
XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX DR WPI; 2000-638250/61.
XX PT New human antibody specific for human interleukin-12 (IL-12) used to
XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX PT disease and multiple sclerosis.
XX PS Claim 75; Page 122; 377pp; English.
XX CC This invention relates to a new human antibody specific for human
XX CC interleukin-12 (IL-12). The invention also includes antigen binding
XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX CC anti-IL-12 antibody heavy and light chain complementarity determining
XX CC region (CDR) amino acid sequences, and also includes variable region
XX CC amino acid sequences. Other variable region amino acid sequences are
XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
XX CC given in AAB40064-B40067. Primers used in the identification and
XX CC construction of the antibodies of the invention are given in AAC61062-
XX CC C61071. The antibody of the invention is a neutralising antibody and has
XX CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
XX CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
XX CC antibacterial and immunosuppressive activity. The antibodies or antigen-
XX CC binding fragments are useful in the treatment of disorders associated
XX CC with detrimental release of human IL-12, especially Crohn's disease,
XX CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX CC manufacture of a pharmaceutical composition to treat human IL-12
```

```
CC disorders
XX XX
SQ Sequence 98 AA;
Query Match 92.1%; Score 82; DB 3; Length 98;
Best Local Similarity 88.2%; Pred. No. 5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKDGSSEKYYADSVRG 17
   |||||
Db 50 NIKDGSSEKYYVDSVKG 66

RESULT 7
AAB40140
ID AAB40140 standard; protein; 98 AA.
XX AC AAB40140;
XX DT 05-FEB-2001 (first entry)
XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 666.
XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
XX KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis.
XX OS Homo sapiens.
XX PN WO200056772-A1.
XX PD 28-SEP-2000.
XX PF 24-MAR-2000; 2000WO-US007946.
XX PR 25-MAR-1999; 99US-0126603P.
XX PA (BADI ) BASF AG.
XX PA (GEMY ) GENETICS INST INC.
XX PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX PI Kaymakalan Z, Iabkovsky B, Sakorafas P, Friedrich S, Myles A;
XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX DR WPI; 2000-638250/61.
XX PT New human antibody specific for human interleukin-12 (IL-12) used to
XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX PT disease and multiple sclerosis.
XX PS Claim 75; Page 122; 377pp; English.
XX CC This invention relates to a new human antibody specific for human
XX CC interleukin-12 (IL-12). The invention also includes antigen binding
XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX CC anti-IL-12 antibody heavy and light chain complementarity determining
XX CC region (CDR) amino acid sequences, and also includes variable region
XX CC amino acid sequences. Other variable region amino acid sequences are
XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
XX CC given in AAB40064-B40067. Primers used in the identification and
XX CC construction of the antibodies of the invention are given in AAC61062-
XX CC C61071. The antibody of the invention is a neutralising antibody and has
XX CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
XX CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
XX CC antibacterial and immunosuppressive activity. The antibodies or antigen-
XX CC binding fragments are useful in the treatment of disorders associated
XX CC with detrimental release of human IL-12, especially Crohn's disease,
XX CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX CC manufacture of a pharmaceutical composition to treat human IL-12
```

CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders

XX Sequence 98 AA;

Query Match 92.1%; Score 82; DB 3; Length 98;

Best Local Similarity 88.2%; Pred. No. 5e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17

DB 50 NIKQDGESEKYVDVSKG 66

RESULT 8

ABG78210

ID ABG78210 standard; protein; 98 AA.

XX AC ABG78210;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #85.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX PS Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

PT or fragment, or construct of fragment with enhanced binding

PT characteristics so as to selectively bind target cell in favor of other

PT cells.

PS Claim 13; Page 191-192; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv

CC molecule, a construct or fragments or a construct of a fragment with

CC enhanced binding characteristics which selectively and/or specifically

CC binds to a target cell in favour of other cells, where binding is

CC primarily determined by a first hypervariable region and Fv is a single

CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

CC association with or attached, coupled, combined, linked or fused to a

CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

CC acute myeloid leukaemia cell). The peptide is also useful for preparing a

CC composition for use in inhibiting the growth of a diseased or cancer

CC cell. This sequence represents a human Fv molecule hypervariable region

CC related peptide of the invention

XX Sequence 98 AA;

Query Match

Best Local Similarity 92.1%; Score 82; DB 5; Length 98;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17

DB 50 NIKQDGESEKYVDVSKG 66

RESULT 9

ABG91901

ID ABG91901 standard; protein; 98 AA.

XX AC ABG91901;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #85.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX KW metastasis; hypervariable region; autoimmune disease; thrombosis;

XX KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;

XX KW myocardial infarction; retinopathic disease; abnormal platelet function;

XX KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

PT diseases, and cancer.

PS Disclosure; Page 268; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and

CC important in physiological phenomena such as cell rolling, metastasis and

CC inflammation, where the epitope is capable of being bound by an antibody,

CC its antigen-binding fragment or its complex comprising at least one

CC antibody or its binding fragment having a first hypervariable region. The

CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

CC tumour or leukaemia cells, increase in number of tumour or leukaemia

CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing

CC mortality of tumour or leukaemia cells, for increasing the susceptibility

CC of diseased cells to damage by anti-disease, anti-cancer or anti-

CC leukaemia agents, or for decreasing the number of tumour or leukaemia

CC cells in a patient, or in the manufacture of a medicament for the above

CC mentioned purposes. The epitopes are useful for diagnosing and treating

CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory

CC diseases, cardiovascular diseases, such as myocardial infarction,

CC retinopathic diseases and other diseases mediated by abnormal platelet

CC function and diseases caused by sulphated tyrosine-dependent protein-

CC protein interactions. This sequence represents a human antibody fragment

CC of the invention

XX Sequence 98 AA;

Query Match

Best Local Similarity 92.1%; Score 82; DB 5; Length 98;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		50 NIKQDGEKYYVDSVKG 66	
QY	1 NIKQDGEKYYVDSVRG 17		
DB	50 NIKQDGEKYYVDSVKG 66		
RESULT 10			
ABO27082			
ID	ABO27082 standard; protein; 98 AA.		
XX			
AC	ABO27082;		
XX			
DT	10-SEP-2003 (first entry)		
XX			
DE	Human germline heavy chain variable region gene segment #15.		
XX			
KW	Human; heavy chain variable region; VH; humanised antibody;		
KW	chimeric antibody; complementarity determining region; CDR;		
KW	canonical CDR structure type.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003039649-A1.		
XX			
PD	27-FEB-2003.		
XX			
PF	12-JUL-2002; 2002US-00194975.		
XX			
PR	12-JUL-2001; 2001US-0305111P.		
XX			
PA	(FOOT/) FOOTE J.		
XX			
PI	Foote J;		
XX			
DR	WPI; 2003-492151/46.		
XX			
PT	Making humanized antibody for converting antibody, by making chimeric		
PT	antibodies containing complementarity determining region from non-human		
PT	antibody and appropriate framework sequences of human antibodies.		
XX			
PS	Example 1; Fig 1; 31pp; English.		
XX			
CC	The invention describes a method of making a humanised antibody,		
CC	comprising making chimeric antibodies containing a complementarity		
CC	determining region (CDR) from a non-human antibody and appropriate		
CC	framework sequences (I) of human antibodies. (I) is selected by using		
CC	canonical CDR structure types of non-human antibody in comparison to		
CC	germline canonical CDR structure types of human antibodies as the basis		
CC	for selection, for humanisation. The method is useful for making a		
CC	humanised antibody or a converted antibody. The method is applicable for		
CC	converting a subject antibody sequence of any subject species to a less		
CC	immunogenic form suitable for use in an object species. The method is		
CC	reliable for identifying suitable human framework sequences to support		
CC	non-human CDR regions and to provide humanised antibodies that retain		
CC	high affinity binding with low immunogenicity in humans, without the need		
CC	for direct comparison of framework sequences, without the need for		
CC	determining critically important amino acid residues in the framework,		
CC	and without the need for multiple iteration and construction to obtain		
CC	humanised antibodies with suitable therapeutic properties. The antibody		
CC	has high affinity and low immunogenicity without need for comparing		
CC	framework sequences between non-human and human antibodies. This sequence		
CC	represents a human heavy chain variable region gene segment used in the		
CC	creation of humanised antibodies		
XX			
SQ	Sequence 98 AA;		
Query Match		92.1%;	Score 82; DB 6; Length 98;
Best Local Similarity		88.2%;	Pred. No. 5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 NIKQDGEKYYVDSVRG 17		
DB	50 NIKQDGEKYYVDSVKG 66		
RESULT 12			
ABR55320			
Query Match		92.1%;	Score 82; DB 7; Length 98;
Best Local Similarity		88.2%;	Pred. No. 5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 NIKQDGEKYYVDSVRG 17		
DB	50 NIKQDGEKYYVDSVKG 66		
RESULT 11			
ADD28039			
ID	ADD28039 standard; protein; 98 AA.		
XX			
AC	ADD28039;		
XX			
DT	15-JAN-2004 (first entry)		
XX			
DE	Lymphoma related immunoglobulin variable region V3-07.		
XX			
KW	B-cell; malignant; immunoglobulin; immunoglobulin variable region;		
KW	Ig variable region; glycosylation site; lymphoma; B cell receptor;		
KW	cytostatic; gene therapy; glycosylation inhibitor;		
KW	non-Hodgkin's lymphoma.		
XX			
OS	Synthetic.		
OS	Homo sapiens.		
XX			
PN	WO2003074059-A2.		
XX			
PD	12-SEP-2003.		
XX			
PF	24-FEB-2003; 2003WO-GB000783.		
XX			
PR	07-MAR-2002; 2002GB-00005395.		
XX			
PA	(CANC-) CANCER RES TECHNOLOGY LTD.		
XX			
PI	Zhu D, Stevenson F;		
XX			
DR	WPI; 2003-902720/82.		
XX			
PT	Classifying a B-cell as malignant or normal by isolating a sequence		
PT	representing an Ig variable region from the B cell, detecting the		
PT	presence of a glycosylation site and classifying the cell as malignant or		
PT	normal.		
XX			
PS	Disclosure; Fig 3; 61pp; English.		
XX			
CC	The present invention describes a method for classifying a B-cell as		
CC	malignant or normal comprising: (a) isolating a sequence representing an		
CC	immunoglobulin (Ig) variable region from the B cell; (b) detecting the		
CC	presence of a glycosylation site; and (c) classifying the cell as		
CC	malignant or normal on the basis of the presence or absence of a		
CC	glycosylation site. Also described: (1) treating a patient suffering from		
CC	or at risk of having lymphoma; (2) screening for substances capable of		
CC	inhibiting glycosylation of the Ig variable region of the B cell receptor		
CC	; and (3) screening for substances (s) capable of inhibiting the		
CC	interaction between lectins of the type found in the germinal centre and		
CC	N-glycans found on the surface of Ig of lymphoma cells. (S) has		
CC	cytostatic activity, and can be used in gene therapy, and as a		
CC	glycosylation inhibitor. The method is useful in classifying a B-cell as		
CC	malignant or normal. The glycosylation inhibitor is useful in preparing a		
CC	medicament for treating non-Hodgkin's lymphoma. The present sequence		
CC	represents an Ig variable region sequence which is used in the		
CC	exemplification of the present invention.		
XX			
SQ	Sequence 98 AA;		
Query Match		92.1%;	Score 82; DB 7; Length 98;
Best Local Similarity		88.2%;	Pred. No. 5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 NIKQDGEKYYVDSVRG 17		
DB	50 NIKQDGEKYYVDSVKG 66		
RESULT 12			
ABR55320			

ID ABR55320 standard; peptide; 109 AA.
 AC ABR55320;
 XX
 DT 29-JUL-2003 (first entry)
 XX
 DE Amino acid sequence of human germline VH gene VH3-7 GL.
 XX
 XX Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;
 KW complementarity determining region; vascular endothelial growth factor;
 KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.
 XX
 OS Homo sapiens.
 XX
 XX WO2003031475-A2.
 PN
 XX
 XX 17-APR-2003.
 PD
 XX 10-OCT-2002; 2002WO-GB004619.
 PF
 XX 10-OCT-2001; 2001GB-00024317.
 XX
 XX (CELL-) CELLTech R & D LTD.
 PA
 XX Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;
 PI
 XX WPI; 2003-441133/41.
 DR
 XX Novel antibody molecules having specificity for human kinase insert
 PT domain-containing receptors, useful for treating inflammation, psoriasis,
 PT rheumatoid arthritis, tumor growth and metastasis.
 XX
 XX Disclosure; Fig 3; 57pp; English.
 PS
 XX The specification describes an antibody molecule which has specificity
 CC for human kinase insert domain-containing receptor (KDR). The antibody
 CC comprises complementarity determining regions (CDRs) from the heavy and
 CC light chain variable domains of the murine monoclonal antibody VR165.
 CC This antibody is specific for human KDR. The antibody of the invention
 CC blocks vascular endothelial growth factor (VEGF) binding to KDR.
 CC Antibodies of the invention are useful for treating a pathology in which
 CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
 CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
 CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
 CC growth or metastasis. ABR55320-21 represent human germline variable
 CC region frameworks, chosen to construct antibodies of the invention
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 92.1%; Score 82; DB 6; Length 109;
 Best Local Similarity 88.2%; Pred. No. 5.6e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NIKQDGESEKYADSVRG 17
 DB 50 NIKQDGESEKYVDSVKG 66
 |||||
 RESULT 13
 AAR66301
 ID AAR66301 standard; protein; 117 AA.
 XX
 AC AAR66301;
 XX
 XX 25-MAR-2003 (revised)
 DT
 DT 02-AUG-1995 (first entry)
 XX
 DE Human immunoglobulin variable heavy chain #7.
 XX
 XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pUB81; E.coli; mammalian.
 XX
 OS Homo sapiens.

XX WO9426895-A1.
 PN
 XX 24-NOV-1994.
 PD
 XX 10-MAY-1993; 93WO-JP000603.
 PF
 XX 10-MAY-1993; 93WO-JP000603.
 PR
 XX (NIBS) JAPAN TOBACCO INC.
 PA
 XX Honjo T, Matsuda F;
 PI
 XX WPI; 1995-006791/01.
 DR
 DR N-PSDB; AAQ78946.
 XX
 XX DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts.
 XX
 XX Claim 17; Page 40-41; 130pp; Japanese.
 PS
 XX Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
 CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
 CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
 CC Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using
 CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
 CC genes. The fragments cover a region of 800 kb. The DNA fragments were
 CC isolated from high molecular weight DNA from human placenta. The DNA was
 CC partially digested with TaqI restriction enzyme. The fragments were
 CC separated by gel electrophoresis and 35-45 kb fractions were collected.
 CC The fragments were ligated with ClaI-digested cosmid vector pUB81. The
 CC ligation products were in vitro packed and infected into E.coli 490A. The
 CC DNA fragments were then subcloned by colony hybridisation. The Vh genes and
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 92.1%; Score 82; DB 2; Length 117;
 Best Local Similarity 88.2%; Pred. No. 6.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NIKQDGESEKYADSVRG 17
 DB 69 NIKQDGESEKYVDSVKG 85
 |||||
 RESULT 14
 ADD94123
 ID ADD94123 standard; protein; 120 AA.
 XX
 AC ADD94123;
 XX
 DT 29-JAN-2004 (first entry)
 DT
 XX Human VHIII/JH6 variable region fusion partial amino acid sequence.
 DE
 XX Grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; antibody; VHIII/JH6; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003046204-A2.
 PN
 XX 05-JUN-2003.
 PD
 XX 26-NOV-2002; 2002WO-US038147.
 PF
 XX 26-NOV-2001; 2001US-00995529.
 PR

```
PR 06-DEC-2001; 2001US-00011250.
XX
XX (CELL-) CELL MATRIX INC.
XX
XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
XX WPI; 2003-513649/48.
XX
XX N-PSDB; ADD94122.
XX
XX New cryptic collagen antibody with one or more complementarity
XX determining regions, useful for diagnosing and treating disorders
XX associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
XX Example 1; SEQ ID NO 8; 232pp; English.
XX
XX This invention relates to a novel grafted antibody or its functional
XX fragment comprising one or more complementarity determining regions
XX (CDRs) of a defined light CDR and a light CDR with at least one amino
XX acid (aa) substitution where the antibody has specific binding activity
XX for a cryptic collagen epitope. The growth of all solid tumours requires
XX new blood vessel growth, angiogenesis, inhibition of which is an approach
XX to limiting tumour growth. The invention may allow development of
XX therapeutics with a cytostatic activity as a collagen agonist or
XX antagonist. The invention is useful for diagnosing and treating disorders
XX associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX present sequence is the partial amino sequence of the human variable
XX region fusion VHIII/JH6 which is related to the invention.
XX
XX SQ Sequence 120 AA;
XX
XX Query Match 92.1%; Score 82; DB 7; Length 120;
XX Best Local Similarity 88.2%; Pred. No. 6.3e-06;
XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 NIKQDGEKYYADSVRG 17
XX ||||| ||||| |||||
XX Db 50 NIKQDGEKYYVDSVKG 66
XX
XX RESULT 15
XX AAB62776
XX ID AAB62776 standard; protein; 125 AA.
XX
XX AC AAB62776;
XX
XX DT 03-APR-2001 (first entry)
XX
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 75.
XX
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO200100678-A1.
XX
XX PD 04-JAN-2001.
XX
XX PF 23-JUN-2000; 2000WO-US017327.
XX
XX PR 30-JUN-1999; 99US-0141701P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Watkins BA, Reitz MS;
XX
XX DR WPI; 2001-112438/12.
XX
XX N-PSDB; AAE29077.
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal.
XX
XX PT
XX PT
```

```
XX Claim 1; Page 69-70; slpp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection
XX
XX SQ Sequence 125 AA;
XX
XX Query Match 92.1%; Score 82; DB 4; Length 125;
XX Best Local Similarity 88.2%; Pred. No. 6.6e-06;
XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 NIKQDGEKYYADSVRG 17
XX ||||| ||||| |||||
XX Db 51 NIKQDGEKYYVDSVKG 67
XX
XX Search completed: June 8, 2004, 18:26:51
XX Job time : 80.2969 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 16.7344 Seconds
(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQDSEKYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	96.6	147	I37780	Ig variable region
2	82	92.1	97	PH0872	Ig heavy chain V r
3	82	92.1	98	PL0123	Ig heavy chain V-I
4	82	92.1	110	PH1655	Ig heavy chain V r
5	82	92.1	114	S36280	Ig heavy chain V r
6	82	92.1	117	S78486	Ig heavy chain V r
7	82	92.1	117	S17079	Ig heavy chain V r
8	82	92.1	122	S31675	Ig heavy chain V r
9	82	92.1	136	S31587	Ig heavy chain V r
10	82	92.1	139	I37781	Ig heavy chain V r
11	79	88.8	140	S22657	Ig variable region
12	77	86.5	123	S31509	Ig heavy chain pre
13	67	75.3	136	S16847	Ig heavy chain - h
14	67	75.3	136	S60296	Ig heavy chain V r
15	66	74.2	98	S29543	Ig heavy chain V r
16	66	74.2	117	S36259	Ig heavy chain V r
17	66	74.2	134	S31688	Ig heavy chain V r
18	66	74.2	135	S31598	Ig heavy chain V r
19	66	74.2	140	S70442	Ig heavy chain V r
20	65	73.0	121	PH1661	Ig heavy chain pre
21	64	71.9	94	PL0120	Ig heavy chain V r
22	64	71.9	97	S44115	Ig heavy chain V-I
23	64	71.9	98	PL0116	Ig heavy chain V r
24	64	71.9	98	S29546	Ig heavy chain V-I
25	64	71.9	109	PH1644	Ig heavy chain V r
26	64	71.9	109	PH1646	Ig heavy chain V r
27	64	71.9	111	PH1643	Ig heavy chain V r
28	64	71.9	111	PH1645	Ig heavy chain V r
29	64	71.9	113	S38490	Ig heavy chain - h

ALIGNMENTS

RESULT 1

I37780

Ig variable region (VDJ) (clone T20-11) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C:Accession: I37780; S25474

R:Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A:Title: Somatic diversification in the heavy chain variable region genes expressed by h

A:Reference number: A36876; MUID:94119917; PMID:8290556

A:Accession: I37780

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-147 <RES>

A:Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 96.6%; Score 86; DB 2; Length 147;
Best Local Similarity 94.1%; Pred No. 5e-07; Mismatches 0; Gaps 0;
Matches 16; Conservative 1; Indels 0;

QY 1 NIKQDSEKYADSVRG 17

Db 63 NIKQDSEKYADSVKG 79

RESULT 2

PH0872

Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996

C:Accession: PH0872

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A:Reference number: PH0862; MUID:92078875; PMID:1660528

A:Accession: PH0872

A:Molecule type: DNA

A:Residues: 1-97 <MAN>

A>Note: a "G" was inserted at the position of between 72nd and 73rd of the DNA sequence

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

F:30-35/Region: complementarity-determining 1

F:49-66/Region: complementarity-determining 2

Query Match 92.1%; Score 82; DB 2; Length 97;
Best Local Similarity 88.2%; Pred No. 1.5e-06; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Indels 0;

QY 1 NIKQDGEKYYADSVRG 17
|||||
Db 49 NIKQDGEKYYVDSVKG 65

RESULT 3

PL0123

Ig heavy chain V-III region (TD-Vr) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C:Accession: PL0123; S26897

R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:8286083; PMID:2840480

A:Accession: PL0123

A:Molecule type: mRNA

A:Residues: 1-98 <BIR>

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A>Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26897

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <ROM>

A:Cross-references: EMBL:Z12354; NID:G32930; PID:CAA78224.1; PID:G32931

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:49-65/Region: complementarity-determining 2

Query Match 92.1%; Score 82; DB 2; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.5e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGEKYYADSVRG 17

|||||

Db 50 NIKQDGEKYYVDSVKG 66

RESULT 4

PH1655

Ig heavy chain V region (clone 2E8) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1655

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1655

A:Molecule type: mRNA

A:Residues: 1-110 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.1%; Score 82; DB 2; Length 110;

Best Local Similarity 88.2%; Pred. No. 1.7e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGEKYYADSVRG 17

|||||

Db 42 NIKQDGEKYYVDSVKG 58

RESULT 5

S36280

Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: S36280

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36280

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-114 <GRI>

A:Cross-references: EMBL:Z18822

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.1%; Score 82; DB 2; Length 114;

Best Local Similarity 88.2%; Pred. No. 1.8e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGEKYYADSVRG 17

|||||

Db 50 NIKQDGEKYYVDSVKG 66

RESULT 6

S78486

Ig heavy chain V region (clone FL13-28) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000

C:Accession: S78486; S31115

R:Raaphorst, F.M.

submitted to the EMBL Data Library, October 1991

A:Reference number: S78486

A:Accession: S78486

A:Molecule type: mRNA

A:Residues: 1-117 <RAA>

A:Cross-references: EMBL:X62965

A:Experimental source: Clone FL13-28

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31115

A:Molecule type: mRNA

A:Residues: 1-4, 'L', 6-32, 'G', 34-52, 'E', 54-73, 'K', 75-97 <RAW>

A:Cross-references: EMBL:X62965

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.1%; Score 82; DB 2; Length 117;

Best Local Similarity 88.2%; Pred. No. 1.8e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGEKYYADSVRG 17

|||||

Db 50 NIKQDGEKYYVDSVKG 66

RESULT 7

S17079

Ig heavy chain V-gene (clone HHG19) - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S60299; S17079

R:Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.

Immunol. Lett. 34, 57-62, 1992

A:Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive im

A:Reference number: S60295; MUID:93122853; PMID:1282498

A:Accession: S60299

A>Status: preliminary

```
A:Molecule type: DNA
A:Residues: 1-117 <KU2>
A:Cross-references: EMBL:X62128; NID:G38340; PIDN:CAA44059.1; PID:G38341
A>Note: the authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72,
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      92.1%; Score 82; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17
   |||||
Db 69 NIKQDGESEKYVDSVKG 85
   |||||

RESULT 8
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31675
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31675
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <CU1>
A:Cross-references: EMBL:Z14175; NID:G31015; PIDN:CRA78544.1; PID:G31016
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-104/Domain: immunoglobulin homology <IMM>

Query Match      92.1%; Score 82; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 1.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17
   |||||
Db 56 NIKQDGESEKYVDSVKG 72
   |||||

RESULT 9
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31587
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31587
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CU1>
A:Cross-references: EMBL:Z14189; NID:G31005; PIDN:CRA78558.1; PID:G31006
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-114/Domain: immunoglobulin homology <IMM>

Query Match      92.1%; Score 82; DB 2; Length 136;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17
   |||||
Db 66 NIKQDGESEKYVDSVKG 82
   |||||
```

```
RESULT 10
I37781
Ig variable region (VDJ) (clone T21-9) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C:Accession: I37781; S25475
R:Demaison, C.; Chastagner, P.; These, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A36876; MUID:94119917; PMID:8290556
A:Accession: I37781
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <RES>
A:Cross-references: EMBL:X67908; NID:G33580; PIDN:CAA48106.1; PID:G33581
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:35-118/Domain: immunoglobulin homology <IMM>

Query Match      92.1%; Score 82; DB 2; Length 139;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17
   |||||
Db 70 NIKQDGESEKYVDSVKG 86
   |||||

RESULT 11
S22657
Ig heavy chain precursor V region (O-81VH) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 06-Feb-1998
C:Accession: S22657
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22657
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: EMBL:X59134
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      88.8%; Score 79; DB 2; Length 140;
Best Local Similarity 82.4%; Pred. No. 7.1e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDGESEKYADSVRG 17
   |||||
Db 69 NVKQDGSARYVDSVKG 85
   |||||

RESULT 12
S31509
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31509
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31509
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <CHA>
A:Cross-references: EMBL:X69864; NID:G33090; PIDN:CAA49498.1; PID:G33091
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-106/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 77; DB 2; Length 123;
Best Local Similarity 82.4%; Pred. No. 1.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKDGSSEKYYADSVRG 17
|||:|||||
Db 58 NIKHDGNEKYYVDSVKG 74

RESULT 13

S16847

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-1996

C;Accession: S16847

R;Kueppers, R.

submitted to the EMBL Data Library, September 1991

A;Reference number: S16847

A;Accession: S16847

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-136 <KUE>

A;Cross-references: EMBL:X62126

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 67; DB 2; Length 136;
Best Local Similarity 68.8%; Pred. No. 0.00072;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKQDGSSEKYYADSVRG 17
:|||||:
Db 70 VKDDGSERYVDSVKG 85

RESULT 14

S60296

Ig heavy-chain variable region (clone WHR) precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000

C;Accession: S60296

R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.

Immunol. Lett. 34, 57-62, 1992

A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm

A;Reference number: S60295; MUID:93122853; PMID:1282498

A;Accession: S60296

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-136 <KUE>

A;Cross-references: EMBL:X62126; NID:G38336; PIDN:CAA44057.1; PID:G38337

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 67; DB 2; Length 136;
Best Local Similarity 68.8%; Pred. No. 0.00072;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKQDGSSEKYYADSVRG 17
:|||||:
Db 70 VKDDGSERYVDSVKG 85

RESULT 15

S29543

Ig heavy chain V region (COS 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999

C;Accession: S29543

R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29543
A;Molecule type: DNA

A;Residues: 1-98 <TOM>

A;Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 0.00075;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKQDGSSEKYYADSVRG 17
:|||||:
Db 51 IRYDGSNKKYYADSVKG 66

Search completed: June 8, 2004, 18:54:10
Job time : 17.7344 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 9.5625 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKQSGSEKYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	70.8	116	1 HV3T HUMAN	P01781 homo sapien
2	57	64.0	122	1 HV3G HUMAN	P01768 homo sapien
3	56	62.9	118	1 HV3V HUMAN	P80419 homo sapien
4	55	61.8	119	1 HV3L HUMAN	P01773 homo sapien
5	55	61.8	126	1 HV3K HUMAN	P01774 homo sapien
6	50	56.2	119	1 HV3M HUMAN	P01775 homo sapien
7	50	56.2	119	1 HV3N HUMAN	P01776 homo sapien
8	49	55.1	119	1 HV3I HUMAN	P01770 homo sapien
9	47	52.8	122	1 HV3A HUMAN	P01762 homo sapien
10	47	52.8	122	1 HV3H HUMAN	P01769 homo sapien
11	46	51.7	114	1 HV3B HUMAN	P01763 homo sapien
12	46	51.7	117	1 HV03 CARAU	P19180 carassius a
13	46	51.7	121	1 HV3J HUMAN	P01771 homo sapien
14	45	50.6	98	1 HV57 MOUSE	P18528 mus musculu
15	45	50.6	116	1 HV05 CARAU	P19181 carassius a
16	44	49.4	115	1 HV3F HUMAN	P01767 homo sapien
17	44	49.4	421	1 YE04 METJA	Q58799 methanococc
18	43	48.3	117	1 HV3C HUMAN	P01764 homo sapien
19	43	48.3	120	1 HV3E HUMAN	P01766 homo sapien
20	42	47.2	117	1 HV53 MOUSE	P18524 mus musculu
21	42	47.2	258	1 YC99 YEAST	P25637 saccharomyc
22	41	46.1	117	1 HV01 CAICR	P01813 calman croc
23	41	46.1	367	1 Y046 MYCTO	P71703 mycobacteri
24	41	46.1	367	1 Y047 MYCTO	P59967 mycobacteri
25	41	46.1	623	1 PBP2 SALTU	P74872 salmonella
26	41	46.1	802	1 FTSK LACPL	P74872 lactobacill
27	41	46.1	877	1 DYN_DROME	P27619 drosophila
28	41	46.1	1085	1 S124 HUMAN	Q9up95 homo sapien
29	41	46.1	1085	1 S124 MOUSE	Q9j1s8 mus musculu
30	41	46.1	1085	1 S124 RABIT	Q28677 oryctolagus
31	41	46.1	1085	1 S124 RAT	Q63632 rattus norv
32	41	46.1	1150	1 S126 HUMAN	Q9uhw9 homo sapien
33	41	46.1	1150	1 S126 MOUSE	Q924n4 mus musculu

RESULT 1
HV3T_HUMAN 34 41 46.1 4447 1 PKSK_BACSU P40803 bacillus su
35 40.5 45.5 197 1 BINL_STAAU P18358 staphylococ
36 40 44.9 97 1 HV56 MOUSE P18527 mus musculu
37 40 44.9 117 1 HV54 MOUSE P18525 mus musculu
38 40 44.9 117 1 HV55 MOUSE P18526 mus musculu
39 40 44.9 198 1 JDP1_MOUSE Q9r022 mus musculu
40 40 44.9 229 1 GPMA_LISIN Q929g8 listeria in
41 40 44.9 229 1 GPMA_LISIN Q9y571 listeria in
42 40 44.9 231 1 PSBQ_ONOVI O22591 onobrychis
43 40 44.9 318 1 FMT_HABIN P44787 haemophilus
44 40 44.9 419 1 RECA_WYCGS Q9f414 mycobacteri
45 40 44.9 463 1 YCES_YEAST P25380 saccharomyc

ALIGNMENTS

RESULT 1
HV3T_HUMAN ID HV3T_HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IGM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IGM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC -!- MACROGLOBULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSF0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 70.8%; Score 63; DB 1; Length 116;
Best Local Similarity 58.8%; Pred. No. 0.00077;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKQSGSEKYADSVRG 17
Db 50 NIKZBGSZBYVDVSKG 66
||||:||||:||||:
||||:||||:||||:

RESULT 2
HV3G_HUMAN ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)

```
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
  location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
  PATIENT WITH MACROGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUM.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 64.0%; Score 57; DB 1; Length 122;
Best Local Similarity 56.2%; Pred. No. 0.0089;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
DB 51 ISYGBBKYABSVRG 66

RESULT 3
HV3V HUMAN
ID HV3V HUMAN STANDARD; PRT; 118 AA.
AC P80419;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
  immunoglobulins."
RL Eur. J. Biochem. 228:886-893(1995).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; S69132; S69132.
DR HSSP; P01810; 2FBT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
```

```
FT DOMAIN 1 110 IG-LIKE.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 13087 MW; 6C21D810ED1B6D1F CRC64;

Query Match 62.9%; Score 56; DB 1; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.013;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NIKDGSSEKYYADSVR 16
DB 50 NIREDETEKFYDSVR 65

RESULT 4
HV3L HUMAN
ID HV3L HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
  IgA1 protease, digestion, Fab and Fc fragments, and the complete
  amino acid sequence of the alpha 1 heavy chain."
RL J. Biol. Chem. 254:2865-2874(1979).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02056; A1HUBR.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 61.8%; Score 55; DB 1; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKDGSSEKYYADSVRG 17
DB 51 ISYGSBKYADSVRG 66

RESULT 5
HV3K HUMAN
ID HV3K HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```



```
RN RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule.";
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 21G2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 61.8%; Score 55; DB 1; Length 126;
Best Local Similarity 62.5%; Pred. No. 0.02; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 2 IKQDGSEKYADSVRG 17
| | | | | | | | | |
Db 51 IWDGSDQHYADSVKG 66

RESULT 6
HV3M HUMAN
ID HV3M HUMAN STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)

Query Match 62.5%; Score 55; DB 1; Length 126;
Best Local Similarity 62.5%; Pred. No. 0.02; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 2 IKQDGSEKYADSVRG 17
| | | | | | | | | |
Db 51 IWDGSDQHYADSVKG 66

RN RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule.";
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 21G2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 61.8%; Score 55; DB 1; Length 126;
Best Local Similarity 62.5%; Pred. No. 0.02; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 4;

QY 2 IKQDGSEKYADSVRG 17
| | | | | | | | | |
Db 51 IWDGSDQHYADSVKG 66

RESULT 6
HV3M HUMAN
ID HV3M HUMAN STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)

Query Match 56.2%; Score 50; DB 1; Length 119;
Best Local Similarity 57.1%; Pred. No. 0.14; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 5;

QY 4 QDGEKYYADSVRG 17
| | | | | | | | | |
Db 53 ENGNDKHYADSVNG 66

RESULT 7
HV3N HUMAN
ID HV3N HUMAN STANDARD; PRT; 119 AA.
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02058; M3HULY.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCF5E CRC64;

Query Match 56.2%; Score 50; DB 1; Length 119;
 Best Local Similarity 57.1%; Pred. No. 0.14; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 1;

Qy 4 QDGSEKYADSVRG 17
 :|:|:|:|:|:|
 Db 53 ENGNDKHYADSVNG 66

RESULT 8
 HV3I HUMAN
 ID HV3I HUMAN STANDARD; PRT; 119 AA.
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region NIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 monoclinal IgG1 immunoglobulin (myeloma protein Nie). Iii. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 [2]
 RN DISULFIDE BOND.
 RP MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A91668; GIHUNI.
 DR HSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT MOD RES 1 112 IG-LIKE.
 FT DISULFID 22 96
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6E5E165B CRC64;

Query Match 55.1%; Score 49; DB 1; Length 119;
 Best Local Similarity 61.5%; Pred. No. 0.21; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 3; Mismatches 2;

Qy 5 DGSEKYADSVRG 17

Db 54 BGBKHVADSVNG 66
 :|:|:|:|:|:|

RESULT 9
 HV3A HUMAN
 ID HV3A HUMAN STANDARD; PRT; 122 AA.
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE (MYELOMA PROTEIN TRO).
 RX MEDLINE=76023781; PubMed=809331;
 RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starosick K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.);
 II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
 structure of the complete IgA-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02045; ALHUTR.
 DR HSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 108 IG-LIKE.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON TER 122 122
 SQ SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 52.8%; Score 47; DB 1; Length 122;
 Best Local Similarity 75.0%; Pred. No. 0.48;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GSEKYADSVRG 17
 :|:|:|:|:|:|
 Db 55 GSTLYADSVNG 66

RESULT 10
 HV3H HUMAN
 ID HV3H HUMAN STANDARD; PRT; 122 AA.
 AC P01769;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region GA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
 RL Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.


```
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RY cryoimmunoglobulin IgG Hil.";
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02054; GIHULH.
CC DR HSSP; P01772; 2FB4.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR Pfam; PF00047; ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Pyrrolidone carboxylic acid.
CC FT DOMAIN 1 112
CC FT MOD RES 1 112
CC FT NON TER 121 121
CC FT SEQUENCE 121 AA; 13566 MW; 480FC53610EFDAB CRC64;
CC QUERY MATCH 51.7%; Score 46; DB 1; Length 121;
CC Best Local Similarity 61.5%; Pred. No. 0.7;
CC Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 DGSEKYYADSVRG 17
Db 54 NGSRTYYGDSVKG 66
RESULT 14
HV57 MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RY the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; JT0501; HVMS96.
CC DR HSSP; P01772; 2FB4.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR Pfam; PF00047; ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region.
CC FT DOMAIN 1 >98
CC FT NON TER 98 98
CC FT SEQUENCE 98 AA; 11007 MW; B8644F7F92BFB95B CRC64;
CC QUERY MATCH 50.6%; Score 45; DB 1; Length 98;
CC Best Local Similarity 56.2%; Pred. No. 0.83;
CC Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2 IKQDSEKYYADSVRG 17
```

```
Db 51 ISDGGSVTYYPDSVKG 66
RESULT 15
HV05 CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
CC NCBI_TaxID=7957;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RP MEDLINE=88144476; PubMed=3125551;
CC RA Wilson M.R., Middleton D., Warr G.W.;
CC RT "Immunoglobulin heavy chain variable region gene evolution: structure
CC and family relationships of two genes and a pseudogene in a teleost
CC fish.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC DR HSSP; P01772; 2FB4.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_v.
CC DR Pfam; PF00047; ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW SIGNAL 1 19
CC FT CHAIN 20 116
CC FT DOMAIN 20 49
CC FT DOMAIN 50 54
CC FT DOMAIN 55 68
CC FT DOMAIN 69 84
CC FT DOMAIN 85 116
CC FT DISULFID 41 114
CC FT NON TER 116 116
CC FT SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;
CC QUERY MATCH 50.6%; Score 45; DB 1; Length 116;
CC Best Local Similarity 66.7%; Pred. No. 1;
CC Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 GSEKYYADSVRG 17
Db 73 GGSTYYADSVKG 84
Search completed: June 8, 2004, 18:56:12
Job time : 10.5625 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 49.1406 Seconds
(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89
Sequence: 1 NIKQDSEKYYADSVRG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	92.1	95	4 Q9ULB6	Q9ULB6 homo sapien
2	66	74.2	113	4 Q9UL90	Q9UL90 homo sapien
3	64	71.9	116	4 Q9UL93	Q9UL93 homo sapien
4	64	71.9	613	4 Q8WUK1	Q8WUK1 homo sapien
5	61	68.5	122	4 Q9UL84	Q9UL84 homo sapien
6	53	59.6	121	4 Q9UL71	Q9UL71 homo sapien
7	52	58.4	147	4 Q9Y509	Q9Y509 homo sapien
8	50	56.2	71	7 Q9GJ71	Q9GJ71 salmo trutt
9	50	56.2	482	4 Q7Z351	Q7Z351 homo sapien
10	50	56.2	493	4 Q8NCL6	Q8NCL6 homo sapien
11	48	53.9	118	4 Q9UL72	Q9UL72 homo sapien
12	48	53.9	593	16 Q92HB9	Q92HB9 rickettsia
13	48	53.9	594	16 Q9ZCY6	Q9ZCY6 rickettsia
14	47.5	53.4	247	5 Q9VZF9	Q9VZF9 drosophila
15	47	52.8	342	2 Q9F5K2	Q9F5K2 rhizobium t
16	47	52.8	360	16 Q987Q4	Q987Q4 rhizobium 1

17	47	52.8	597	4	Q96BB9	Q96BB9 homo sapien
18	46	51.7	844	12	Q91LD2	Q91LD2 white spot
19	46	51.7	844	12	Q8GQZ0	Q8GQZ0 white spot
20	46	51.7	984	16	O67280	O67280 aquifex aso
21	45	50.6	119	11	Q920E7	Q920E7 mus musculu
22	45	50.6	150	4	Q9NQF2	Q9NQF2 homo sapien
23	45	50.6	169	4	Q9NQF1	Q9NQF1 homo sapien
24	45	50.6	463	4	Q7Z4G4	Q7Z4G4 homo sapien
25	45	50.6	550	16	Q83H75	Q83H75 tropheryma
26	45	50.6	550	16	Q820B7	Q820B7 tropheryma
27	45	50.6	1852	5	Q812U9	Q812U9 plasmodium
28	45	50.6	5488	16	Q31782	Q31782 bacillus su
29	44	49.4	71	7	Q9GJ67	Q9GJ67 salmo trutt
30	44	49.4	71	7	Q9GJ70	Q9GJ70 salmo trutt
31	44	49.4	71	7	Q9GJ72	Q9GJ72 salmo trutt
32	44	49.4	71	7	Q9GJ69	Q9GJ69 salmo trutt
33	44	49.4	71	7	Q9GJ68	Q9GJ68 salmo trutt
34	44	49.4	71	7	Q9GJ64	Q9GJ64 salmo trutt
35	44	49.4	118	16	Q82Y10	Q82Y10 enterococcu
36	44	49.4	140	4	Q9UNM8	Q9UNM8 homo sapien
37	44	49.4	472	4	Q8NBZ1	Q8NBZ1 homo sapien
38	44	49.4	472	4	Q9Y646	Q9Y646 homo sapien
39	44	49.4	513	10	Q8S658	Q8S658 oryza sativ
40	44	49.4	513	10	Q7XFV9	Q7XFV9 oryza sativ
41	44	49.4	541	4	Q9Y5X6	Q9Y5X6 homo sapien
42	44	49.4	1104	5	Q812S2	Q812S2 plasmodium
43	44	49.4	1812	5	Q8I538	Q8I538 plasmodium
44	43	48.3	71	7	Q9GJ66	Q9GJ66 salmo trutt
45	43	48.3	71	7	Q9GJ63	Q9GJ63 salmo trutt

ALIGNMENTS

RESULT 1

Q9ULB6 PRELIMINARY; PRT; 95 AA.
ID Q9ULB6
AC Q9ULB6; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; --
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1 95
FT NON_TER 95 95
SQ SEQUENCE 95 AA; 10527 MW; 90A9C6D16D22574A CRC64;

Query Match 92.1%; Score 82; DB 4; Length 95;
Best Local Similarity 88.2%; Pred. No. 9.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 49 NIKQDSEKYYVDSVKG 65

RESULT 2

```
Q9UL90
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57DD19086D07F CRC64;

Query Match 74.2%; Score 66; DB 4; Length 113;
Best Local Similarity 75.0%; Pred. No. 0.0051;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
| : ||| ||||| :|
Db 51 IRYDGSNKYYADSVKG 66

RESULT 3
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; PLO120; PLO120.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;
```

```
Query Match 71.9%; Score 64; DB 4; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
| : ||| ||||| :|
Db 50 ISYDGSNKYYADSVKG 65

RESULT 4
Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX ISSUES=Ions11;
RA Strausberg R.;
RL EMBL; BC020240; AAH20240.1; -.
DR PIR; PLO120; PLO120.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 71.9%; Score 64; DB 4; Length 613;
Best Local Similarity 75.0%; Pred. No. 0.072;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
| : ||| ||||| :|
Db 70 ISYDGSNKYYADSVKG 85

RESULT 5
Q9UL84
ID Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
```

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DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match
Best Local Similarity 68.5%; Score 61; DB 4; Length 122;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
Db 51 ISNDGSKNYADSVRG 66

RESULT 6
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035043; AAD56279.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match
Best Local Similarity 59.6%; Score 53; DB 4; Length 121;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
Db 51 ISGDGSGTYADSVRG 66

RESULT 7
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
DE VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;

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RA Cao J., Vesicio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953 (1995).
DR EMBL: S80860; AAD14339.1; -.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005887; C:integral to plasma membrane; NAS.
DR GO: GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO: GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR GO: GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match
Best Local Similarity 58.4%; Score 52; DB 4; Length 147;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKQDSEKYYADSVRG 17
Db 51 ISYDGSQYYAGSVKG 66

RESULT 8
Q9GJ71 PRELIMINARY; PRT; 71 AA.
AC Q9GJ71
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MHC class II alpha chain (Fragment).
DE SATR-DA.
OS Salmo trutta (Brown trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8032;
RN [1]
RP SEQUENCE FROM N.A.
RA Stet R.J.M., Jordan W.C.;
RT "Class II alpha chain in brown trout (Salmo trutta).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ293950; CAC08187.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR001003; MHC II alpha.
DR Pfam: PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 7699 MW; 0E3D9764E397FF72 CRC64;

Query Match
Best Local Similarity 56.2%; Score 50; DB 7; Length 71;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGSEKYYADSVRG 17
Db 14 DGEKQYADFIKG 26

RESULT 9
Q7Z351 PRELIMINARY; PRT; 482 AA.
ID Q7Z351
AC Q7Z351
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN DKFZp686N02209.

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DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI	TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	fetus.";	
RRL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
DR	EMBL; AF035042; RAD56278.1; -.	
DR	PIR; S21205; S21205.	
DR	HSP; P01772; 2FB4.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
DR	NON_TER 1	
FT	NON_TER 118 118	
FT	SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;	
SQ		
Query Match 53.9%; Score 48; DB 4; Length 118;		
Best Local Similarity 47.1%; Pred. No. 4.8;		
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;		
QY	1 NIKQDGSEKYYADSVRG 17	
DB	49 SVTYSGSSYYADSVRG 65	
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RESULT 12		
Q92HB9	PRELIMINARY; PRT; 593 AA.	
ID	Q92HB9	
AC	Q92HB9; 2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	penicillin-binding protein.	
GN	PEPAL OR RC0852	
OS	Rickettsia conorii	
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;	
OC	Rickettsiaceae; Rickettsiae; Rickettsia.	
NCBI	TaxID=781;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Malish 7;	
RX	MEDLINE=21442074; PubMed=11557893;	
RA	Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,	
RA	Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,	
RA	Racult D.;	
RT	"Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";	
RL	Science 293:2093-2098(2001).	
DR	EMBL; AF008640; AAL03390.1; -.	
DR	PIR; D97806; D97806.	
DR	GO; GO:0008658; Fipenicillin binding; IEA.	
DR	GO; GO:0009273; P-cell wall biosynthesis (sensu Bacteria); IEA.	
DR	InterPro; IPR005311; PBP dimer.	
DR	InterPro; IPR001460; Transpeptidase.	
DR	Pfam; PF03717; PBP dimer; 1.	
DR	Pfam; PF00905; Transpeptidase; 1.	
DR	Complete proteome.	
QY	SEQUENCE 593 AA; 65518 MW; F1CA3B85086C66F1 CRC64;	
Query Match 53.9%; Score 48; DB 16; Length 593;		
Best Local Similarity 52.9%; Pred. No. 30;		


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Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 194 NIGKSGIEKYYDNKLRG 210

RESULT 13
Q9ZCV6 PRELIMINARY; PRT; 594 AA.
ID Q9ZCV6 PRELIMINARY; PRT; 594 AA.
AC Q9ZCV6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Penicillin-binding protein (PBPAL).
GN RP565.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140 (1998).
DR EMBL; AJ235272; CAA15013.1; -.
DR PIR; C71661; C71661.
DR GO; GO:0008658; P:cell wall biosynthesis (sensu Bacteria); IEA.
DR GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
DR InterPro; IPR005311; PBP dimer.
DR InterPro; IPR001460; Transpeptidase.
DR Pfam; PF03717; PBP dimer; 1.
DR Pfam; PF09005; Transpeptidase; 1.
KW Complete proteome.
SQ SEQUENCE 594 AA; 67195 MW; 669AB06BAD4A28AC CRC64;

Query Match
Best Local Similarity 53.9%; Score 48; DB 16; Length 594;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIKQDSEKYYADSVRG 17
Db 194 NIGKSGIEKYYDNKLRG 210

RESULT 14
Q9ZVF9 PRELIMINARY; PRT; 247 AA.
ID Q9ZVF9 Q9SZQ3;
AC Q9ZVF9; Q9SZQ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG1259 protein (RE69226p).
GN CG1259.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RL "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

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RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacieb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003480; AAF47864.2; -.
DR EMBL; AY070590; AAL48061.1; -.
DR FlyBase; FBgn0035513; CGI259.
DR InterPro; IPR000618; Insect_cuticle.
DR Pfam; PF00379; Chitin_bind_4; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
SQ SEQUENCE 247 AA; 24279 MW; 3C46B29935A7AAD1 CRC64;

Query Match 53.4%; Score 47.5; DB 5; Length 247;
Best Local Similarity 52.6%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 2 IKQDSEK--YVADSVRG 17
Db 179 IEPDGRIRVSYADSING 197

RESULT 15
Q9FSK2 PRELIMINARY; PRT; 342 AA.
AC Q9FSK2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable ABC-transporter binding protein.
GN ORF342.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIAT 899;
RA Becker B.U., Neumann-Silkow F., Mueller P.;
RT "ORF 342, a potential binding protein of an ABC transporter in
RT Rhizobium tropici CIAT 899.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317885; AAG31660.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006059; SBP_bac_1.
DR InterPro; IPR001188; SpeTm/putr-bndng.
DR Pfam; PF01547; SBP_bac_1; 1.
DR PRINTS; PR00909; SPERMNDNDNG.
SQ SEQUENCE 342 AA; 37997 MW; CCBBBD9D01767628 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 342;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSEKYVADSVRG 17
Db 294 GAERYSDMKG 305

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Search completed: June 8, 2004, 18:30:03
Job time : 51.1406 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:20:03 ; Search time 6.48438 Seconds
(without alignments)
39.808 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	98	1	US-07-942-245-37
2	31	100.0	117	3	US-08-545-809A-95
3	31	100.0	312	4	US-09-079-029-10
4	28	90.3	5	2	US-08-318-157B-23
5	28	90.3	5	4	US-09-253-794-23
6	28	90.3	10	1	US-08-208-886C-83
7	28	90.3	10	1	US-08-208-886C-87
8	28	90.3	10	1	US-08-704-744-85
9	28	90.3	10	1	US-08-704-744-89
10	28	90.3	10	1	US-08-469-557-64
11	28	90.3	10	1	US-08-463-557-68
12	28	90.3	10	2	US-08-290-793B-64
13	28	90.3	10	2	US-08-290-793B-68
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19	28	90.3	119	2	US-08-318-157B-10
20	28	90.3	119	2	US-08-318-157B-11
21	28	90.3	119	2	US-08-318-157B-12
22	28	90.3	119	2	US-08-318-157B-13
23	28	90.3	119	2	US-08-318-157B-14
24	28	90.3	119	2	US-08-318-157B-15
25	28	90.3	119	2	US-08-318-157B-17
26	28	90.3	119	2	US-08-318-157B-57
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28 28 90.3 119 3 US-08-767-128-6 Sequence 6, Appli
29 28 90.3 119 4 US-09-253-794-2 Sequence 2, Appli
30 28 90.3 119 4 US-09-253-794-8 Sequence 8, Appli
31 28 90.3 119 4 US-09-253-794-9 Sequence 9, Appli
32 28 90.3 119 4 US-09-253-794-10 Sequence 10, Appl
33 28 90.3 119 4 US-09-253-794-11 Sequence 11, Appl
34 28 90.3 119 4 US-09-253-794-12 Sequence 12, Appl
35 28 90.3 119 4 US-09-253-794-13 Sequence 13, Appl
36 28 90.3 119 4 US-09-253-794-14 Sequence 14, Appl
37 28 90.3 119 4 US-09-253-794-15 Sequence 15, Appl
38 28 90.3 119 4 US-09-253-794-17 Sequence 17, Appl
39 28 90.3 119 4 US-09-253-794-57 Sequence 57, Appl
40 28 90.3 119 4 US-09-253-794-58 Sequence 58, Appl
41 28 90.3 211 4 US-09-512-563C-46 Sequence 46, Appl
42 28 90.3 218 2 US-08-399-889-25 Sequence 25, Appl
43 28 90.3 218 3 US-09-167-364-25 Sequence 25, Appl
44 28 90.3 218 3 US-09-439-897-4 Sequence 4, Appli
45 28 90.3 241 1 US-08-235-838-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-37
; Sequence 37, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-37

Query Match 100.0%; Score 31; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5

Db 31 SYWMS 35

```
RESULT 2
US-08-545-809A-95
; Sequence 95, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-95

Query Match 100.0%; Score 31; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 50 SYWMS 54
|||||

RESULT 3
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuttharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: F1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match 100.0%; Score 31; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 70 SYWMS 74
|||||

RESULT 4
US-08-318-157B-23
; Sequence 23, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CSA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-23
```

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 1 TYWMS 5

RESULT 5
US-09-253-794-23
; Sequence 23, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J. L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-253-794-23

Query Match 90.3%; Score 28; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 1 TYWMS 5

RESULT 6
US-08-208-886C-83
; Sequence 83, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dallie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424

APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-83

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 6 SYWMT 10

RESULT 7
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dallie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-208-886C-87

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
||||:
DB 6 SYWMT 10

RESULT 8

US-08-704-744-85
Sequence 85, Application US/08704744
Patent No. 5705154

GENERAL INFORMATION:

APPLICANT: Dalié, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:
INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-704-744-85

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
||||:
DB 6 SYWMT 10

RESULT 9

US-08-704-744-89
Sequence 89, Application US/08704744
Patent No. 5705154

GENERAL INFORMATION:

APPLICANT: Dalié, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-704-744-89

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
||||:
DB 6 SYWMT 10

RESULT 10

US-08-469-557-64
Sequence 64, Application US/08469557
Patent No. 5770403

GENERAL INFORMATION:

APPLICANT: Dalia, Barbara
APPLICANT: Le Hung
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/499,327
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-557-64

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 6 SYWMT 10

RESULT 11
US-08-469-557-68
Sequence 68, Application US/08469557
Patent No. 5770403
GENERAL INFORMATION:
APPLICANT: Dalia, Barbara
APPLICANT: Le Hung
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-557-68

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.3%; Score 28; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 ||||:
Db 6 SYWMT 10

RESULT 12

US-08-290-793B-64
; Sequence 64, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,793B
; FILING DATE: August 16, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-290-793B-64

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.3%; Score 28; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 ||||:
Db 6 SYWMT 10

RESULT 13

US-08-290-793B-68
; Sequence 68, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,793B
; FILING DATE: August 16, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

US-08-290-793B-64

STRANDEDNESS: single
TOPOLOGY: linear
US-08-290-793B-68

Query Match 90.3%; Score 28; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 6 SYWMT 10

RESULT 14
US-08-767-128-2

; Sequence 2, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:

US-08-767-128-2

Query Match 90.3%; Score 28; DB 3; Length 118;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 31 SYWMN 35

RESULT 15

US-08-767-128-8
; Sequence 8, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:

US-08-767-128-8

Query Match 90.3%; Score 28; DB 3; Length 118;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
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|
Db 31 SYWMN 35

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Job time : 21.4844 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 18:21:58 ; Search time 16.6406 Seconds
(without alignments)
84.534 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	100.0	5	9	US-09-832-312-61	Sequence 61, Appl
2	31	100.0	5	11	US-09-829-495-61	Sequence 61, Appl
3	31	100.0	53	12	US-10-424-599-259490	Sequence 259490,
4	31	100.0	98	12	US-10-453-698-55	Sequence 55, Appl
5	31	100.0	98	12	US-10-029-926B-85	Sequence 85, Appl
6	31	100.0	98	14	US-10-194-975-15	Sequence 15, Appl
7	31	100.0	98	15	US-10-308-817-55	Sequence 55, Appl
8	31	100.0	98	15	US-10-032-037B-85	Sequence 85, Appl
9	31	100.0	98	15	US-10-029-988B-85	Sequence 85, Appl
10	31	100.0	98	15	US-10-032-423A-85	Sequence 6, Appl
11	31	100.0	117	9	US-09-982-992A-6	Sequence 8, Appl
12	31	100.0	120	10	US-09-995-529-8	Sequence 8, Appl
13	31	100.0	120	12	US-09-995-529-8	Sequence 8, Appl
14	31	100.0	241	10	US-09-880-748-1889	Sequence 1889, Ap
15	31	100.0	241	12	US-10-293-418-1889	Sequence 1889, Ap

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16 31 100.0 247 10 US-09-880-748-1470 Sequence 1470, Ap
17 31 100.0 247 12 US-10-293-418-1470 Sequence 1470, Ap
18 31 100.0 247 14 US-10-322-673-48 Sequence 48, Appl
19 31 100.0 251 10 US-09-880-748-1594 Sequence 1594, Ap
20 31 100.0 251 12 US-10-293-418-1594 Sequence 1594, Ap
21 31 100.0 251 12 US-10-293-418-3245 Sequence 3245, Ap
22 31 100.0 290 12 US-10-406-830-4 Sequence 4, Appl
23 31 100.0 312 13 US-10-052-798-10 Sequence 10, Appl
24 31 100.0 312 14 US-10-288-917-10 Sequence 10, Appl
25 31 100.0 312 15 US-10-423-448-10 Sequence 10, Appl
26 31 100.0 395 9 US-09-738-626-4698 Sequence 4698, Ap
27 28 90.3 5 9 US-09-253-794-23 Sequence 23, Appl
28 28 90.3 5 10 US-09-977-797A-76 Sequence 76, Appl
29 28 90.3 10 12 US-10-239-656-14 Sequence 14, Appl
30 28 90.3 20 14 US-10-032-221B-30 Sequence 30, Appl
31 28 90.3 42 12 US-10-424-599-161302 Sequence 161302,
32 28 90.3 46 9 US-09-864-761-48095 Sequence 48095, A
33 28 90.3 59 12 US-10-424-599-211834 Sequence 211834,
34 28 90.3 79 14 US-10-032-221B-26 Sequence 26, Appl
35 28 90.3 85 12 US-10-424-599-268484 Sequence 268484,
36 28 90.3 88 14 US-10-032-221B-33 Sequence 33, Appl
37 28 90.3 88 14 US-10-032-221B-34 Sequence 34, Appl
38 28 90.3 100 9 US-09-840-459-36 Sequence 36, Appl
39 28 90.3 117 12 US-10-239-656-13 Sequence 13, Appl
40 28 90.3 117 12 US-09-948-004-16 Sequence 16, Appl
41 28 90.3 118 14 US-10-270-073-3 Sequence 3, Appl
42 28 90.3 118 15 US-10-435-614-11 Sequence 11, Appl
43 28 90.3 118 15 US-10-435-614-13 Sequence 13, Appl
44 28 90.3 119 9 US-09-253-794-2 Sequence 2, Appl
45 28 90.3 119 9 US-09-253-794-8 Sequence 8, Appl
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ALIGNMENTS

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RESULT 1
US-09-832-312-61
; Sequence 61, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-61
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SYWMS 5
Db 1 SYWMS 5
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RESULT 2
US-09-829-495-61
; Sequence 61, Application US/09829495
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; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Petrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-829-495-61

Query Match      100.0%; Score 31; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SYWMS 5
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Db      1 SYWMS 5

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US-10-424-599-259490
; Sequence 259490, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 259490
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_76345C.1.pep
;
US-10-424-599-259490

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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SYWMS 5
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Db      45 SYWMS 49

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US-10-453-698-55
; Sequence 55, Application US/10453698
; Publication No. US20040038308A1
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; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
;
US-10-453-698-55

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Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      31 SYWMS 35

RESULT 5
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; Sequence 85, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-029-926B-85

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SYWMS 5
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Db      31 SYWMS 35

RESULT 6
US-10-194-975-15
; Sequence 15, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-194-975-15

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Matches 5; Conservative 0; Mismatches 0;

QY 1 SYWMS 5
Db 31 SYWMS 35

RESULT 7
US-10-308-817-55
; Sequence 55, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-55

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Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 31 SYWMS 35

RESULT 8
US-10-032-037B-85
; Sequence 85, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
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US-10-032-037B-85

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 31 SYWMS 35

RESULT 9
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; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
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; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
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US-10-029-988B-85

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Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 SYWMS 35

RESULT 10
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; Sequence 85, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-85

Query Match 100.0%; Score 31; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 31 SYWMS 35

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; Sequence 6, Application US/09982992A
; Patent No. US20020164337A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M. et al.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TRE.
; FILE REFERENCE: P06922US02/BAS
; CURRENT APPLICATION NUMBER: US/09/982,992A
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/277,287
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/241,832
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
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taps 0;

Qy 1 SYWMS 5
| | | | |
Db 31 SYWMS 35

Search completed: June 8, 2004, 18:52:57
Job time : 21.6406 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 18:27:04 ; Search time 4.92188 Seconds
(without alignments)
97.718 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62
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Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	31	100.0	114	2	S36280
5	31	100.0	115	2	S38714
6	31	100.0	117	2	S78486
7	31	100.0	117	2	S17079
8	31	100.0	118	2	S00700
9	31	100.0	122	2	A33989
10	31	100.0	122	2	S31675
11	31	100.0	136	2	S13587
12	31	100.0	139	2	I37781
13	31	100.0	147	2	I37780
14	31	100.0	207	2	F95966
15	31	100.0	939	2	A82275
16	31	100.0	942	2	B84469
17	31	100.0	942	2	T37539
18	31	100.0	1254	1	A32686
19	31	100.0	1844	2	T31890
20	28	90.3	101	2	H37262
21	28	90.3	103	2	PH0986
22	28	90.3	106	2	S26315
23	28	90.3	108	2	S26316
24	28	90.3	110	2	S26317
25	28	90.3	117	2	G45722
26	28	90.3	118	2	C30560
27	28	90.3	120	2	PD0080
28	28	90.3	126	2	E71185
29	28	90.3	161	2	S49488

ALIGNMENTS

RESULT 1

PL0123

Ig heavy chain V-III region (TD-Vr) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C:Accession: PL0123; S26897

R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:88286083; PMID:2840480

A:Accession: PL0123

A:Molecule type: mRNA

A:Residues: 1-98 <BIR>

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL f

A:Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26897

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z12354; NID:G32930; PIDN:CAA78224.1; PID:G32931

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 31; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

DB 31 SYWMS 35

RESULT 2

S26460

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26460

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26460

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <KAV>

hypothetical oligo
22K antigen - fluk
22.6k tegument ant
gene sj22 protein
conserved hypochet
hypothetical prote
collagen alpha 3(I
hypothetical prote
collagen alpha 3(I
collagen alpha 5(I
probable transport
collagen alpha 1(I
collagen alpha 2(I
C05B5.4 protein (c
collagen alpha 4(I
conserved hypochet

30 28 90.3 180 2 T39395
31 28 90.3 190 2 A45601
32 28 90.3 190 2 A54518
33 28 90.3 191 2 S43178
34 28 90.3 204 2 B82166
35 28 90.3 216 2 A72291
36 28 90.3 220 2 B49736
37 28 90.3 226 2 T29404
38 28 90.3 246 2 I48302
39 28 90.3 253 2 I48304
40 28 90.3 254 2 E83619
41 28 90.3 258 2 B61228
42 28 90.3 261 2 A34476
43 28 90.3 309 2 S43573
44 28 90.3 312 2 I48303
45 28 90.3 314 2 AC2690

A;Cross-references: EMBL:X59106; NID:G51707; PIDN:CAA41832.1; PID:G51708
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 13 SYWMS 17

RESULT 3

Ig heavy chain V region (clone 2E8) - human (fragment)

A;Species: Homo sapiens (man)
 C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C;Accession: PH1655
 R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, B.H.
 J. Exp. Med. 178, 331-336, 1993
 A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcus aureus
 A;Reference number: PH1642; MUID:93301610; PMID:8315389
 A;Accession: PH1655
 A;Molecule type: mRNA
 A;Residues: 1-110 <HIL>

A;Experimental source: B cell
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 23 SYWMS 27

RESULT 4

Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)

A;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C;Accession: S36280
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36256; MUID:93178448; PMID:7679990
 A;Accession: S36280
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-114 <GRI>

A;Cross-references: EMBL:Z18822
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 31 SYWMS 35

RESULT 5

Ig heavy chain V region - mouse

A;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C;Accession: S38714
 R;Gimanis, A.Y.
 submitted to the EMBL Data Library, November 1993
 A;Reference number: S38713

A;Accession: S38714
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-115 <CIM>

A;Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;14-99/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 30 SYWMS 34

RESULT 6

Ig heavy chain V region (clone FL13-28) - human (fragment)

A;Species: Homo sapiens (man)
 C;Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
 C;Accession: S78486; S31115
 R;Raaphorst, F.M.
 submitted to the EMBL Data Library, October 1991

A;Reference number: S78486
 A;Accession: S78486
 A;Molecule type: mRNA
 A;Residues: 1-117 <RAA>

A;Cross-references: EMBL:X62965

A;Experimental source: clone FL13-28

R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31115

A;Molecule type: mRNA

A;Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97 <RAW>

A;Cross-references: EMBL:X62965

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 31 SYWMS 35

RESULT 7

Ig heavy chain V-gene (clone HHG19) - human

A;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C;Accession: S60299; S17079
 R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
 Immunol. Lett. 34, 57-62, 1992

A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive im

A;Reference number: S60295; MUID:93122853; PMID:1282498

A;Accession: S60299

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <KU2>

A;Cross-references: EMBL:X62128; NID:G38340; PIDN:CAA44059.1; PID:G38341

A;Note: the authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72

C;Genetics:

A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 50 SYWMS 54

RESULT 8

Ig heavy chain V region - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
 C;Accession: S00700
 R;Cuisinier, A.M.; Honjo, T.
 Nucleic Acids Res. 15, 5888, 1987
 A;Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy chain
 A;Reference number: S00700; MUID: 87289054; PMID: 3112743
 A;Accession: S00700
 A;Molecule type: DNA
 A;Residues: 1-118 <YAM>
 A;Cross-references: EMBL:Y00380; NID:G64810; PIDN:CAA68452.1; PID:G64811
 A;Note: the sequence was determined from the germline gene
 C;Genetics:

A;Introns: 15/3

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 50 SYWMS 54

RESULT 9

A33989
 Ig heavy chain V-1-D-J region - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 16-Aug-1996
 C;Accession: A33989
 R;Hsu, E.; Schwager, J.; Alt, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989
 A;Title: Evolution of immunoglobulin genes: V-H families in the amphibian Xenopus.
 A;Reference number: A33989; MUID: 90046727; PMID: 2510156
 A;Accession: A33989

A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-122 <HSU>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 31 SYWMS 35

RESULT 10

S31675

Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31675
 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A;Reference number: S31585
 A;Accession: S31675
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-122 <CUI>
 A;Cross-references: EMBL:Z14175; NID:g31015; PIDN:CAA78544.1; PID:g31016
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;21-104/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 37 SYWMS 41

RESULT 11

S31587
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31587
 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A;Reference number: S31585
 A;Accession: S31587
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-136 <CUI>
 A;Cross-references: EMBL:Z14189; NID:g31005; PIDN:CAA78558.1; PID:g31006
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;31-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 |||||
 Db 47 SYWMS 51

RESULT 12

I37781
 Ig variable region (VDJ) (clone T21-9) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
 C;Accession: I37781; S25475
 R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
 A;Reference number: A36876; MUID: 94113917; PMID: 8290556
 A;Accession: I37781

A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-139 <RES>
 A;Cross-references: EMBL:X67908; NID:g33580; PIDN:CAA48106.1; PID:g33581
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;35-118/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
|||||
Db 51 SYWMS 55

RESULT 13

I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
R;Accession: I37780; S25474
C;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by B
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <RES>
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
|||||
Db 44 SYWMS 48

RESULT 14

P95966
Probable aldehyde or xanthine dehydrogenase, iron-sulfur subunit protein [imported] - Si
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F95966
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95966
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49398.1; PID:gl5140884; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smb21559
A;Genome: plasmid

Query Match 100.0%; Score 31; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
|||||
Db 178 SYWMS 182

RESULT 15

AE2275
hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2275
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2275
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-939 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAH75455.1; PID:gl7132890; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3756

Query Match 100.0%; Score 31; DB 2; Length 939;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
|||||
Db 931 SYWMS 935

Search completed: June 8, 2004, 18:54:09
Job time : 5.92188 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:31:59 ; Search time 2.8125 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	1254	1	DPOG YEAST
2	28	90.3	168	1	LSPA_VIBVU
3	28	90.3	169	1	LSPA_VIBPA
4	28	90.3	180	1	ORN_SCHPO
5	28	90.3	190	1	TEGU_SCHMA
6	28	90.3	315	1	YK04_CABEL
7	28	90.3	342	1	TORT_ECO57
8	28	90.3	342	1	TORT_ECOLI
9	28	90.3	359	1	DNLI_BPT7
10	28	90.3	385	1	YWM_BACSU
11	28	90.3	393	1	Y306_MYCGE
12	28	90.3	455	1	YAO6_SCHPO
13	28	90.3	471	1	CA34_BOVIN
14	28	90.3	583	1	PHBC_AZOCA
15	28	90.3	745	1	FSP1_RAT
16	28	90.3	754	1	CA54_CANFA
17	28	90.3	1002	1	YAJ7_ANASP
18	28	90.3	1669	1	CA14_HUMAN
19	28	90.3	1669	1	CA14_MOUSE
20	28	90.3	1670	1	CA34_HUMAN
21	28	90.3	1685	1	CA54_HUMAN
22	28	90.3	1691	1	CA64_HUMAN
23	28	90.3	1707	1	CA24_MOUSE
24	28	90.3	1712	1	CA24_HUMAN
25	28	90.3	1758	1	CA24_CAEEL
26	28	90.3	1763	1	CA24_ASCSU
27	28	90.3	2210	1	RRL_BEOSM
28	28	90.3	2297	1	MORX_BACSU
29	28	90.3	3587	1	SF2_SCHPO
30	28	90.3	4540	1	DYHC_PARTE
31	27	87.1	116	1	HV36_MOUSE
32	27	87.1	117	1	HV04_MOUSE
33	27	87.1	117	1	HV05_MOUSE

34	27	87.1	117	1	HV06_MOUSE	P01750 mus musculus
35	27	87.1	117	1	HV09_MOUSE	P01753 mus musculus
36	27	87.1	117	1	HV10_MOUSE	P01754 mus musculus
37	27	87.1	117	1	HV41_MOUSE	P01811 mus musculus
38	27	87.1	117	1	HV42_MOUSE	P01812 mus musculus
39	27	87.1	117	1	HV49_MOUSE	P06328 mus musculus
40	27	87.1	118	1	HV39_MOUSE	P01809 mus musculus
41	27	87.1	119	1	HV37_MOUSE	P01807 mus musculus
42	27	87.1	119	1	HV38_MOUSE	P01808 mus musculus
43	27	87.1	119	1	HV40_MOUSE	P01810 mus musculus
44	27	87.1	120	1	HV50_MOUSE	P06329 mus musculus
45	27	87.1	139	1	HV07_MOUSE	P01751 mus musculus

ALIGNMENTS

RESULT 1
DPOG YEAST
ID DPOG YEAST STANDARD; PRT; 1254 AA.
AC P15801; Q08785;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase gamma (EC 2.7.7) (Mitochondrial DNA polymerase
DE catalytic subunit).
GN MIPI OR YOR330C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90062193; PubMed=2684980;
RA Foury F.;
RT "Cloning and sequencing of the nuclear gene MIPI encoding the
RT catalytic subunit of the yeast mitochondrial DNA polymerase.";
RL J. Biol. Chem. 264:20552-20560 (1989).
RN [2]
RP REVISIONS.
RA Foury F.;
RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051586; PubMed=8896263;
RA Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
RT "Sequence of 29 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I.";
RL Yeast 12:999-1004 (1996).
RN [4]
RP SEQUENCE OF 987-1254 FROM N.A.
RC STRAIN=GRP88;
RA Song J.M., Cheung E., Rabinowitz J.C.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the replication of mitochondrial DNA.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -!- COFACTOR: Magnesium.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
CC alpha, beta, gamma, delta, and epsilon which are responsible for
CC different reactions of DNA synthesis.
CC -!- SIMILARITY: Belongs to the DNA polymerase type-A family.
CC
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CC

DR EMBL; J05117; AAA17543.1; -;
DR EMBL; Z49821; CAA89977.1; -;
DR EMBL; Z75238; CAA9652.1; ALT_INIT.
DR EMBL; U42227; AAA85442.1; -;
DR PIR; S62062; A32686.
DR GernOnline; 143918; -;
DR SGD; S0005857; MPI.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0006261; P:DNA dependent DNA replication; IDA.
DR InterPro; IPR001098; DNA_pol.
DR InterPro; IPR002297; DNA_polG.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00867; DNAPOIG.
DR SMART; SMO0482; POLAC; 1.
DR PROSITE; PS00447; DNA_POLYMERASE_A; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Mitochondrion; Magnesium.
FT DOMAIN 150 189 CONSENSUS FOR POLYMERASES MOTIF II.
FT DOMAIN 198 198 CONSENSUS FOR POLYMERASES MOTIF I.
FT DOMAIN 225 255 CONSENSUS FOR POLYMERASES MOTIF VI.
FT CONFLICT 8 8 S -> F (IN REF. 1).
FT CONFLICT 35 35 T -> A (IN REF. 1).
FT CONFLICT 222 222 I -> V (IN REF. 1).
FT CONFLICT 357 357 E -> K (IN REF. 1).
FT CONFLICT 540 541 TH -> MN (IN REF. 1).
FT CONFLICT 616 616 S -> N (IN REF. 1).
FT CONFLICT 661 661 A -> T (IN REF. 1).
FT CONFLICT 978 978 S -> P (IN REF. 1).
FT CONFLICT 986 986 N -> S (IN REF. 1).
SQ SEQUENCE 1254 AA; 143501 MW; 80BE686E8EA9F2EC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 599 SYWMS 603

RESULT 2
LSPA VIBVU STANDARD; PRT; 168 AA.
ID LSPA VIBVU
AC Q8DE88;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
peptidase) (Signal peptidase II) (SPase II).
GN LSPA OR VV10506.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein specifically catalyzes the removal of
signal peptides from prolipoproteins (By similarity).
CC -!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
membrane prolipoproteins. Hydrolyzes Xaa-Xbb-Xcc-|-Cys, in which
Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc
is often Gly or Ala, and the Cys is alkylated on sulfur with a
diacylglyceryl group.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- SIMILARITY: Belongs to peptidase family A8.
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CC
CC EMBL; AE016798; AAC09025.1; -;
CC HAMAP; MF_00161; -; 1.
CC InterPro; IPR001872; Peptidase_A8.
CC Pfam; PF01252; Peptidase_A8; 1.
CC PRINTS; PR00781; LIPOSIGPTASE.
CC PRODOM; PD004304; SigPase_A8; 1.
CC TIGRFAMS; TIGR00077; lspa; 1.
CC PROSITE; PS00855; SPase_II; 1.
KW Hydrolase; aspartyl protease; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 12 34 Potential.
FT TRANSMEM 70 92 Potential.
FT TRANSMEM 104 126 Potential.
FT TRANSMEM 136 158 Potential.
FT ACT_SITE 119 119 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 168 AA; 19200 MW; 825297099B2D7BA3 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 168;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 89 TYWMS 93

RESULT 3
LSPA VIBPA STANDARD; PRT; 169 AA.
ID LSPA VIBPA
AC Q87S89;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
peptidase) (Signal peptidase II) (SPase II).
GN LSPA OR VP0535.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nejima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -!- FUNCTION: This protein specifically catalyzes the removal of
signal peptides from prolipoproteins (By similarity).
CC -!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
membrane prolipoproteins. Hydrolyzes Xaa-Xbb-Xcc-|-Cys, in which
Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc
is often Gly or Ala, and the Cys is alkylated on sulfur with a
diacylglyceryl group.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- SIMILARITY: Belongs to peptidase family A8.
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CC -----
 CC EMBL: AF005074; BAC58798.1; --
 CC HAMAP: MF 00161; -- 1.
 CC InterPro: IPR001872; Peptidase_A8.
 CC Pfam: PF01452; Peptidase_A8; 1.
 CC PRINTS: PR00781; LIPOSIGTASE.
 CC PROSITE: PS00855; SPASE II; 1.
 CC KW Hydrolase; Aspartyl protease; Transmembrane; Inner membrane;
 CC Complete proteome.
 CC FT TRANSMEM 15 34 Potential.
 CC FT TRANSMEM 47 66 Potential.
 CC FT TRANSMEM 70 92 Potential.
 CC FT TRANSMEM 104 126 Potential.
 CC FT TRANSMEM 136 158 Potential.
 CC FT ACT_SITE 119 119 BY SIMILARITY.
 CC FT ACT_SITE 146 146 BY SIMILARITY.
 CC SQ SEQUENCE 169 AA; 19265 MW; F9FA101EC910A74F CRC64;

Query Match 90.3%; Score 28; DB 1; Length 169;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

DB 89 TYWMS 93

RESULT 4

ORN SCHPO
 ID ORN SCHPO STANDARD; PRT; 180 AA.
 AC O94626;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable oligoribonuclease (EC 3.1.21.1).
 GN SPBCL347.07.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."

RL Nature 415:871-880(2002).

CC -!- FUNCTION: 3'-to-5' exoribonuclease specific for small
 CC oligoribonucleotides (By similarity).

CC -!- SIMILARITY: Belongs to the oligoribonuclease family.

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CC EMBL: AL035548; CAB37438.1; --
 CC PIR: T39395; T39395.
 CC GeneDB SPombe; SPBCL347.07; --
 CC InterPro: IPR006055; Exonuclease.
 CC Pfam: PF00929; Exonuclease; 1.
 CC SMART: SM00479; EXOIII; 1.
 CC KW Hypothetical protein; Hydrolase; Exonuclease; Nuclease.
 CC FT ACT_SITE 130 130 POTENTIAL.
 CC SQ SEQUENCE 180 AA; 20785 MW; 7AB466905131B603 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 180;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

DB 176 SYWMS 180

RESULT 5

TEGU SCHWA
 ID TEGU SCHWA STANDARD; PRT; 190 AA.
 AC P14202;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tegument antigen (I(H)A) (Antigen SMA22.6) (A12).
 OS Schistosoma mansoni (Blood fluke).
 CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 CC Schistosomatidae; Schistosomatidae; Schistosoma.
 CC NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Puerto Rican.
 RX MEDLINE=87014570; PubMed=2429181;
 RA Stein L.D.; David J.R.;
 RT "Cloning of a developmentally regulated tegument antigen of
 RT Schistosoma mansoni."
 RL Mol. Biochem. Parasitol. 20:253-264 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91304514; PubMed=1852171;
 RA Jeffs S.A.; Hagan P.; Allen R.; Correa-Oliveira R.; Smithers S.R.,
 RA Simpson A.J.G.;
 RT "Molecular cloning and characterisation of the 22-kilodalton adult
 RT Schistosoma mansoni antigen recognised by antibodies from mice
 RT protectively vaccinated with isolated tegumental surface membranes."
 RL Mol. Biochem. Parasitol. 46:159-168 (1991).
 CC -!- TISSUE SPECIFICITY: Adult tegument.
 CC -!- DEVELOPMENTAL STAGE: This antigen occurs in adults and sporocysts
 CC but not in cercariae, eggs or newly transformed schistosomula. It
 CC is a developmentally regulated protein.
 CC -!- SIMILARITY: TO S.MANSONI ANTIGEN SM21.7.

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CC	EMBL; M29837; AAA29856.1; -.	
DR	EMBL; M37003; AAA29922.1; -.	
DR	PIR; A54518; A54518.	
DR	InterPro; IPR001372; Dynein_light1.	
DR	InterPro; IPR002048; EF-hand.	
DR	Pfam; PF00036; efnh; 2.	
DR	SMART; SM00054; EFN; 2.	
DR	PROSITE; PS00019; EF_HAND; UNKNOWN_1.	
KW	Antigen.	
QY	SEQUENCE 190 AA; 22578 MW; F265EFA29AA7ACDB CRC64;	
DB	Query Match 90.3%; Score 28; DB 1; Length 190;	
	Best Local Similarity 80.0%; Pred. No. 1.4e+02;	
	Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SYWMS 5	
DB	160 SYWMS 164	
RESULT 6		
YK04 CAEEL	STANDARD; PRT; 315 AA.	
AC	P34232; 1994 (Rel. 28, Created)	
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	01-NOV-1995 (Rel. 32, Last annotation update)	
DE	Hypothetical 35.9 kDa protein C05B5.4 in chromosome III.	
GN	C05B5.4.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-Bristol N2;	
RA	Mortimore B.J.;	
RL	Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.	
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DR	EMBL; Z32679; CAA83591.1; -.	
DR	PIR; B88571; B88571.	
DR	WormPep; C05B5.4; C800880.	
KW	Hypothetical protein.	
QY	SEQUENCE 315 AA; 35918 MW; D6665F5FAB040BCF CRC64;	
DB	Query Match 90.3%; Score 28; DB 1; Length 315;	
	Best Local Similarity 80.0%; Pred. No. 2.2e+02;	
	Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SYWMS 5	
DB	281 TYWMS 285	
RESULT 7		
TORT ECO57	STANDARD; PRT; 342 AA.	
ID	TORT ECO57	
AC	P58358;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Periplasmic protein tort precursor.	
GN	TORT OR Z1411 OR ECS1149.	
OS	Escherichia coli.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC	Enterobacteriaceae; Escherichia.	
OX	NCBI_TaxID=83334;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;	
RC	MEDLINE=21074935; PubMed=11206551;	
RA	Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,	
RA	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,	
RA	Posfal G., Hackett J., Klink N., Boutin A., Shao Y., Miller L.,	
RA	Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,	
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,	
RA	Welch R.A., Blattner F.R.;	
RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";	
RL	Nature 409:529-533(2001).	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=O157:H7 / RIMD 050952;	
RC	MEDLINE=21156231; PubMed=11258796;	
RA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,	
RA	Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,	
RA	Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,	
RA	Kuhara S., Shiba T., Hattori M., Shinagawa H.;	
RT	"Complete genome sequence of enterohemorrhagic Escherichia coli	
RT	O157:H7 and genomic comparison with a laboratory strain K-12.";	
RL	DNA Res. 8:11-22(2001).	
CC	!- FUNCTION: Upon binding a putative inducer it probably interacts	
CC	with torts and allows it to play a role in the induction of the	
CC	tortCAD operon for trimethylamine N-oxide reductase (By	
CC	similarity).	
CC	!- SUBCELLULAR LOCATION: Periplasmic (By similarity).	
CC	!- SIMILARITY: Belongs to the bacterial extracellular solute-binding	
CC	protein family 2.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	or send an email to license@isb-sib.ch).	
DR	EMBL; AE005293; AAG55541.1; -.	
DR	EMBL; AP002554; BAB34572.1; -.	
DR	PIR; A85635; A85635.	
DR	PIR; E90772; E90772.	
DR	InterPro; IPR001761; PeriplaBP_LacI.	
DR	Pfam; PF00532; Peripla_BP_Like; 1.	
KW	Transport; Periplasmic; Signal; Complete proteome.	
FT	CHAIN 1 18 BY SIMILARITY.	
FT	SIGNAL 19 342 PERIPLASMIC PROTEIN TORT.	
QY	SEQUENCE 342 AA; 37950 MW; 8B44A1B064DBA54D CRC64;	
DB	Query Match 90.3%; Score 28; DB 1; Length 342;	
	Best Local Similarity 80.0%; Pred. No. 2.4e+02;	
	Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SYWMS 5	
DB	57 SYWMS 61	
RESULT 8		
TORT ECO1	STANDARD; PRT; 342 AA.	
ID	TORT ECO1	
AC	P36683; P75888;	
DT	01-FEB-1995 (Rel. 31, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Periplasmic protein tort precursor.	
GN	TORT OR B0994.	
OS	Escherichia coli.	

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MC4100;
 RX MEDLINE=94364937; PubMed=8083154;
 RA Simon G., Mejean V., Jourlin C., Chippaux M., Pascal M.-C.;
 RT "The *corK* gene of *Escherichia coli* encodes a response regulator
 RT protein involved in the expression of the trimethylamine N-oxide
 RT reductase genes.";
 RL J. Bacteriol. 176:5601-5606(1994).
 RN [2]
 RP REVISIONS TO 29-30, SEQUENCE OF 19-24, AND CHARACTERIZATION.
 RC STRAIN=K12;
 RX MEDLINE=96165284; PubMed=8576063;
 RA Jourlin C., Simon G., Pommier J., Chippaux M., Mejean V.;
 RT "The periplasmic Tort protein is required for trimethylamine N-oxide
 RT reductase gene induction in *Escherichia coli*.";
 RL J. Bacteriol. 178:1219-1223 (1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayaashi K., Horiho A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 CC -!- FUNCTION: Upon binding a putative inducer it probably interacts
 CC with *tors* and allows it to play a role in the induction of the
 CC *torCAD* operon for trimethylamine N-oxide reductase.
 CC -!- SUBCELLULAR LOCATION: Periplasmic.
 CC -!- SIMILARITY: Belongs to the bacterial extracellular solute-binding
 CC protein family 2.
 CC
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 CC
 DR EMBL; X94231; CAAG3921.1; -;
 DR EMBL; AE000201; RAC74079.1; -;
 DR EMBL; D90736; BAA36136.1; -;
 DR EMBL; D90737; BAA35761.1; -;
 DR PIR; H64840; H64840.
 DR Ecogene; EGI2616; tort.
 DR InterPro; IPR001761; PeriplaBP/LacI.
 DR Pfam; PF00532; Peripla_BP_like; 1.
 KW Transport; Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 18
 FT CHAIN 19 342 PERIPLASMIC PROTEIN TORT.
 FT CONFLICT 59 59 W -> S (IN REF. 1).
 FT CONFLICT 230 230 A -> R (IN REF. 1).
 FT SEQUENCE 342 AA; 37864 MW; 82FC7AEDF3B2DB9 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 342;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 Db 57 SYWLS 61
 RESULT 9
 DNLI BPT7
 ID DNLI BPT7 STANDARD; PRT; 359 AA.
 AC P00969;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
 GN 1.3
 OS Bacteriophage T7.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC T7-like viruses.
 OX NCBI_TaxID=10760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83241725; PubMed=6864790;
 RA Dunn J.J., Studier F.W.;
 RT "Complete nucleotide sequence of bacteriophage T7 DNA and the
 RT locations of T7 genetic elements.";
 RL J. Mol. Biol. 166:477-535(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82078034; PubMed=7310871;
 RA Dunn J.J., Studier F.W.;
 RT "Nucleotide sequence from the genetic left end of bacteriophage T7
 RT DNA to the beginning of gene 4.";
 RL J. Mol. Biol. 148:303-330(1981).
 RN [3]
 RP SEQUENCE OF 278-359 FROM N.A.
 RX MEDLINE=81053683; PubMed=7001354;
 RA Dunn J.J., Studier F.W.;
 RT "The transcription termination site at the end of the early region of
 RT bacteriophage T7 DNA.";
 RL Nucleic Acids Res. 8:2119-2132 (1980).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=81054683; PubMed=6254001;
 RA Saito H., Tabor S., Tamanoi F., Richardson C.C.;
 RT "Nucleotide sequence of the primary origin of bacteriophage T7 DNA
 RT replication: relationship to adjacent genes and regulatory
 RT elements.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=96222302; PubMed=8653795;
 RA Subramanya H.S., Doherty A.J., Ashford S.R., Wigley D.B.;
 RT "Crystal structure of an Arp-dependent DNA ligase from bacteriophage
 RT T7.";
 RL Cell 85:607-615 (1996).
 CC -!- FUNCTION: DNA LIGASE, WHICH IS EXPRESSED IN THE EARLY STAGE OF
 CC LYTIC DEVELOPMENT, HAS BEEN IMPLICATED IN T7 DNA SYNTHESIS AND
 CC GENETIC RECOMBINATION. IT MAY ALSO PLAY A ROLE IN T7 DNA REPAIR.
 CC -!- CATALYTIC ACTIVITY: ATP + {deoxyribonucleotide}(N) +
 CC {deoxyribonucleotide}(N) = AMP + diphosphate +
 CC -!- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.
 CC
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CC -----CAA24322.1; --
DR ENBL; V01124; CAA24326.1; --
DR ENBL; V01126; CAA24326.1; --
DR ENBL; V01127; CAA24336.1; --
DR ENBL; V01146; CAA24393.1; --
DR PIR; E94615; LOBP37.
DR PDB; 1A01; 25-MAR-98.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF01068; DNA_ligase; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; 1.
DR PROSITE; PS00333; DNA_LIGASE_A2; 1.
DR PROSITE; PS0160; DNA_LIGASE_A3; 1.
DR DNA repair; DNA replication; DNA recombination; ATP-binding; Ligase;
KW 3D-structure.
KW BINDING.
FT FT TURN 34 34 AMP (BY SIMILARITY).
FT FT TURN 3 4
FT FT STRAND 9 13
FT FT HELIX 16 26
FT FT STRAND 29 33
FT FT STRAND 38 45
FT FT TURN 46 47
FT FT STRAND 49 53
FT FT TURN 55 56
FT FT STRAND 59 59
FT FT HELIX 61 66
FT FT STRAND 68 69
FT FT HELIX 71 78
FT FT TURN 85 86
FT FT STRAND 87 96
FT FT TURN 101 103
FT FT HELIX 104 109
FT FT STRAND 117 117
FT FT STRAND 139 139
FT FT TURN 141 143
FT FT STRAND 144 153
FT FT HELIX 154 159
FT FT STRAND 163 166
FT FT HELIX 167 184
FT FT TURN 186 187
FT FT STRAND 189 192
FT FT STRAND 195 198
FT FT HELIX 201 212
FT FT TURN 213 215
FT FT STRAND 219 222
FT FT TURN 224 225
FT FT STRAND 227 228
FT FT STRAND 231 239
FT FT STRAND 243 253
FT FT TURN 257 259
FT FT STRAND 267 271
FT FT TURN 273 274
FT FT STRAND 277 281
FT FT HELIX 286 299
FT FT TURN 300 302
FT FT TURN 321 324
FT FT STRAND 326 331
FT FT STRAND 333 334
FT FT TURN 336 337
FT FT STRAND 340 341
FT FT STRAND 344 348
SQ SEQUENCE 359 AA; 41133 MW; 43DA453B71BDF8DC CRC64;

Query Match 90.3%; Score 28; DB 1; Length 359;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWMS 5
DB 50 SYWLS 54

```

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RESULT 10
YWBM_BACSU
ID_YWBM_BACSU STANDARD; PRT; 385 AA.
AC P39596;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ywbm.
GN YWBM OR IPA-28D OR BSU38270.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
RA Rapoport G., Danchin A.;
RA "Bacillus subtilis genome project: cloning and sequencing of the 97
RA kb region from 325 degrees to 333 degrees.";
RL Mol. Microbiol. 10:371-384(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Hailech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche B., Roche M., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- SIMILARITY: TO E.COLI YCDO.
CC -----
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CC -----
DR ENBL; X73124; CAA51584.1; --
DR ENBL; Z99123; CAB15853.1; --
DR PIR; S39683; S39683.
DR Subtilist; BGI0574; ywbm.
DR InterPro; IPR007399; DUF451.

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DR Pfam; PF04302; DUP451; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 385 AA; 42796 MW; 1F9DCH6BA385A3C7 CRC64;

Query Match
  90.3%; Score 28; DB 1; Length 385;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 78 SYWLS 82

RESULT 11.
Y306_MYCGE STANDARD; PRT; 393 AA.
AC P47548;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG306.
GN MG306.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bost K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403 (1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC -----
DR EMBL; U39711; AAC71528.1; -.
DR PIR; H64233; H64233.
DR TIGR; MG306; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 15 35 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 131 151 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT TRANSMEM 289 309 POTENTIAL.
FT TRANSMEM 349 369 POTENTIAL.
SQ SEQUENCE 393 AA; 45750 MW; D740FDA979EC364A CRC64;

Query Match
  90.3%; Score 28; DB 1; Length 393;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 173 SYWLS 177

RESULT 12
YAO6_SCHPO STANDARD; PRT; 455 AA.
ID YAO6_SCHPO

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AC Q1085;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C11D3.06 in chromosome I.
GN SPAC11D3.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Holzer E., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.-J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the multi antimicrobial extrusion (MATE)
CC family.
CC -----
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CC -----
DR EMBL; Z68166; CRA92307.1; -.
DR PIR; T37517; T37517.
DR GenDB Spombe; SPAC11D3.06; -.
DR InterPro; IPR002528; MATE.
DR Pfam; PF01554; MATE; 2.
DR TIGRfams; TIGR00797; mate; 1.
KW Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 184 204 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 280 300 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT TRANSMEM 405 425 POTENTIAL.
SQ SEQUENCE 455 AA; 49086 MW; FF41087BC6405327 CRC64;

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Query Match          90.3%; Score 28; DB 1; Length 455;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWMS 5
DB      196 SYWLS 200
      |||||
      |||||

RESULT 13
CA34 BOVIN
ID CA34_BOVIN STANDARD; PRT; 471 AA.
AC Q28084;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Collagen alpha 3(IV) chain (Fragment).
GN COL4A3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN R1
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA MEDLINE=91093146; PubMed=1985905;
RA Morrison K.E., Germlo G.G., Reiders S.T.;
RT "Use of the polymerase chain reaction to clone and sequence a cDNA
RL encoding the bovine alpha 3 chain of type IV collagen.";
RN J. Biol. Chem. 266:34-39(1991).
[2]
RN R2
RP SEQUENCE OF 227-258.
RC TISSUE=Kidney;
RA MEDLINE=90202779; PubMed=2318822;
RA Gunwar S., Saus J., Noelken M.E., Hudson B.G.;
RT "Glomerular basement membrane. Identification of a fourth chain,
RT alpha 4, of type IV collagen.";
RL J. Biol. Chem. 265:5466-5469(1990).
[3]
RN R3
RP SEQUENCE OF 227-254.
RA MEDLINE=88330844; PubMed=3417661;
RA Saus J., Wieslander J., Langeveld J.P.M., Quinones S., Hudson B.G.;
RT "Identification of the Goodpasture antigen as the alpha 3(IV) chain
RT of collagen IV.";
RL J. Biol. Chem. 263:13374-13380(1988).
[4]
RN R4
RP SEQUENCE OF 227-244.
RA MEDLINE=87222419; PubMed=2438283;
RA Butkowski R.J., Langeveld J.P.M., Wieslander J., Hamilton J.,
RA Hudson B.G.;
RT "Localization of the Goodpasture epitope to a novel chain of basement
RT membrane collagen.";
RL J. Biol. Chem. 262:7874-7877(1987).
-!- FUNCTION: Type IV collagen is the major structural component of
CC glomerular basement membranes (GBM), forming a 'chicken-wire'
CC meshwork together with laminins, proteoglycans and entactin/
CC nidogen.
CC
CC -!- SUBUNIT: There are six type IV collagen isoforms, alpha 1(IV)-
CC alpha 6(IV), each of which can form a triple helix structure
CC with 2 other chains to generate type IV collagen network.
CC
CC -!- SUBCELLULAR LOCATION: Cell surface (Potential).
CC
CC -!- DOMAIN: Alpha chains of type IV collagen have a noncollagenous
CC domain (NC1) at their C-terminus, frequent interruptions of the
CC G-X-Y repeats in the long central triple-helical domain (which may
CC cause flexibility in the triple helix), and a short N-terminal
CC triple-helical 7S domain.
CC
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC
CC -!- PTM: Type IV collagens contain numerous cysteine residues which
CC are involved in inter- and intramolecular disulfide bonding. 12 of
CC these, located in the NC1 domain, are conserved in all known type
CC IV collagens.

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-!- SIMILARITY: TO OTHER TYPE IV COLLAGENS.
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-----
CC EMBL; M63139; AAA62708.1; -.
CC PIR; A39024; A39024.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR001442; Procollagn4_C.
CC Pfam; PF01413; C4; 2.
CC Pfam; PF01391; Collagen; 4.
CC ProDom; PD003923; ProcollagnC4; 1.
CC SMART; SM00111; C4; 2.
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Glycoprotein; Basement membrane; Collagen; Cell adhesion.
FT NON_TER 1 1
FT DOMAIN <1 238 TRIPLE-HELICAL REGION.
FT SITE 239 471 NONHELICAL REGION (NC1).
FT SITE 106 108 CELL ATTACHMENT SITE (POTENTIAL).
FT MOD_RES 232 232 HYDROXYLATION.
FT MOD_RES 238 238 HYDROXYLATION.
FT DISULFID 261 352 OR 349 (BY SIMILARITY).
FT DISULFID 294 349 OR 352 (BY SIMILARITY).
FT DISULFID 306 312 BY SIMILARITY.
FT DISULFID 371 466 OR 463 (BY SIMILARITY).
FT DISULFID 405 463 OR 466 (BY SIMILARITY).
FT DISULFID 417 423 BY SIMILARITY.
FT CONFLICT 253 253 S -> Y (IN REF. 3).
SQ SEQUENCE 471 AA; 47585 MW; C03B66F14E7008DE CRC64;

Query Match          90.3%; Score 28; DB 1; Length 471;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYWMS 5
DB      321 SYWLS 325
      |||||
      |||||

RESULT 14
PHEC AZOCA STANDARD; PRT; 583 AA.
AC O66392;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Poly-beta-hydroxybutyrate polymerase (EC 2.3.1.-) (Poly(3-
DE hydroxybutyrate) polymerase) (PHB polymerase) (PHB synthase) (Poly(3-
DE hydroxyalkanoate) polymerase) (PHA polymerase) (PHA synthase)
DE (Polyhydroxyalkanoic acid synthase).
GN PHEC.
OS Azorhizobium caulinodans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Azorhizobium.
OX NCBI_TaxID=7;
[1]
RN R1
RP SEQUENCE FROM N.A.
RC STRAIN=ORS571;
RA MEDLINE=98422458; PubMed=9748438;
RA Mandon K., Michel-Reydellet N., Encarnacion S., Kaminski P.A.,
RA Leija A., Cevallos M.A., Elmerich C., Mora J.;
RT "Poly-beta-hydroxybutyrate turnover in Azorhizobium caulinodans is
RT required for growth and affects nifA expression.";
RL J. Bacteriol. 180:5070-5076(1998).
CC -!- FUNCTION: POLYMERIZES D(-)-3-HYDROXYBUTYRYL-COA TO CREATE PHB
CC WHICH CONSISTS OF THOUSANDS OF HYDROXYBUTYRATE MOLECULES LINKED
CC END TO END. PHB SERVES AS AN INTRACELLULAR ENERGY RESERVE MATERIAL
CC WHEN CELLS GROW UNDER CONDITIONS OF NUTRIENT LIMITATION.

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CC -!- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; third step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the PHA/PHB synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ006237; CAA06928.1; -
CC PHB biosynthesis; Transferrase; Acyltransferase.
CC FT ACT SITE 320 320
CC SEQUENCE 583 AA; 64739 MW; C205763D6DD1A18 CRC64;
CC -----
Query Match 90.3%; Score 28; DB 1; Length 583;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMS 5
DB 50 NYWMS 54
-----
RESULT 15
FSPI_RAT
ID FSPI_RAT STANDARD; PRT; 745 AA.
AC Q63517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucine-rich primary response protein 1 (Follicle-stimulating hormone
DE primary response protein).
GN FSHPRH1 OR LRPR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Testis;
RX MEDLINE=95278605; PubMed=7758824;
RA Slegtenhorst-Begdeman K.E., Post M., Baarends W.M., Themmen A.P.M.,
RA Grootegeed J.A.;
RT "Regulation of gene expression in Sertoli cells by
RT follicle-stimulating hormone (FSH): cloning and characterization of
RT LRPR1, a primary response gene encoding a leucine-rich protein.";
RL Mol. Cell. Endocrinol. 108:115-124(1995)
CC -!- FUNCTION: Involved in the response of gonadal tissues to follicle-
CC stimulating hormone.
CC -!- TISSUE SPECIFICITY: Highly expressed in testis, ovary and spleen.
CC A much lower mRNA level is found in brain and lung, and no
CC expression is detected in liver, kidney, heart, muscle, pituitary
CC gland, prostate, epididymis and seminal vesicle.
CC -!- INDUCTION: By follicle-stimulating hormone (FSH).
CC -!- SIMILARITY: SOME, TO S.FOMEE MIS6.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X90355; CAA62018.1; -
CC PIR; I57665; I57665.
CC SEQUENCE 745 AA; 85650 MW; 3C9D1AD066D4FD85 CRC64;
CC -----
Query Match 90.3%; Score 28; DB 1; Length 745;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;

```

```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMS 5
DB 383 SYWLS 387
Search completed: June 8, 2004, 18:56:11
Job time : 4.8125 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2004, 18:17:03 ; Search time 14.4531 Seconds
(without alignments)
109.152 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	95	4	Q9ULB6
2	31	100.0	207	16	Q92UT9 rhizobium m
3	31	100.0	291	16	Q88RV9 pseudomonas
4	31	100.0	395	16	Q8NRH2 corynebacte
5	31	100.0	399	16	Q8FQ16 corynebacte
6	31	100.0	399	16	Q8YQK3 corynebacte
7	31	100.0	942	3	Q13690 schizosacch
8	31	100.0	942	10	Q9SL18 arabidopsis
9	28	90.3	57	8	Q955K1 mytilus tro
10	28	90.3	79	16	Q837B5 mytilus tro
11	28	90.3	89	8	Q8LXR7 mytilus tro
12	28	90.3	105	8	Q8LXS2 mytilus edu
13	28	90.3	107	8	Q8LXS3 mytilus edu
14	28	90.3	108	8	Q8LXS0 mytilus edu
15	28	90.3	108	8	Q8LXS1 mytilus edu
16	28	90.3	108	8	Q8LXA4 mytilus edu

17	28	90.3	108	8	Q8LXR9 mytilus edu
18	28	90.3	108	8	Q8LVQ8 mytilus edu
19	28	90.3	108	8	Q8LXR8 mytilus gal
20	28	90.3	108	8	Q8LVU9 mytilus tro
21	28	90.3	123	4	Q8N2S7 homo sapien
22	28	90.3	125	8	Q8LXA5 mytilus edu
23	28	90.3	126	17	Q59434 pyrococcus
24	28	90.3	128	8	Q8LVQ0 mytilus tro
25	28	90.3	128	8	Q8LJUQ2 mytilus edu
26	28	90.3	128	8	Q8LUQ1 mytilus gal
27	28	90.3	142	2	Q83XV2 gamma-prote
28	28	90.3	148	11	Q9DAL1 mus musculu
29	28	90.3	151	10	Q9FFY3 arabidopsis
30	28	90.3	154	8	Q94NC3 mytilus edu
31	28	90.3	154	8	Q94NC1 mytilus tro
32	28	90.3	154	8	Q94NC2 mytilus gal
33	28	90.3	154	8	Q94N95 mytilus tro
34	28	90.3	154	8	Q955K3 mytilus edu
35	28	90.3	154	8	Q955K4 mytilus edu
36	28	90.3	154	8	Q955K2 mytilus tro
37	28	90.3	154	8	Q955K5 mytilus edu
38	28	90.3	160	16	Q7V1G4 prochloroco
39	28	90.3	161	11	Q61430 mus musculu
40	28	90.3	178	8	Q8WB24 ostrinia fu
41	28	90.3	178	8	Q8WBV3 ostrinia nu
42	28	90.3	179	11	P70165 mus musculu
43	28	90.3	185	5	O45206 schistosoma
44	28	90.3	185	5	Q86RB3 schistosoma
45	28	90.3	191	5	Q03528 schistosoma

ALIGNMENTS

RESULT 1

Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6; (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2F8A.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1_95
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 100.0%; Score 31; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5

Db 30 SYWMS 34

RESULT 2


```

OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.,
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005217; BAC17943.1; -.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000733; Flav_monooxygenase.
DR InterPro; IPR002938; Mox_FAD_binding.
DR InterPro; IPR003042; Rng_monooxygenase.
DR Pfam; PF01494; FAD binding 3; 1.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RNCNNOXGNASE.
KW Monooxygenase; Complete proteome.
SQ SEQUENCE 399 AA; 44698 MW; 6EF0DF41B4F30C14 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 399;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 347 SYWMS 351

RESULT 6
Q8YQR3 PRELIMINARY; PRT; 939 AA.
AC Q8YQR3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Alr3756.
GN ALR3756.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003594; BAB75455.1; -.
DR PIR; AE2275; AE2275.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 939 AA; 104233 MW; 8FE0A7CA6C1759A5 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 931 SYWMS 935

RESULT 7
O13690 PRELIMINARY; PRT; 942 AA.
ID O13690;
AC O13690;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)

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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative guanine nucleotide exchange factor.
GN SPAC11E3.11c.
OS Schizosaccharomyces pombe (Fission yeast)
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Murphy L., Harris D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; Z98595; CAB11190.1; -.
DR PIR; T37539; T37539.
DR GenedB SPombe; SPAC11E3.11c; -.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000904; Sec7.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF01369; Sec7; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00222; Sec7; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50190; SEC7; 1.
SQ SEQUENCE 942 AA; 105909 MW; A677CE2B619ECDFA CRC64;

Query Match 100.0%; Score 31; DB 3; Length 942;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
DB 539 SYWMS 543

RESULT 8
Q9SL18 PRELIMINARY; PRT; 942 AA.
ID Q9SL18;
AC Q9SL18;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mutator-like transposase.
GN AT2G05490.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;

```

RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006220; AA224558.1; -.
 DR PIR; B84469; B84469.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000566; Lipocln_cytrFABP.
 DR InterPro; IPR004332; MuDR.
 DR InterPro; IPR006564; Znf_PZ.
 DR InterPro; IPR007527; Znf_SWIM.
 DR Pfam; PF03108; MuDR; 1.
 DR Pfam; PF04434; SWIM; 1.
 DR SMART; SM00575; Znf_PZ; 1.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 SQ SEQUENCE 942 AA; 106737 MW; 0DE83F5F5AC0B71E CRC64;

Query Match 100.0%; Score 31; DB 10; Length 942;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 63 SYWMS 67

RESULT 9

ID Q955K1 PRELIMINARY; PRT; 57 AA.
 AC Q955K1;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I) (Fragment).
 DE COI.
 GN COI.
 OS Mytilus trossulus (Blue mussel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidae; Mytilidae; Mytilus.
 OX NCBI_TaxID=6551;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MMT4;
 RA Wares J.P., Cunningham C.W.;
 RT "Comparative phylogeography of the North Atlantic";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERROCYTOCHROME C + 2 H(2)O.
 CC -!- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF242032; AAK66961.1; -.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0009481; F:a3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009482; F:b3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009485; F:cb3-type cytochrome c oxidase; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000883; COXI.

DR Pfam; PF00115; COXI; 1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6521 MW; 370D7C4075ADEA71 CRC64;
 Query Match 90.3%; Score 28; DB 8; Length 57;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 42 SYWMS 46

RESULT 10

ID Q837E5 PRELIMINARY; PRT; 79 AA.
 AC Q837E5;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 DE EF0898.
 GN EF0898.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Nelson W.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vanathavan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant Enterococcus faecalis";
 RT Science 299:2071-2074(2003).
 RL EMBL; AE016949; AA080706.1; -.
 DR TIGR; EF0898; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 79 AA; 8676 MW; E8A25E6CDB2689C CRC64;

Query Match 90.3%; Score 28; DB 16; Length 79;
 Best Local Similarity 80.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
 |||||
 Db 54 SYWMS 58

RESULT 11

ID Q8LXR7 PRELIMINARY; PRT; 89 AA.
 AC Q8LXR7;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I) (Fragment).
 DE COI.
 GN COI.
 OS Mytilus trossulus (Blue mussel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidae; Mytilidae; Mytilus.
 OX NCBI_TaxID=6551;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC STRAIN=759NF;
RA Rignos C., Hickerson M.J., Henzler C.M., Cunningham C.W.;
RT "A multilocus study of differential patterns of male and female trans-
RL Atlantic gene flow in the blue mussel, Mytilus edulis."
CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
CC C + 2 H(2)O.
CC -!- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AV101434; AA63589.1; -
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.
DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000893; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PRO1165; CYCOXIDASE1.
KW Copper; Electron transport; Heme; Inner membrane; Membrane;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 9638 MW; 85CA357AE7D8F8C4 CRC64;

Query Match 90.3%; Score 28; DB 8; Length 89;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 18 SYWLS 22

RESULT 12
Q8LXS2 PRELIMINARY; PRT; 105 AA.
AC Q8LXS2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I)
DE (Fragment).
GN COI.
OS Mytilus edulis (Blue mussel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=376WH;
RA Rignos C., Hickerson M.J., Henzler C.M., Cunningham C.W.;
RT "A multilocus study of differential patterns of male and female trans-
RL Atlantic gene flow in the blue mussel, Mytilus edulis."
CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

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CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
CC C + 2 H(2)O.
CC -!- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AV101412; AA63567.1; -
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.
DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
DR GO; GO:0009485; F:cb3-type cytochrome c oxidase; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000893; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PRO1165; CYCOXIDASE1.
KW Copper; Electron transport; Heme; Inner membrane; Membrane;
KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11372 MW; 13F4DAF375E5AE73 CRC64;

Query Match 90.3%; Score 28; DB 8; Length 105;
Best Local Similarity 80.0%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 15 SYWLS 19

RESULT 13
Q8LXS3 PRELIMINARY; PRT; 107 AA.
AC Q8LXS3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I)
DE (Fragment).
GN COI.
OS Mytilus edulis (Blue mussel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=366ME;
RA Rignos C., Hickerson M.J., Henzler C.M., Cunningham C.W.;
RT "A multilocus study of differential patterns of male and female trans-
RL Atlantic gene flow in the blue mussel, Mytilus edulis."
CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).

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CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
 CC -1- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AY101407; AAM63562.1; -.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON TER 1
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11598 MW; 5B6104D10C023051 CRC64;
 Query Match 90.3%; Score 28; DB 8; Length 107;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYNMS 5
 DB 17 SYMLS 21
 RESULT 14
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 ID Q8LXS0 PRELIMINARY; PRT; 108 AA.
 AC Q8LXS0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I) (Fragment).
 DE COI.
 GN Mytilus edulis (Blue mussel).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A.NC1;
 RA Riginos C.; Hickerson M.J.; Henzler C.M.; Cunningham C.W.;
 RA "A multilocus study of differential patterns of male and female trans-Atlantic gene flow in the blue mussel, Mytilus edulis.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
 CC -1- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL; AY101420; AAM63575.1; -.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
 DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON TER 1
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11680 MW; 28D7CD8208416745 CRC64;
 Query Match 90.3%; Score 28; DB 8; Length 108;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYNMS 5
 DB 18 SYMLS 22
 RESULT 15
 Q8LXS1
 ID Q8LXS1 PRELIMINARY; PRT; 108 AA.
 AC Q8LXS1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I) (Fragment).
 DE COI.
 GN Mytilus edulis (Blue mussel).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A.WH10;
 RA Riginos C.; Hickerson M.J.; Henzler C.M.; Cunningham C.W.;
 RA "A multilocus study of differential patterns of male and female trans-Atlantic gene flow in the blue mussel, Mytilus edulis.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
 CC -1- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AY101417; AAM63572.1; -.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.

DR GO: GO:0009482; F:ba3-type cytochrome c oxidase; IEA.
 DR GO: GO:0009483; F:caa3-type cytochrome c oxidase; IEA.
 DR GO: GO:0009485; F:cb3-type cytochrome c oxidase; IEA.
 DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; F:electron transport; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11712 MW; 28D7C826D3297545 CRC64;

Query Match 90.3%; Score 28; DB 8; Length 108;
 Best Local Similarity 80.0%; Pred.No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 Db 18 SYWLS 22

Search completed: June 8, 2004, 18:30:01
 Job time : 17.4531 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:16:13 ; Search time 22.7344 Seconds
(without alignments)
62.141 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	5	4	AAB61293	Aab61293 Anti-TANG
2	31	100.0	5	6	ABU11259	Abu11259 Human TAN
3	31	100.0	98	2	AAR52066	Aar52066 Heavy cha
4	31	100.0	98	2	AAR72074	Aar72074 DP54 VH r
5	31	100.0	98	3	AAB40138	Aab40138 Anti-hi11
6	31	100.0	98	3	AAB40140	Aab40140 Anti-hi11
7	31	100.0	98	5	ABG78210	Abg78210 Human Fv
8	31	100.0	98	5	ABG91901	Abg91901 Human ant
9	31	100.0	98	6	ABO27082	AbO27082 Human ger
10	31	100.0	98	7	ADD28039	Add28039 Lymphoma
11	31	100.0	109	6	ABR55320	AbR55320 Amino aci
12	31	100.0	117	2	AAR66301	Aar66301 Human imm
13	31	100.0	117	5	AAE25526	Aae25526 S. aureus
14	31	100.0	120	7	ADD94123	Add94123 Human VHI
15	31	100.0	123	4	AAE62777	Aae62777 Human HIV
16	31	100.0	123	4	AAE62778	Aae62778 Human HIV
17	31	100.0	125	4	AAE62776	Aae62776 Human HIV
18	31	100.0	157	6	ABR55915	AbR55915 Human mAb
19	31	100.0	157	6	ABR55886	AbR55886 Human mAb
20	31	100.0	241	5	ABP45878	Abp45878 Human Bly
21	31	100.0	247	5	ABP45459	Abp45459 Human Bly
22	31	100.0	247	6	AAO31142	Aao31142 Human CMO
23	31	100.0	251	5	ABP45583	Abp45583 Human Bly
24	31	100.0	264	5	AAU75152	Aau75152 Protein f
25	31	100.0	265	5	AAU75154	Aau75154 Protein f

26	31	100.0	265	5	AAU75149	Aau75149 Amino aci
27	31	100.0	265	5	AAU75153	Aau75153 Protein f
28	31	100.0	271	2	AAW90180	Aaw90180 Human C10
29	31	100.0	312	2	AAW83323	Aaw83323 Single ch
30	31	100.0	312	5	ABB09604	Abb09604 Amino aci
31	31	100.0	312	6	ABG74385	Abg74385 Single ch
32	31	100.0	395	4	AGS09444	AgS09444 C glutami
33	31	100.0	395	7	ADD13735	Add13735 C. glutam
34	28	90.3	5	2	AAR85499	Aar85499 ScFv(FWPS
35	28	90.3	5	2	AAR97316	Aar97316 Humanised
36	28	90.3	5	2	AAV05038	Aav05038 Tumour an
37	28	90.3	5	5	ABB07357	Abb07357 22A5 Igm
38	28	90.3	5	5	AAO17609	Aao17609 Human FAP
39	28	90.3	5	7	ADC82794	Adc82794 CDR regio
40	28	90.3	10	5	AAU72831	Aau72831 Anti-NGK2
41	28	90.3	20	5	AAU75604	Aau75604 Human ttp
42	28	90.3	20	6	ADA20268	Ada20268 Human tum
43	28	90.3	46	4	AAI18657	Aai18657 Peptide #
44	28	90.3	46	5	ABG40558	Abg40558 Human pep
45	28	90.3	59	3	AAV64781	Aav64781 Human 5'

ALIGNMENTS

RESULT 1

AAAB61293	ID	AAAB61293 standard; peptide; 5 AA.
XX	AC	AAAB61293;
XX	DT	04-APR-2001 (first entry)
XX	DE	Anti-TANGO 268 scFv CDR, SEQ ID NO: 61.
XX	KW	Human; antibody; scFv; CDR; complementarity determining region;
XX	KW	TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
XX	KW	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX	KW	platelet membrane glycoprotein receptor; bleeding disorder;
XX	KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX	KW	ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX	OS	Homo sapiens.
XX	PN	WO200100810-A1.
XX	PD	04-JAN-2001.
XX	PF	30-JUN-2000; 2000WO-US018152.
XX	PR	30-JUN-1999; 99US-00345468.
XX	PR	06-DEC-1999; 99US-00454824.
XX	PR	14-FEB-2000; 2000US-00503387.
XX	PA	(MILL-) MILLENNIUM PHARM INC.
XX	PI	Busfield SJ, Vilelial J, Jandrot-Perrus M, Vainchencker W;
XX	PI	Gill DS, Qian MD, Kingsbury G;
XX	DR	WPI; 2001-080877/09.

New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.

Claim 31; Page 102; 227pp; English.

The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPII. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 31; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYNWS 5
 |||||
 Db 1 SYNWS 5

RESULT 2

ABU11259
 ID ABU11259 standard; peptide; 5 AA.

AC ABU11259;

DT 06-FEB-2003 (first entry)

DE Human TANGO 268 VHCOR1 Peptide #3.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPII;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchenker W;

XX Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO
 XX 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Disclosure; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPII)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopaenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 31; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYNWS 5
 |||||
 Db 1 SYNWS 5

RESULT 3

AAR52066

ID AAR52066 standard; protein; 98 AA.

AC AAR52066;

DT 11-OCT-1996 (first entry)

DE Heavy chain variable region of human PL0123 antibody.

XX antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..30

FT /label= framework_region_1

FT /note= "FR 1"

FT Region 31..35

FT /label= complementarity_determining_region_1

FT /note= "CDR 1"

FT Region 36..49

FT /note= "FR 2"

FT Region 50..59

FT /note= "CDR 2"

FT Region 60..98

FT /note= "FR 3"

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-00307051.

XX 09-SEP-1992; 92US-00942245.

XX

PA (IMMU-) IMMUNOGEN INC.
 PT Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;
 XX WPI; 1994-120230/15.
 DR
 XX Method of resurfacing of rodent antibodies to produce humanised antibody
 PT forms - for producing non human antibodies with improved therapeutic
 PT efficiency by presenting human surface on V-region.
 XX
 PS Example 1; Fig 4B; 230pp; English.
 CC
 CC Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with most similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see AAR52061). Experiment 3 was carried out using the
 CC present sequence which represents the human PL0123 Ab light chain
 CC variable region with 74 percent homology with anti-N901 Ab. N901/PL0123
 CC (AAR52067) was prepd. by resurfacing. Sequence numbering starts at
 CC position 118 in the specification
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 31; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 DB 31 SYWMS 35
 |||||
 RESULT 4
 AAR72074
 ID AAR72074 standard; protein; 98 AA.
 XX
 AC AAR72074;
 XX
 XX 25-MAR-2003 (revised)
 DT 26-SEP-1995 (first entry)
 XX
 XX DP54 VH region.
 DE
 XX Graves ophthalmopathy associated immunoglobulin protein; orbital antigen;
 KW monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Region 41..44
 FT /label= CDR1
 FT Region 49..67
 FT /label= CDR2
 XX
 FN WO9508336-A1.
 XX
 PD 30-MAR-1995.
 XX
 XX 22-SEP-1994; 94WO-US010756.
 PF
 XX 22-SEP-1993; 93US-00124469.
 PR
 XX (NICH-) NICHOLS INST DIAGNOSTICS.
 PA Rapoport B, McLachlan SM;
 XX
 PI WPI; 1995-139383/18.
 DR N-PSDB; AAR89332.
 DR
 XX

PT Graves' ophthalmopathy-associated monoclonal antibody - produced by
 PT molecular cloning of immunoglobulin genes by PCR.
 XX
 PS Disclosure; Page 72; 94pp; English.
 XX
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and
 CC clones encoding autoimmune-associated immunoglobulin fragments were
 CC obtained. 2/15 clones of H chain (IgG1) genes showed homology to the
 CC germline gene DP54 (AAQ89332), which encodes the protein given in
 CC AAR72074. The DNA (AAQ89333) and corresp. amino acid (AAR72075) sequences
 CC of the VH region of a representative clone, OF7H1.19, are provided.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 98 AA;
 Query Match 100.0%; Score 31; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 DB 31 SYWMS 35
 |||||
 RESULT 5
 AAB40138
 ID AAB40138 standard; protein; 98 AA.
 XX
 AC AAB40138;
 XX
 DT 05-FEB-2001 (first entry)
 DT
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 664.
 DE
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antischlerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX WO200056772-A1.
 FN
 XX 28-SEP-2000.
 PD
 XX 24-MAR-2000; 2000WO-US007946.
 PF
 XX 25-MAR-1999; 99US-0126603P.
 PR
 XX (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Wildom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 PT
 PS Claim 75; Page 122; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771

CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 31; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 Db 31 SYWMS 35
 RESULT 6
 ID AAB40140
 XX AAB40140 standard; protein; 98 AA.
 AC AAB40140;
 DT 05-FEB-2001 (first entry)
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 666.
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 OS
 XX WO2000056772-A1.
 EN 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US007946.
 XX 25-MAR-1999; 99US-0126603P.
 XX (BADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 DR
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 PT
 XX Claim 75; Page 122; 377pp; English.
 PS
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are

CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 31; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYWMS 5
 Db 31 SYWMS 35
 RESULT 7
 ID ABG78210
 XX ABG78210 standard; protein; 98 AA.
 AC ABG78210;
 DT 15-NOV-2002 (first entry)
 DE Human Fv molecule hypervariable region related peptide #85.
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.
 OS
 XX WO200259264-A2.
 EN 01-AUG-2002.
 XX 31-DEC-2001; 2001WO-US049440.
 XX 29-DEC-2000; 2000US-00751181.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Flaksin D, Feretz T;
 XX WPI; 2002-619166/66.
 DR
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 PT
 XX Claim 13; Page 191-192; 232pp; English.
 PS
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 98 AA;

Query Match 100.0%; Score 31; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 Db 31 SYWMS 35

RESULT 8
 ABG91901
 ID ABG91901 standard; protein; 98 AA.

XX AC ABG91901;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #85.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in

XX PT Physiological phenomena such as cell rolling, metastasis and
 XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 XX PT diseases, and cancer.

XX PS Disclosure; Page 268; Opp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above

CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 XX Sequence 98 AA;

Query Match 100.0%; Score 31; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
 Db 31 SYWMS 35

RESULT 9
 ABO27082
 ID ABO27082 standard; protein; 98 AA.

XX AC ABO27082;

XX DT 10-SEP-2003 (first entry)

XX DE Human germline heavy chain variable region gene segment #15.

XX KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.

XX OS Homo sapiens.

XX PN US2003039649-A1.

XX PD 27-FEB-2003.

XX PF 12-JUL-2002; 2002US-00194975.

XX PR 12-JUL-2001; 2001US-0305111P.

XX PA (FOOT/) FOOTE J.

XX PI Foote J;

XX DR WPI; 2003-492151/46.

XX PT Making humanized antibody for converting antibody, by making chimeric
 XX PT antibodies containing complementarity determining region from non-human
 XX PT antibody and appropriate framework sequences of human antibodies.

XX PS Example 1; Fig 1; 31pp; English.

XX CC The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing

CC framework sequences between non-human and human antibodies. This sequence
CC represents a human heavy chain variable region gene segment used in the
CC creation of humanised antibodies
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 31; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
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|
DB 31 SYWMS 35

RESULT 10
ADD28039
ID ADD28039 standard; protein; 98 AA.

XX AC ADD28039;
XX DT 15-JAN-2004 (first entry)
XX DE Lymphoma related immunoglobulin variable region V3-07.

XX KW B-cell; malignant; immunoglobulin; immunoglobulin variable region;
XX KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
XX KW cytostatic; gene therapy; glycosylation inhibitor;
XX KW non-Hodgkin's lymphoma.

XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003074059-A2.

XX PD 12-SEP-2003.

XX PF 24-FEB-2003; 2003WO-GB000783.

XX PR 07-MAR-2002; 2002GB-00005395.

XX PA (CANC-) CANCER RES TECHNOLOGY LTD.

XX PI Zhu D, Stevenson F;

XX PS WPI; 2003-902720/82.

XX CC Classifying a B-cell as malignant or normal by isolating a sequence
XX CC representing an Ig variable region from the B cell; detecting the
XX CC presence of a glycosylation site and classifying the cell as malignant or
XX CC normal.

XX PS Disclosure; Fig 3; 61pp; English.

XX CC The present invention describes a method for classifying a B-cell as
XX CC malignant or normal comprising: (a) isolating a sequence representing an
XX CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the
XX CC presence of a glycosylation site; and (c) classifying the cell as
XX CC malignant or normal on the basis of the presence or absence of a
XX CC glycosylation site. Also described: (1) treating a patient suffering from
XX CC or at risk of having lymphoma; (2) screening for substances capable of
XX CC inhibiting glycosylation of the Ig variable region of the B cell receptor
XX CC ; and (3) screening for substances (S) capable of inhibiting the
XX CC interaction between lectins of the type found in the germinal centre and
XX CC N-glycans found on the surface of Ig of lymphoma cells. (S) has
XX CC cytostatic activity, and can be used in gene therapy, and as a
XX CC glycosylation inhibitor. The method is useful in classifying a B-cell as
XX CC malignant or normal. The glycosylation inhibitor is useful in preparing a
XX CC medicament for treating non-Hodgkin's lymphoma. The present sequence
XX CC represents an Ig variable region sequence which is used in the
XX CC exemplification of the present invention.

XX SQ Sequence 98 AA;

Query Match 100.0%; Score 31; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
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|
DB 31 SYWMS 35

RESULT 11
ABR55320
ID ABR55320 standard; peptide; 109 AA.

XX AC ABR55320;

XX DT 29-JUL-2003 (first entry)

XX DE Amino acid sequence of human germline VH gene VH3-7 GL.

XX KW Antibody; kinase insert domain-containing receptor; KDR; antibody VRI65;
XX KW complementarity determining region; vascular endothelial growth factor;
XX KW CDK; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.

XX OS Homo sapiens.

XX PN WO2003031475-A2.

XX PD 17-APR-2003.

XX PF 10-OCT-2002; 2002WO-GB004619.

XX PR 10-OCT-2001; 2001GB-00024317.

XX PA (CELL-) CELLTech R & D LTD.

XX PI Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;

XX PS WPI; 2003-441133/41.

XX CC Novel antibody molecules having specificity for human kinase insert
XX CC domain-containing receptors, useful for treating inflammation, psoriasis,
XX CC rheumatoid arthritis, tumor growth and metastasis.

XX PS Disclosure; Fig 3; 57pp; English.

XX CC The specification describes an antibody molecule which has specificity
XX CC for human kinase insert domain-containing receptor (KDR). The antibody
XX CC comprises complementarity determining regions (CDRs) from the heavy and
XX CC light chain variable domains of the murine monoclonal antibody VRI65.
XX CC This antibody is specific for human KDR. The antibody of the invention
XX CC blocks vascular endothelial growth factor (VEGF) binding to KDR.

XX CC Antibodies of the invention are useful for treating a pathology in which
XX CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
XX CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
XX CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
XX CC growth or metastasis. ABR55320-21 represent human germline variable
XX CC region frameworks, chosen to construct antibodies of the invention

XX SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
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|
|
|
DB 31 SYWMS 35

RESULT 12
AAR66301
ID AAR66301 standard; protein; 117 AA.

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XX AC AAR66301;
XX DT 25-MAR-2003 (revised)
XX DT 02-AUG-1995 (first entry)
XX DE Human immunoglobulin variable heavy chain #7.
XX KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
XX KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX OS Homo sapiens.
XX PN WO9426895-A1.
XX PD 24-NOV-1994.
XX PF 10-MAY-1993; 93WO-JP000603.
XX PR 10-MAY-1993; 93WO-JP000603.
XX PA (NIBS) JAPAN TOBACCO INC.
XX PI Honjo T, Matsuda F;
XX DR WPI: 1995-006791/01.
XX DR N-PSDB; AAQ78946.
XX PT DNA fragment comprising human immunoglobulin Vh genes - for the
XX PT production of human immunoglobulin in mammalian hosts.
XX PS Claim 17; Page 40-41; 130pp; Japanese.
XX CC Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
XX CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
XX CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
XX CC Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using
XX CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
XX CC genes. The fragments cover a region of 800 kb. The DNA fragments were
XX CC isolated from high molecular weight DNA from human placenta. The DNA was
XX CC partially digested with Taqi restriction enzyme. The fragments were
XX CC separated by gel electrophoresis and 35-45 kb fractions were collected.
XX CC The fragments were ligated with ClaI-digested cosmid vector pJB81. The
XX CC ligation products were in vitro packed and infected into E.coli 490A. The
XX CC fragments were then subcloned by colony hybridisation. The Vh genes and
XX CC the DNA fragments encoding them are useful in producing human
XX CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 31; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 50 SYWMS 54
|||||

RESULT 13
AAE25526
ID AAE25526 standard; protein; 117 AA.
XX AC AAE25526;
XX DT 04-NOV-2002 (first entry)
XX DE S. aureus Map10 antibody H07VHD-1 (variable heavy chain) protein.
XX KW Map10 protein; infection; immunological response; passive immunisation;
XX KW vaccine; antibacterial; variable heavy chain; H07VHD-1 protein.
XX DE Human VHIII/JH6 variable region fusion partial amino acid sequence.

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OS XX Staphylococcus aureus.
FH XX Key Location/Qualifiers
FT Region 31..35
FT /note= "Complementarity determining region (CDR) "
FT Region 53..66
FT /note= "Complementarity determining region (CDR) "
FT Region 99..106
FT /note= "Complementarity determining region (CDR) "
XX PN WO200234788-A1.
XX PD 02-MAY-2002.
XX PF 22-OCT-2001; 2001WO-US032550.
XX PR 20-OCT-2000; 2000US-0241832P.
XX PR 21-MAR-2000; 2001US-0277287P.
XX PA (INHI-) INHIBITEX INC.
XX PI Patti JM, Domanski P, Patel P;
XX DR WPI: 2002-547435/58.
XX DR N-PSDB; AAD41846.
XX PT Antibody capable of binding subdomains of Map10 protein, a surface
XX PT localized protein from Staphylococcus aureus, useful for preventing and
XX PT treating staphylococcal infection in humans or animals.
XX PS Claim 11; Page 48; 52pp; English.
XX CC The present sequence relates to novel antibodies which are capable of
XX CC binding to the subdomains Map10 protein, a surface localised protein from
XX CC Staphylococcus aureus. Sequences of the invention prevent S.aureus
XX CC infection in a human or animal and inhibit binding of staphylococcal
XX CC bacteria to eukaryotic cells. They are also useful for diagnosing an
XX CC infection of S.aureus in a sample and for treating or preventing S.aureus
XX CC infection in humans or animals. Antibodies of the invention are useful
XX CC for inducing an immunological response in a human or animal and for
XX CC identifying antibodies to the Map10 protein in a sample. They are also
XX CC useful in preventing adherence of Staphylococcal bacteria, in production
XX CC facilities or laboratories to isolate additional quantities of the
XX CC proteins, such as by affinity chromatography and in the development of
XX CC vaccines for passive immunisation against staphylococcal infections. The
XX CC antibodies prevent or reduce bacterial infection on in-dwelling medical
XX CC devices to make them safer to use, including sutures, replacement heart
XX CC valves, cardiac assist devices, hard and soft contact lenses, intraocular
XX CC lens implants, other implants, such as corneal inlays, kerato-prostheses,
XX CC vascular stents, dental prostheses, pacemakers and heart valves. The
XX CC present sequence is a DNA encoding Staphylococcus aureus Map10 antibody
XX CC H07VHD-1 (variable heavy chain) protein
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 31; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMS 5
Db 31 SYWMS 35
|||||

RESULT 14
ADD94123
ID ADD94123 standard; protein; 120 AA.
XX AC ADD94123;
XX DT 29-JAN-2004 (first entry)
XX DE Human VHIII/JH6 variable region fusion partial amino acid sequence.

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XX KW grafted antibody; complementarity determining region; CDR; light CDR;
XX KW heavy CDR; cryptic collagen epitope; solid tumour;
XX KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
XX KW collagen agonist; collagen antagonist; cancer metastasis;
XX KW anti-cryptic collagen; antibody; VHIII/JH6; human.
XX OS Homo sapiens.
XX FN WO2003046204-A2.
XX PD 05-JUN-2003.
XX PF 26-NOV-2002; 2002WO-US038147.
XX PR 26-NOV-2001; 2001US-00995529.
XX PR 06-DEC-2001; 2001US-00011250.
XX PA (CELL-) CELL MATRIX INC.
XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX PF; 2003-513649/48.
XX DR N-PSDB; ADD94122.
XX PS New cryptic collagen antibody with one or more complementarity
XX PT determining regions, useful for diagnosing and treating disorders
XX PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX PS Example 1; SEQ ID NO 8; 232pp; English.
XX CC This invention relates to a novel grafted antibody or its functional
XX CC fragment comprising one or more complementarity determining regions
XX CC (CDRs) of a defined light CDR and a light CDR with at least one amino
XX CC acid (aa) substitution where the antibody has specific binding activity
XX CC for a cryptic collagen epitope. The growth of all solid tumours requires
XX CC new blood vessel growth, angiogenesis, inhibition of which is an approach
XX CC to limiting tumour growth. The invention may allow development of
XX CC therapeutics with a cytostatic activity as a collagen agonist or
XX CC antagonist. The invention is useful for diagnosing and treating disorders
XX CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX CC present sequence is the partial amino sequence of the human variable
XX CC region fusion VHIII/JH6 which is related to the invention.
XX SQ Sequence 120 AA;

Query Match 100.0%; Score 31; DB 7; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 31 SYWMS 35

RESULT 15
AAB62777
ID AAB62777 standard; protein; 123 AA.
XX AC AAB62777;
XX DT 03-APR-2001 (first entry)
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 76.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX KW envelope glycoprotein; gp120; diagnosis.
XX OS Homo sapiens.
XX OS WO200100678-A1.
XX FN 04-JAN-2001.
FD

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XX PF 23-JUN-2000; 2000WO-US017327.
XX PF 30-JUN-1999; 99US-0141701P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Watkins BA, Reitz MS;
XX PF; 2001-112438/12.
XX DR N-PSDB; AAF29078.
XX PT Novel human monoclonal antibody immunoreactive with human
XX PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX PT in biological sample and providing passive immunotherapy to HIV-1
XX PT infected mammal.
XX PS Claim 1; Page 70; 81pp; English.
XX CC The present invention provides the protein and coding sequences for the
XX CC variable regions of human monoclonal antibodies which are immunoreactive
XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection
XX SQ Sequence 123 AA;

Query Match 100.0%; Score 31; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMS 5
Db 32 SYWMS 36

Search completed: June 8, 2004, 18:26:48
Job time : 31.7344 secs

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:12:56 ; Search time 22 Seconds
(without alignments)
795.509 Million cell updates/sec

Title: US-09-610-118-3
Perfect score: 1786
Sequence: 1 MSFSPALFCLGLCLGRVPA.....KSHGGDGGGRQDVHSGRLCS 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	3	US-09-345-468-3
2	1786	100.0	339	4	US-09-414-453A-3
3	1678	94.0	319	3	US-09-345-468-5
4	1678	94.0	319	4	US-09-414-453A-5
5	1304	73.0	249	3	US-09-345-468-9
6	1304	73.0	249	4	US-09-414-453A-9
7	1122	62.8	313	3	US-09-345-468-16
8	1122	62.8	313	4	US-09-414-453A-16
9	1080.5	60.5	292	3	US-09-345-468-18
10	1080.5	60.5	292	4	US-09-414-453A-18
11	937	52.5	267	3	US-09-345-468-19
12	937	52.5	267	4	US-09-414-453A-19
13	498	27.9	448	4	US-09-310-463-18
14	498	27.9	448	4	US-08-842-248A-18
15	477	26.7	289	4	US-09-310-463-12
16	477	26.7	289	4	US-08-842-248A-12
17	455	25.5	299	4	US-09-310-463-30
18	454	25.4	631	3	US-09-345-468-12
19	454	25.4	631	4	US-09-414-453A-12
20	449	25.1	631	4	US-09-310-463-20
21	449	25.1	631	4	US-08-842-248A-20
22	441	24.7	483	4	US-09-310-463-16
23	441	24.7	483	4	US-08-842-248A-16
24	438.5	24.6	489	4	US-09-310-463-14
25	438.5	24.6	489	4	US-08-842-248A-14
26	438	24.5	431	3	US-08-985-950-14
27	438	24.5	431	3	US-08-985-950-20

ALIGNMENTS

RESULT 1
US-09-345-468-3
; Sequence 3, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Valdivia, J.
; APPLICANT: Jandrot-Ferrus, M.
; APPLICANT: Valchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-3

Query Match 100.0%; Score 1786; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 9, 9e-158;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSFSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYRLH	60
DB	1	MSFSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYRLH	60
QY	61	KLSSRYQDQAVLFIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQP	120
DB	61	KLSSRYQDQAVLFIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQP	120
QY	121	GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC	180
DB	121	GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC	180
QY	181	YSPSRDYLWSAPDPLELVVTGTSVTPSRILPTEPPSSVAEFSATAELTVSFTNKVPT	240
DB	181	YSPSRDYLWSAPDPLELVVTGTSVTPSRILPTEPPSSVAEFSATAELTVSFTNKVPT	240
QY	241	TETSSITTSKESDPAGAPQYTKGNLVRCICGAVILILAGFLAEDWHSRKRRLH	300
DB	241	TETSSITTSKESDPAGAPQYTKGNLVRCICGAVILILAGFLAEDWHSRKRRLH	300
QY	301	RGRVQRPLPPLPPLPQTRKSHGGDGGGRQDVHSGRLCS	339
DB	301	RGRVQRPLPPLPPLPQTRKSHGGDGGGRQDVHSGRLCS	339

RESULT 2
US-09-414-453A-3
; Sequence 3, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-3

Query Match 100.0%; Score 1786; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 9.9e-158;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRL 60
DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRL 60
QY 61 KLSSSRYQDQAVLFIAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP 120
DB 61 KLSSSRYQDQAVLFIAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP 120
QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
DB 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YFSSRDPLWSAPSDPLELVGTSTVPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
DB 181 YFSSRDPLWSAPSDPLELVGTSTVPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRICLGAVALIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRICLGAVALIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPLPQTRKSHGGQDGRQDVHSRGLCS 339
DB 301 RGRAVORPLPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 3
US-09-345-468-5
; Sequence 5, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-5

Query Match 94.0%; Score 1678; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 9.7e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLKLSSSRYQDQAVLFIAMKR 80
DB 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLKLSSSRYQDQAVLFIAMKR 60
QY 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPVSSGGDVTLCQTRYGF 140
DB 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPVSSGGDVTLCQTRYGF 120
QY 141 DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCSYFSGRDPYLSAPSDEPLEL 200
DB 121 DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCSYFSGRDPYLSAPSDEPLEL 180
QY 201 VVTGTSVTPSRPLTEPPSSVAEPSEATAELTVSFTNKVFTTETSRTTSPKESDSPAG 260
DB 181 VVTGTSVTPSRPLTEPPSSVAEPSEATAELTVSFTNKVFTTETSRTTSPKESDSPAG 240
QY 261 ARQYTKGNLVRICLGAVALIILAGFLAEDWHSRRKRLRHGRAVORPLPLPQTRK 320
DB 241 ARQYTKGNLVRICLGAVALIILAGFLAEDWHSRRKRLRHGRAVORPLPLPQTRK 300
QY 321 SHGGQDGRQDVHSRGLCS 339
DB 301 SHGGQDGRQDVHSRGLCS 319

RESULT 4
US-09-414-453A-5
; Sequence 5, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-5

Query Match 94.0%; Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 9.7e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLKLSSSRYQDQAVLFIAMKR 80
DB 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLKLSSSRYQDQAVLFIAMKR 60
QY 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPVSSGGDVTLCQTRYGF 140
DB 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPVSSGGDVTLCQTRYGF 120
QY 141 DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCSYFSGRDPYLSAPSDEPLEL 200
DB 121 DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCSYFSGRDPYLSAPSDEPLEL 180
QY 201 VVTGTSVTPSRPLTEPPSSVAEPSEATAELTVSFTNKVFTTETSRTTSPKESDSPAG 260
DB 181 VVTGTSVTPSRPLTEPPSSVAEPSEATAELTVSFTNKVFTTETSRTTSPKESDSPAG 240
QY 261 ARQYTKGNLVRICLGAVALIILAGFLAEDWHSRRKRLRHGRAVORPLPLPQTRK 320


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Db 241 ARQYTKGNLVRLICGAVLIIILAGFLAEDWHSRRRLRHGRAVORPLPPLPLPQTRK 300
QY 321 SHGGQDGRQDVHSRGLCS 339
Db 301 SHGGQDGRQDVHSRGLCS 319

RESULT 5
US-09-345-468-9
; Sequence 9, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; FILE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-9
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Query Match 73.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.6e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYQDQAVLFIAMKR 80
Db 1 QSGPLPKSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYQDQAVLFIAMKR 60

QY 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLCQTRYGF 140
Db 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLCQTRYGF 120

QY 141 DQFALYKEGDPAKYKNPERWYRASFPPIITVTAHSGTYRCYCFSSRDPLYWGAAPSDELEL 200
Db 121 DQFALYKEGDPAKYKNPERWYRASFPPIITVTAHSGTYRCYCFSSRDPLYWGAAPSDELEL 180

QY 201 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 260
Db 181 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 240

QY 261 ARQYTKGN 269
Db 241 ARQYTKGN 249
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RESULT 6
US-09-414-453A-9
; Sequence 9, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; FILE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-9

Query Match 73.0%; Score 1304; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.6e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYQDQAVLFIAMKR 80
Db 1 QSGPLPKSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYQDQAVLFIAMKR 60

QY 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLCQTRYGF 140
Db 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLCQTRYGF 120

QY 141 DQFALYKEGDPAKYKNPERWYRASFPPIITVTAHSGTYRCYCFSSRDPLYWGAAPSDELEL 200
Db 121 DQFALYKEGDPAKYKNPERWYRASFPPIITVTAHSGTYRCYCFSSRDPLYWGAAPSDELEL 180

QY 201 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 260
Db 181 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 240

QY 261 ARQYTKGN 269
Db 241 ARQYTKGN 249
```

```
RESULT 7
US-09-345-468-16
; Sequence 16, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; FILE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-16
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Query Match 62.8%; Score 1122; DB 3; Length 313;
Best Local Similarity 69.4%; Pred. No. 4e-96;
Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

QY 1 MSPSPALFCLGLC-LGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPGVDLYRL 59
Db 1 MSPASPTFCIGLCVLQVIQTQSGLPKPSLQAQSSSLVPLGQSVILRCQGGPPDVLRL 60

QY 60 EKLSSRYQDQAVLFIAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 119
Db 61 EKLKEKVEDQDFLPIPTWERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH 120

QY 120 PGFAVSSGGDVTLCQTRYGDFQFALYKEGDPAKYKNPERWYRASFPPIITVTAHSGTYR 179
Db 121 PSSAVPQGRDVLTKQSPYSDFEVLVYKEGDTGPKYRPEKWKYRANFPPIITVTAHSGTYR 180

QY 180 CYSFSSRDPLYWGAAPSDELELVVGTSTVTPSRLPTEPPSSVAFSEATAELTVSTNKVF 239
Db 181 CYSFSSSDPLYWGAAPSDELVVLTGLSATPQCVPTFESFPVTESRRRPSILP---TNKIS 237

QY 240 TTETSRITTSRKESDSPAGPARQYTKGNLVRIICLGAFLIILAGFLAEDWHSRRRLR 299
Db 238 TTEKPMNITASPEGLSPPIGFAHQAQGNLVRIICLGAFLIILGLLAEDWHSRRKCLQ 297
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QY 300 HGRAVORLPLPLP 313
Db 298 HRMRALQRLPLPLP 311

RESULT 8

US-09-414-453A-16
; Sequence 16, Application US/09414453A

; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-414-453A-16

Query Match 62.8%; Score 1122; DB 4; Length 313;

Best Local Similarity 69.4%; Pred. No. 4e-96;

Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

QY 1 MSPSPALCLGLC-LGRVPAQSGPLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYL 59
Db 1 MSPASPTFCIGLVLQVITQTSQGLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYL 60
QY 60 EKLSSRYQDQAVLFIIPAMKRSAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 119
Db 61 EKLKPEYEDQDFLFIPTMERSNAGRYCSYQNGSHWSLPSDQLELVATGVFAKPSLSAH 120
QY 120 PGPVSSGGDVTLCQTRGVDFDQFALYKGGDPAPYKNPERWYASPIITVTAHSGTYR 179
Db 121 PSSAVPQGRDVTLCQSPSYDFEFLVYKGGDTGPKRPEKWRANFPIITVTAHSGTYR 180
QY 180 CYSFSSRDPLYWAPSDPLELVGTGVSPTSLPTEPPSSVAFSEATAELTVSFNKNVF 239
Db 181 CYSFSSSPYLWAPSDPLVLVWGLSATPSQVPTESFPVTSSRRPSILP---TNKIS 237
QY 240 TTETSRITSPKESDSPAGPARQYTKGNLVRICLGAVALIILAGFLAEDHRSRKLRL 299
Db 238 TTEKPMNITASPEGLSPPIGFAHQYAKGNLVRICLGAVALIILAGFLAEDHRSRKLRL 297

QY 300 HGRAVORLPLPLP 313
Db 298 HRMRALQRLPLPLP 311

RESULT 9

US-09-345-468-18
; Sequence 18, Application US/09345468

; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 18
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-18

Query Match

Best Local Similarity 71.3%; Score 1080.5; DB 3; Length 292;

Matches 209; Conservative 22; Mismatches 59; Indels 3; Gaps 1;

QY 21 QSGPLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIAMKR 80
Db 1 QSGPLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYRLEKLPKPEYEDQDFLFIPTMR 60
QY 81 SLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 140
Db 61 SNAGRYCSYQNGSHWSLPSDQLELVATGVFAKPSLSAHPSSAVPQGRVTLKQSPYSF 120
QY 141 DQFALYKGGDPAPYKNPERWYASPIITVTAHSGTYRCSYFSSRDPLYWAPSDPLEL 200
Db 121 DEFVLYKGGDTGPKRPEKWRANFPIITVTAHSGTYRCSYFSSSSPYLWAPSDPLVL 180
QY 201 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFNKNVFTTTSRITSPKESDSPAGP 260
Db 181 VVTGLSATPSQVPTESFPVTSSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGF 237
QY 261 ARQYTKGNLVRICLGAVALIILAGFLAEDHRSRKLRLHRCRAVORLPLPLP 313
Db 238 AHQYAKGNLVRICLGAVALIILGLLAEDHRSRKLRLHRCRAVORLPLPLP 290

RESULT 10

US-09-414-453A-18

; Sequence 18, Application US/09414453A

; Patent No. 6383779

; GENERAL INFORMATION:

; APPLICANT: Busfield, S.

; APPLICANT: Villevall, J.

; APPLICANT: Jandrot-Perrus, M.

; APPLICANT: Vainchenker, W.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-147

; CURRENT APPLICATION NUMBER: US/09/414,453A

; CURRENT FILING DATE: 1999-10-07

; PRIOR APPLICATION NUMBER: 09/345,468

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 18

; LENGTH: 292

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-414-453A-18

Query Match

Best Local Similarity 71.3%; Score 1080.5; DB 4; Length 292;

Matches 209; Conservative 22; Mismatches 59; Indels 3; Gaps 1;

QY 21 QSGPLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIAMKR 80
Db 1 QSGPLPKPSLQALPSSLYPLEKPVTLRCQGGPGVDLYRLEKLPKPEYEDQDFLFIPTMR 60
QY 81 SLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 140
Db 61 SNAGRYCSYQNGSHWSLPSDQLELVATGVFAKPSLSAHPSSAVPQGRVTLKQSPYSF 120
QY 141 DQFALYKGGDPAPYKNPERWYASPIITVTAHSGTYRCSYFSSRDPLYWAPSDPLEL 200
Db 121 DEFVLYKGGDTGPKRPEKWRANFPIITVTAHSGTYRCSYFSSSSPYLWAPSDPLVL 180
QY 201 VVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFNKNVFTTTSRITSPKESDSPAGP 260
Db 181 VVTGLSATPSQVPTESFPVTSSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGF 237

QY 261 ARQYTKNLVRLICGLAVIIILLAGFTLAEADWHSRKRRLRHGRAVQRLPPLP 313
Db 238 AHQYAKGNLVRICGLGATIIILGLLAEADWHSRKKCLQHRMRALQRLPPLP 290

RESULT 11
US-09-345-468-19
; Sequence 19, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevial, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-19

Query Match 52.5%; Score 937; DB 3; Length 267;
Best Local Similarity 67.8%; Pred. No. 4.8e-79;
Matches 183; Conservative 21; Mismatches 62; Indels 4; Gaps 2;
QY 1 MSPSPALFCLGLC-LGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGPVGVLDYRL 59
Db 1 MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLOAQPSLVPLGQSVILRCQGPVGVLDYRL 60
QY 60 EKLSSSRYOQAVLFIIPAMKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 119
Db 61 EKLKPEYEDQDFLFTWERSNAGRYCSYQNGSHWSLPSDQLELIATGVIAKPSLSAH 120
QY 120 PGAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYR 179
Db 121 PSSAVPQGRDVTLCQSPYSFDEFVLYKEGDTGPKRPEKWRANFPIITVTAHSGTYR 180
QY 180 CYFSFSSRDPLYWASDPDPLELVVTGTSVTPSRPLTPPPSSVAEFSATAELTVSFNKKVF 239
Db 181 CYFSFSSPYLWASDPDPLVLVVTGLSATPSQVPTESFPVTSSRRPSILP---TNKIS 237
QY 240 TTETSRITTSPKESDSPAGPARQYVTGN 269
Db 238 TTEKPNITASPEGLSPPIGFAHQHYAKGN 267

RESULT 12
US-09-414-453A-19
; Sequence 19, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevial, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-414-453A-19

Query Match 52.5%; Score 937; DB 4; Length 267;
Best Local Similarity 67.8%; Pred. No. 4.8e-79;
Matches 183; Conservative 21; Mismatches 62; Indels 4; Gaps 2;
QY 1 MSPSPALFCLGLC-LGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGPVGVLDYRL 59
Db 1 MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLOAQPSLVPLGQSVILRCQGPVGVLDYRL 60
QY 60 EKLSSSRYOQAVLFIIPAMKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 119
Db 61 EKLKPEYEDQDFLFTWERSNAGRYCSYQNGSHWSLPSDQLELIATGVIAKPSLSAH 120
QY 120 PGAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYR 179
Db 121 PSSAVPQGRDVTLCQSPYSFDEFVLYKEGDTGPKRPEKWRANFPIITVTAHSGTYR 180
QY 180 CYFSFSSRDPLYWASDPDPLELVVTGTSVTPSRPLTPPPSSVAEFSATAELTVSFNKKVF 239
Db 181 CYFSFSSPYLWASDPDPLVLVVTGLSATPSQVPTESFPVTSSRRPSILP---TNKIS 237
QY 240 TTETSRITTSPKESDSPAGPARQYVTGN 269
Db 238 TTEKPNITASPEGLSPPIGFAHQHYAKGN 267

RESULT 13
US-09-310-463-18
; Sequence 18, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: human
US-09-310-463-18

Query Match 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 5.7e-38;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;
QY 1 MSPSPALFCLGLC-LGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGPVGVLDYRL 59
Db 1 MIPTFTALLCLGLSLGPRTHMQAGPLPKPTLWAEPGSVISWGNSTIWCQGTLEAREYRL 60
QY 60 EKLSSSRYOQ-----QAVLFIIPAMKRSLAGRYCSYQNGSLWSLPSDQLELVATGV 110
Db 61 DKEESPAPWDRQNPLEPKKARFSPMTEDYAGRYCYRSPVGSQSPDLELVMTGA 120
QY 111 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPY-----KNPERWYRAF 165
Db 121 YSKPTLSALPSLVTSKGKSVTLCCQSRSPMDTFLIKERAAHPLHLRSEHGAQHQAEF 180
QY 166 PIITVTAHSGTYRCYFSFSSRDPLYWASDPDPLELVVTGTSVTPSRPLTPPEPSSVAEFS 225
Db 181 PMSPVTSVHGGTYRCYFSHSHGSHYLLSHPSDPLELVSGSLGEPSPPT----- 229
QY 226 ATAELTVSFNKKVFITETTSRSTTSPKESDSPAGPARQYVTGN-----NLVRICLGAVI 279
Db 230 -----RSVSTAAGPEDQPLMPTGTGSPVHSGLRHWEVLIGLVVLSIL 270

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:15:18 ; Search time 49 Seconds
(without alignments)
1946.404 Million cell updates/sec

Title: US-09-610-118-3

Perfect score: 1786

Sequence: 1 MSPSPALFCLGICLRVPA.....KSHGGQGGQDVHSRGLCS 339

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Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1786	100.0	339	9 US-09-832-312-3	Sequence 3, Appli
2	1786	100.0	339	11 US-09-829-495-3	Sequence 3, Appli
3	1786	100.0	339	14 US-10-157-031-387	Sequence 387, App
4	1782	99.8	339	9 US-09-832-312-34	Sequence 34, Appl
5	1782	99.8	339	9 US-09-832-312-36	Sequence 38, Appl
6	1782	99.8	339	9 US-09-832-312-38	Sequence 38, Appl
7	1782	99.8	339	9 US-09-832-312-40	Sequence 40, Appl
8	1782	99.8	339	11 US-09-829-495-34	Sequence 34, Appl
9	1782	99.8	339	11 US-09-829-495-36	Sequence 36, Appl
10	1782	99.8	339	11 US-09-829-495-38	Sequence 38, Appl
11	1782	99.8	339	11 US-09-829-495-40	Sequence 40, Appl
12	1759	98.5	339	14 US-10-446-826-5	Sequence 5, Appli
13	1678	94.0	319	9 US-09-832-312-5	Sequence 5, Appli
14	1678	94.0	319	11 US-09-829-495-5	Sequence 5, Appli
15	1304	73.0	249	9 US-09-832-312-9	Sequence 9, Appli

16	1304	73.0	249	11 US-09-829-495-9	Sequence 9, Appli
17	1304	73.0	369	14 US-10-446-826-37	Sequence 37, Appl
18	1122	62.8	313	9 US-09-832-312-16	Sequence 16, Appl
19	1122	62.8	313	9 US-09-832-312-48	Sequence 48, Appl
20	1122	62.8	313	11 US-09-829-495-16	Sequence 16, Appl
21	1122	62.8	313	11 US-09-829-495-48	Sequence 48, Appl
22	1118	62.6	313	9 US-09-832-312-42	Sequence 42, Appl
23	1118	62.6	313	9 US-09-832-312-44	Sequence 44, Appl
24	1118	62.6	313	9 US-09-832-312-46	Sequence 46, Appl
25	1118	62.6	313	11 US-09-829-495-42	Sequence 42, Appl
26	1118	62.6	313	11 US-09-829-495-44	Sequence 44, Appl
27	1118	62.6	313	11 US-09-829-495-46	Sequence 46, Appl
28	1080.5	60.5	292	9 US-09-832-312-18	Sequence 18, Appl
29	1080.5	60.5	292	11 US-09-829-495-18	Sequence 18, Appl
30	937	52.5	267	9 US-09-832-312-19	Sequence 19, Appl
31	937	52.5	267	11 US-09-829-495-19	Sequence 19, Appl
32	499	27.9	448	16 US-10-408-765A-1701	Sequence 1701, Ap
33	498	27.9	447	9 US-09-870-759-50	Sequence 50, Appl
34	498	27.9	447	10 US-09-751-708A-50	Sequence 50, Appl
35	498	27.9	448	14 US-10-139-662-18	Sequence 18, Appl
36	498	27.9	448	14 US-10-139-683-18	Sequence 18, Appl
37	498	27.9	448	14 US-10-143-618-18	Sequence 18, Appl
38	498	27.9	448	16 US-10-429-160-54	Sequence 54, Appl
39	492	27.5	472	11 US-09-907-421-8	Sequence 8, Appl
40	491	27.5	447	10 US-09-978-418-36	Sequence 36, Appl
41	477	26.7	289	14 US-10-139-662-12	Sequence 12, Appl
42	477	26.7	289	14 US-10-139-683-12	Sequence 12, Appl
43	477	26.7	289	14 US-10-143-618-12	Sequence 12, Appl
44	457	25.6	632	14 US-10-114-153-92	Sequence 92, Appl
45	455	25.5	299	10 US-09-796-753-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-09-832-312-3
; Sequence 3, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-3

Query Match 100.0%; Score 1786; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGICLRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCGPGVDLYRLE 60
Db 1 MSPSPALFCLGICLRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCGPGVDLYRLE 60
QY 61 KLSRSRYQDQAVLFIPAMKRSYQNGSLWSLPSDQLELVATGVFAKPSLSAQF 120
Db 61 KLSRSRYQDQAVLFIPAMKRSYQNGSLWSLPSDQLELVATGVFAKPSLSAQF 120

QY 121 GPAVSSGGDVTLCQCTRYGDFQFALYKKGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQCTRYGDFQFALYKKGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
DB 301 RGRAVORPLPPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
RESULT 2
US-09-829-495-3
; Sequence 3, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-3
Query Match 100.0%; Score 1786; DB 11; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MSPSPALFCLGCLGRVPAQSGPLKPSLQALPSSLVPLEKPVTLRCOGPGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSSRYQDQAVLFIIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
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DB 121 GPAVSSGGDVTLCQCTRYGDFQFALYKKGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
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DB 301 RGRAVORPLPPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

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RESULT 3
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, I. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-387
Query Match 100.0%; Score 1786; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPSPALFCLGCLGRVPAQSGPLKPSLQALPSSLVPLEKPVTLRCOGPGVDLYRLE 60
DB 1 MSPSPALFCLGCLGRVPAQSGPLKPSLQALPSSLVPLEKPVTLRCOGPGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSSRYQDQAVLFIIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQCTRYGDFQFALYKKGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQCTRYGDFQFALYKKGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLETPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
DB 301 RGRAVORPLPPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
RESULT 4
US-09-832-312-34
; Sequence 34, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30

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; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-34

Query Match          99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
QY 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
Db 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339

RESULT 5
US-09-832-312-36
; Sequence 36, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-36

Query Match          99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
QY 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
Db 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
```

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Db 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
Db 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339

RESULT 6
US-09-832-312-38
; Sequence 38, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-38

Query Match          99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQPPGVDLVRL 60
QY 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
Db 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLEPTEPPSSVAEFSEATAELTVFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDQVHSGRLCS 339
```

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RESULT 7
US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40

Query Match          99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
Db 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
QY 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
Db 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 8
US-09-829-495-34
; Sequence 34, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villaveal J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-34

Query Match          99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
Db 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
QY 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
Db 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
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; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-34

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
Db 61 KLSRSRYQDAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQF 120
QY 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GRAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
Db 241 TETSRITTSPEKSDSPAGPARQYTKGNLVICLGAIVILILAGFLAEDWHSRRRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 9
US-09-829-495-36
; Sequence 36, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villaveal J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-36
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Query Match 99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60
DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60

QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120

QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180

QY 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240
DB 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQGGQDGVHSGRLCS 339
DB 301 RGRAVORPLPPLPQTRKSHGGQGGQDGVHSGRLCS 339

RESULT 10
US-09-829-495-38
; Sequence 38, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-38

Query Match 99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60
DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60

QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120

QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180

QY 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240
DB 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQGGQDGVHSGRLCS 339
DB 301 RGRAVORPLPPLPQTRKSHGGQGGQDGVHSGRLCS 339

RESULT 11
US-09-829-495-40
; Sequence 40, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-40

Query Match 99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.7e-139;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60
DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE 60

QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQ 120

QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKPNPERWYRASFPFIITVTAHSGTYRC 180

QY 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240
DB 181 YPSSRDYPLWSPAPDPLELVVTGTSVTPSRPLTPPSSVAEFSSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQGGQDGVHSGRLCS 339

```
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
|||||
RESULT 12
US-10-446-826-5
; Sequence 5, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-5

Query Match 98.5%; Score 1759; DB 14; Length 339;
Best Local Similarity 99.1%; Pred. No. 3.8e-137;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSPSPALFCGLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLE 60
Db 1 MSPSPALFCGLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLE 60

QY 61 KLSRRYQOAVLFTPAMKRSAGRYRCSYQNGSLWLSLSDQLELVATGVFAKPSLSAQP 120
Db 61 KLSRRYQOAVLFTPAMKRSAGRYRCSYQNGSLWLSLSDQLELVATGVFAKPSLSAQP 120

QY 121 GPVSSGGVDTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 180
Db 121 GPVSSGGVDTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 180

QY 181 YSFSSRDPLYMSAPSDPLBLVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLBLVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240

QY 241 TETSSITTSPKESDSPAGPARQYTKGNLVLCIGAVILIIAGFLAEDWHSRRKRLRH 300
Db 241 TETSSITTSPKESDSPAGPARQYTKGNLVLCIGAVILIIAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 13
US-09-832-312-5
; Sequence 5, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09

Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
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RESULT 14
US-09-829-495-5
; Sequence 5, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT

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Best Local Similarity 100.0%; Pred. No. 1.7e-130;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLEKLSRRYQOAVLFTPAMKR 80
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLEKLSRRYQOAVLFTPAMKR 60

QY 81 SLAGRYRCSYQNGSLWLSLSDQLELVATGVFAKPSLSAQPGPAVSSGGVDTLQCQTRYGF 140
Db 61 SLAGRYRCSYQNGSLWLSLSDQLELVATGVFAKPSLSAQPGPAVSSGGVDTLQCQTRYGF 120

QY 141 DOFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 200
Db 121 DOFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

QY 201 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTTSRITTSKESDSPAGP 260
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTTSRITTSKESDSPAGP 240

QY 261 ARQYTKGNLVLCIGAVILIIAGFLAEDWHSRRKRLRHGRAVQRPLPPLPQTRK 320
Db 241 ARQYTKGNLVLCIGAVILIIAGFLAEDWHSRRKRLRHGRAVQRPLPPLPQTRK 300

QY 321 SHGGQDGRQDVHSRGLCS 339
Db 301 SHGGQDGRQDVHSRGLCS 319
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; ORGANISM: Homo sapiens
US-09-829-495-5

Query Match      94.0%; Score 1676; DB 11; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.7e-130;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQDOAVLFIPAMKR 80
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QY 81 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCOTRYGF 140
Db 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCOTRYGF 120

QY 141 DQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLEL 200
Db 121 DQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLEL 180

QY 201 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSPKESDSPAGP 260
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QY 261 AROYTYTKGN 269
Db 241 AROYTYTKGN 249

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Job time : 65 secs

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-9

Query Match      73.0%; Score 1304; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQDOAVLFIPAMKR 80
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQDOAVLFIPAMKR 60

QY 81 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCOTRYGF 140
Db 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCOTRYGF 120

QY 141 DQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLEL 200
Db 121 DQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLEL 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:13:32 ; Search time 184 Seconds
(without alignments)
1798.273 Million cell updates/sec

Title: US-09-610-118-3

Perfect score: 1786

Sequence: 1 MFSPFALFCLGLGRVFA.....KSHGGDGGGRQDVHSGELCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*
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33: /cgn2_6/ptodata/2/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description

1	1786	100.0	339	1	PCT-US00-18152-3	Sequence 3, Appli
2	1786	100.0	339	1	PCT-US02-11122-3	Sequence 3, Appli
3	1786	100.0	339	18	US-09-453-699-3	Sequence 3, Appli
4	1786	100.0	339	18	US-09-453-699A-3	Sequence 3, Appli
5	1786	100.0	339	18	US-09-454-824-3	Sequence 3, Appli
6	1786	100.0	339	19	US-09-503-387-3	Sequence 3, Appli
7	1786	100.0	339	20	US-09-610-118-3	Sequence 3, Appli
8	1786	100.0	339	22	US-09-791-537-66967	Sequence 66967, A
9	1786	100.0	339	23	US-09-829-495-3	Sequence 3, Appli
10	1786	100.0	339	27	US-10-157-031-387	Sequence 387, App
11	1782	99.8	339	1	PCT-US00-18152-34	Sequence 34, Appl
12	1782	99.8	339	1	PCT-US00-18152-36	Sequence 36, Appl
13	1782	99.8	339	1	PCT-US00-18152-38	Sequence 38, Appl
14	1782	99.8	339	1	PCT-US02-11122-34	Sequence 34, Appl
15	1782	99.8	339	1	PCT-US02-11122-36	Sequence 36, Appl
16	1782	99.8	339	1	PCT-US02-11122-38	Sequence 38, Appl
17	1782	99.8	339	1	PCT-US02-11122-40	Sequence 40, Appl
18	1782	99.8	339	20	US-09-610-118-34	Sequence 34, Appl
19	1782	99.8	339	20	US-09-610-118-36	Sequence 36, Appl
20	1782	99.8	339	20	US-09-610-118-38	Sequence 38, Appl
21	1782	99.8	339	20	US-09-610-118-40	Sequence 40, Appl
22	1782	99.8	339	23	US-09-829-495-34	Sequence 34, Appl
23	1782	99.8	339	23	US-09-829-495-36	Sequence 36, Appl
24	1782	99.8	339	23	US-09-829-495-38	Sequence 38, Appl
25	1782	99.8	339	23	US-09-829-495-40	Sequence 40, Appl
26	1782	99.8	339	23	US-09-829-495-42	Sequence 42, Appl
27	1777	99.5	339	33	US-60-452-680-19073	Sequence 19073, A
28	1777	99.5	339	33	US-60-453-050-11421	Sequence 11421, A
29	1777	99.5	339	33	US-60-453-135-11421	Sequence 11421, A
30	1777	99.5	339	33	US-60-455-444-5986	Sequence 5986, Ap
31	1777	99.5	339	33	US-60-465-241-5986	Sequence 5986, Ap
32	1777	99.5	339	33	US-60-466-412-11421	Sequence 11421, A
33	1770	99.1	339	26	US-10-030-306-1	Sequence 1, Appli
34	1759	98.5	339	20	US-09-653-255B-5	Sequence 5, Appli
35	1759	98.5	339	30	US-10-446-826-5	Sequence 5, Appli
36	1678	94.0	319	1	PCT-US00-18152-5	Sequence 5, Appli
37	1678	94.0	319	1	PCT-US02-11122-5	Sequence 5, Appli
38	1678	94.0	319	18	US-09-453-699-5	Sequence 5, Appli
39	1678	94.0	319	18	US-09-453-699A-5	Sequence 5, Appli
40	1678	94.0	319	18	US-09-454-824-5	Sequence 5, Appli
41	1678	94.0	319	19	US-09-503-387-5	Sequence 5, Appli
42	1678	94.0	319	20	US-09-610-118-5	Sequence 5, Appli
43	1678	94.0	319	23	US-09-829-495-5	Sequence 5, Appli
44	1678	94.0	319	25	US-09-959-802-3	Sequence 3, Appli
45	1678	94.0	319	25	US-09-959-802A-3	Sequence 3, Appli

ALIGNMENTS

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PCT-US00-18152-3
; Sequence 3, Application PC/TUS0018152
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-211-228
; CURRENT APPLICATION NUMBER: PCT/US00/18152
; CURRENT FILING DATE: 2000-06-30
; EARLIER APPLICATION NUMBER: 09/503,387
; EARLIER FILING DATE: 2/14/00
; EARLIER APPLICATION NUMBER: 09/454,824
; EARLIER FILING DATE: 12/6/99
; EARLIER APPLICATION NUMBER: 09/345,468
; EARLIER FILING DATE: 6/30/99
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-18152-3

Query Match 100.0%; Score 1786; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60

QY 61 KLSRSSYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
DB 61 KLSRSSYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120

QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
DB 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180

QY 181 YSFSSRDPLYMSAPSDPLELVVGTSTVPSRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVGTSTVPSRLTEPPSSVAEFSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
DB 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

RESULT 2
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; Sequence 3, Application PCT/TUS0211122
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234-228
; CURRENT APPLICATION NUMBER: PCT/US02/11122
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/829,495
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-11122-3

Query Match 100.0%; Score 1786; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60

QY 61 KLSRSSYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
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QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
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QY 181 YSFSSRDPLYMSAPSDPLELVVGTSTVPSRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVGTSTVPSRLTEPPSSVAEFSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

DB 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

RESULT 3
US-09-453-699-3
; Sequence 3, Application US/09453699
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Martine J.
; APPLICANT: Vanchecker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-172
; CURRENT APPLICATION NUMBER: US/09/453,699
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-453-699-3

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Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KLSRSSYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
DB 61 KLSRSSYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120

QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
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QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
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; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/453,699A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339


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/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 6/30/99
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/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-610-118-3

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Best Local Similarity 100.0%; Pred. No. 2.2e-143;
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QY 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120

QY 121 GRAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GRAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180

QY 181 YSFSSRDPLWMSAPSDPLELVVTGTSVTPSRSLPTEPPSSVAEPSEATABLETVSFTNKVFT 240
Db 181 YSFSSRDPLWMSAPSDPLELVVTGTSVTPSRSLPTEPPSSVAEPSEATABLETVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRCICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRCICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 9
US-09-829-495-3
/ Sequence 3, Application US/09829495
/ GENERAL INFORMATION:
/ APPLICANT: Busfield SJ
/ APPLICANT: Villerval J
/ APPLICANT: Jandrot-perrus M
/ APPLICANT: Vainchenker W
/ APPLICANT: Gill DS
/ APPLICANT: Qian MD
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/829,495
/ CURRENT FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,387
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-829-495-3

Query Match      100.0%; Score 1786; DB 23; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLR 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLR 60

QY 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120

QY 121 GRAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GRAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPFIITVTAHSGTYRC 180

QY 181 YSFSSRDPLWMSAPSDPLELVVTGTSVTPSRSLPTEPPSSVAEPSEATABLETVSFTNKVFT 240
Db 181 YSFSSRDPLWMSAPSDPLELVVTGTSVTPSRSLPTEPPSSVAEPSEATABLETVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRCICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRCICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 8
US-09-791-537-66967
/ Sequence 66967, Application US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Bionomix, Inc.
/ APPLICANT: Danzer, Joseph
/ APPLICANT: Debe, Derek
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ FILE REFERENCE: 261/210
/ CURRENT APPLICATION NUMBER: US/09/791,537
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 153055
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 66967
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-791-537-66967

Query Match      100.0%; Score 1786; DB 22; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLR 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLR 60

QY 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSSRYQDQAVLFIPAMKRSLAGRYCSYQNSLWSLPSDQLELVATGVFAKPSLSAQ 120
```



```
|||||
Db 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339

RESULT 10
US-10-157-031-387
; Sequence 387, Application US/10157031
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, I. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157.031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-387

Query Match 100.0%; Score 1786; DB 27; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
Db 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
Db 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
QY 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339
Db 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339

RESULT 11
PCT-US00-18152-34
; Sequence 34, Application PC/TUS00018152
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-211-228
; CURRENT APPLICATION NUMBER: PCT/US00/18152
; CURRENT FILING DATE: 2000-06-30
; EARLIER FILING DATE: 2/14/00
; EARLIER FILING DATE: 2/14/00
; EARLIER FILING DATE: 12/6/99
; EARLIER FILING DATE: 12/6/99
; EARLIER FILING DATE: 6/30/99
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-18152-34

Query Match 99.8%; Score 1782; DB 1; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-143;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
Db 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-18152-34

Query Match 99.8%; Score 1782; DB 1; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-143;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
Db 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
Db 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
QY 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339
Db 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339

RESULT 12
PCT-US00-18152-36
; Sequence 36, Application PC/TUS00018152
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-211-228
; CURRENT APPLICATION NUMBER: PCT/US00/18152
; CURRENT FILING DATE: 2000-06-30
; EARLIER FILING DATE: 2/14/00
; EARLIER FILING DATE: 2/14/00
; EARLIER FILING DATE: 12/6/99
; EARLIER FILING DATE: 12/6/99
; EARLIER FILING DATE: 6/30/99
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-18152-36

Query Match 99.8%; Score 1782; DB 1; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-143;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
Db 61 KLSSRYQDQAVLFIPAMKSLAGRCYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWAPSDDPLELVVTGTSVTPSKRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
Db 241 TETSRITTSKESDSPAGPARQYTTKGNLVRIICLGAVILIIILAGFLAEDWHSRKLRLH 300
QY 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339
Db 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGRLCS 339
```


Qy	121	GPVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRC	180
Db	121	GPVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRC	180
Qy	181	YSFSSRDPYLWSAPSDPLELVVTGTSVTPSELPTPEPSSVAEFSEATAELTVSFTNKVFT	240
Db	181	YSFSSRDPYLWSAPSDPLELVVTGTSVTPSELPTPEPSSVAEFSEATAELTVSFTNKVFT	240
Qy	241	TETSRITTSPKESDSPAGPARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRKKLRH	300
Db	241	TETSRITTSPKESDSPAGPARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRKKLRH	300
Qy	301	RGRAVQRPLPLPLPQTRKSHGGQDGGQDQDVHSRGLCS	339
Db	301	RGRAVQRPLPLPLPQTRKSHGGQDGGQDQDVHSRGLCS	339

Search completed: June 8, 2004, 18:19:59
Job time : 185 secs

mis Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:12:38 ; Search time 20 Seconds
(without alignments)
1630.446 Million cell updates/sec

Title: US-09-610-118-3

Perfect score: 1786

Sequence: 1 MSPSPTALFCLGLCLGRVPA.....KSHGGQDGRQDVHSGRLCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	2 JC7509	Glycoprotein VI-1
2	428.5	24.0	466	2 JC5897	killer cell inhibi
3	426.5	23.9	264	2 I46020	FC gamma 2 recepto
4	392	21.9	287	2 JH0332	IGA (Fc) receptor,
5	372.5	20.9	841	2 JC5894	killer cell inhibi
6	365.5	20.5	635	2 JC5896	killer cell inhibi
7	358.5	20.1	239	2 G02630	Fc alphaRb - human
8	356.5	20.0	680	2 JC5895	killer cell inhibi
9	335	18.8	444	2 G01925	KIR (cl-11) NK rec
10	330	18.5	296	2 B53434	cell surface glyco
11	328	18.4	348	2 A56247	natural killer cel
12	327	18.3	444	2 G01924	KIR (cl-2) NK rece
13	323.5	18.1	341	2 I61725	natural killer ass
14	322	18.0	1327	2 T09402	immunoglobulin-li
15	317.5	17.8	335	2 A53434	cell surface glyco
16	316	17.7	455	2 G01923	KIR (cl-5) NK rece
17	315	17.6	427	2 G02034	killer cell inhibi
18	289.5	16.2	303	2 A40807	membrane glycoprot
19	182	10.2	184	2 T46433	hypothetical prote
20	145	8.1	237	2 A42013	alpha-1-B-glycopro
21	142.5	8.0	474	1 OMHUIB	alpha-1-B-glycopro
22	126.5	7.1	3707	2 S18252	heparan sulfate pr
23	124.5	7.0	267	2 T56110	FC-gamma RIIB-alp
24	118.5	6.6	267	2 A35902	FC gamma (IgG) rec
25	118	6.6	4391	2 A38096	perlecan precursor
26	116	6.5	2774	2 A43359	microtubule-associ
27	115	6.4	283	1 FCMSG1	FC gamma (IgG) rec
28	114.5	6.4	1259	2 A43425	Bravo/Nr-CAM cell
29	113.5	6.4	592	2 D70863	hypothetical prote

30	113.5	6.4	1268	1 A39640	neural cell adhesi
31	110.5	6.2	1612	2 T30805	du1t1 protein - mo
32	110	6.2	270	2 A34636	FC-gamma receptor
33	109.5	6.1	4162	2 T42633	connectin/titin -
34	108	6.0	257	2 S00682	IgE Fc receptor al
35	107	6.0	261	2 S29360	FC gamma (IgG) rec
36	106.5	6.0	3375	2 T19821	hypothetical prote
37	106	5.9	285	2 S36903	FC gamma (IgG) rec
38	106	5.9	739	2 JN0581	vascular cell adhe
39	106	5.9	931	2 T49710	related to glucan
40	106	5.9	1607	2 T02837	long chain fatty a
41	105.5	5.9	330	2 A40071	FC gamma (IgG) rec
42	105.5	5.9	330	2 I49660	FC-gamma-1/gamma-2
43	104.5	5.9	267	2 I72882	FC gamma receptor
44	104.5	5.9	1651	2 T14160	transmembrane rece
45	104	5.8	1367	1 S48478	glucan 1,4-alpha-g

ALIGNMENTS

RESULT 1

JC7509

glycoprotein VI-1 - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: JC7509; PC7101

R:Exoni: Y; Uchiyama, T.; Takayama, H.

R:Exoni: Y; Uchiyama, T.; Takayama, H.

A:Title: Molecular-cloning, genomic structure, chromosomal localization, and alternative

A:Reference number: JC7509; MUID:20483673; PMID:11027634

A:Contents: Platelet

A:Accession: JC7509

A:Molecule type: mRNA

A:Residues: 1-339 <EZU>

A:Cross-references: DDBJ:AB043819

A:Accession: PC7101

A:Molecule type: protein

A:Residues: 28-41;62-79;114-142 <EZ2>

C:Comment: This protein, which belongs to the immunoglobulin superfamily, is the major c

or gamma chain as a signal transducing subunit, and plays some roles in cancer cells.

C:Genetics:

A:Gene: gpVI-1

A:Map position: 19q13.4

A:Introns: 62/1; 95/1; 353/1; 638/1; 692/1; 752/1; 803/1

C:Keywords: glycoprotein; immunoglobulin; platelet

Query Match 100.0%; Score 1786; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.5e-123; Mismatches 0; Indels 0; Gaps 0;
Matches 339; Conservative 0;

Qy	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE	60
Db	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLE	60
Qy	61	KLSSRYQDQAVLPIPAWKSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP	120
Db	61	KLSSRYQDQAVLPIPAWKSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP	120
Qy	121	GPVSSGGDVTLCOTYGFQDQFALYKEGDPAPKPNRWYRASFPITVTAAHSGTYRC	180
Db	121	GPVSSGGDVTLCOTYGFQDQFALYKEGDPAPKPNRWYRASFPITVTAAHSGTYRC	180
Qy	181	YFSSRDYPLWSAPSDPLELVVTGTSVTPSRLETPSPSSVAEFSEATAELTVFTNKVFT	240
Db	181	YFSSRDYPLWSAPSDPLELVVTGTSVTPSRLETPSPSSVAEFSEATAELTVFTNKVFT	240
Qy	241	TETSRSTTSPKSSDSAPGARQYVTKGNLVRLCLGAVILLIILAGFLAEDWHRRKRLRH	300
Db	241	TETSRSTTSPKSSDSAPGARQYVTKGNLVRLCLGAVILLIILAGFLAEDWHRRKRLRH	300
Qy	301	RGRAVQPLPPLPPLQTRKSHGGQDGRQDVHSGRLCS	339

Db 301 RGRAVQRLPPLPQLTRKSHGQDGRQDVHSHGLCS 339

RESULT 2

JCS897

killer cell inhibitory receptor p91 precursor - human

C;Species: Homo sapiens (man)

C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C;Accession: JCS897

R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya

J. Biochem. 123, 358-366, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A;Reference number: JCS894; MUID:98218758; PMID:9538215

A;Accession: JCS897

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-466 <YAM>

A;Cross-references: GB:AF041034; NID:g2791689; PIDN:AA896926.1; PID:g2791690

C;Comment: This protein function as inhibitory cell-surface molecule against cell activa

C;Genetics:

A;Map position: 19q13.3-13.4

F;1-23/Domain: signal sequence #status predicted <SIG>

Query Match 24.0%; Score 428.5; DB 2; Length 466;

Best Local Similarity 36.1%; Pred. No. 9.2e-24;

Matches 126; Conservative 43; Mismatches 127; Indels 53; Gaps 13;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPQVD--L 56

Db 1 MTPILATLCLGLSLGPRTHVQAGHLPKPTLWAEFGSVIIQGSPTVTLRCQGSLSQAEYHL 60

QY 57 YLEKLSS--SRQD--QAVLFIPAMKRSIAGRYCSYQNGSLWSLPSQLLELVATGVF 111

Db 61 YRENKSASWTRIQEPKNGQFPPIPSITWEHAGHYHCQYVSHNSSEYSPLELVVTGAY 120

QY 112 AKPSLSAQGPVSSGGDVTLCQOTRYGDFQALYKEGDPAPYKPNPRM-----YR 162

Db 121 SKPTLSALPFPVTLGGNVTLQCVSQAQDFGILCKEGD---EHPQLNSHSHARGSSR 177

QY 163 ASPPIITVTAHSGTYRCYFSRSDPYLWAGSPDPLELVVTGTVTSRLTPTEPPSSVAE 222

Db 178 AIFSVGVPSPNRRWSHRCYGYDLSNPVYVSSPSLLELVLPVGSKPS-LSVQGPVVP 236

QY 223 FSBATAELT--VSFTNKVFTTTSRTITTPKESDSDPAGPARQYTKGNLVRI-----C 274

Db 237 GESITLCQVSDGVDRFVLYKEGDLRLQLEGRQPQ-AGLSQANFTLGPVSRSYGGYRC 295

QY 275 LGAVILIIAGFTAEADWHSRRKRLRHGRAVQRLPPLPPLPQTRKSHG 323

Db 296 YGAY-----NLSSEWSA-----PSDPLDIL-ITQIHG 322

RESULT 3

I46020

FC gamma 2 receptor precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C;Accession: I46020; S53115

R;Zhang, G.; Young, J.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A;Title: Identification of a novel class of mammalian Fc gamma receptor.

A;Reference number: I46020; MUID:95363119; PMID:7636215

A;Accession: I46020

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-264 <ZIA>

A;Cross-references: EMBL:Z37506; NID:g732571; PIDN:CAA85736.1; PID:g732572

C;Keywords: immunoglobulin receptor

Query Match 23.9%; Score 426.5; DB 2; Length 264;

Best Local Similarity 32.5%; Pred. No. 6.5e-24;

Matches 112; Conservative 37; Mismatches 87; Indels 109; Gaps 8;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPQVDLYRL 59

Db 1 MAETLFALLCLGLSVGLRTQVQAGTFPKPIIAEPPSSVWPLGSSVTLCOQPPNTKSFSL 60

QY 60 EKLSSS-----RYDQAVLFIPAMKRSIAGRYCSYQNGSLWSLPSQLLELVATG- 109

Db 61 NKEGDSPTWNIHPSLEPMDKANFFISNVREQQAGRYHCSHFIGNVWSESEP:DLII VAGE 120

QY 110 -----VFAPKPSLSAQGPVSSGGDVTLCQOTRYGDFQALYKEG--DPAPYKNP-- 159

Db 121 EPAGRLDRPSSLVSRPSPVAPENVTLLCQSGNRDITFLLSKEGAHRLRLRSQDQD 180

QY 160 WYRASPIITVTAHSGTYRCYFSRSDPYLWAGSPDPLELVVTGTVTSRLTPTEPPSS 219

Db 181 WYQAEFSLSPVTSAGHGTYRCYRSLSTNPYLLSQSEPLALIVAD----- 225

QY 220 VAEFSEATAEITVSFTNKVFTTTSRTITTPKESDSDPAGPARQYTKGNLVRI:CLGAVI 279

Db 226 -----YTQNLIRMGUAAVS 240

QY 280 LIILAGFLAEADWHSRRKRLRHGRAVQRLPPLPPLPQTRKSHG 324

Db 241 LILL-L-GIL-----LCQAHDHGG 257

RESULT 4

JH0332

IgA (Fc) receptor, myeloid cell (CD89) precursor - human

N;Alternate names: myeloid glycoprotein CD89

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999

C;Accession: JH0332; I37224; S14405

R;Maliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.; Shen, L.

J. Exp. Med. 172, 1665-1672, 1990

A;Title: Expression cloning of a human Fc receptor for IgA.

A;Reference number: JH0332; MUID:91079769; PMID:2258698

A;Accession: JH0332

A;Molecule type: mRNA

A;Residues: 1-287 <NAL>

A;Cross-references: GB:X54150; NID:g31329; PIDN:CAA38089.1; PID:g31330

A;Experimental source: myeloid cell liver V937

R;de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.

J. Immunol. 155, 1203-1209, 1995

A;Title: Structure of the gene for the human myeloid IgA Fc receptor (CD89).

A;Reference number: I37224; MUID:95363085; PMID:7636188

A;Accession: I37224

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-287 <RES>

A;Cross-references: EMBL:X87767; NID:g963041; PIDN:CAA61039.1; PID:g1054737

C;Genetics:

A;Gene: GDB:FCAR; CD89

A;Cross-references: GDB:127543; OMIM:147045

A;Map position: 19q13.2-19q13.4

A;Introns: 12/1; 24/1; 121/1; 217/1

C;Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-287/Product: IgA receptor Fc alpha #status predicted <MFC>

F;228-246/Domain: transmembrane #status predicted <TRA>

F;65,79,141,177,186/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 21.9%; Score 392; DB 2; Length 287;

Best Local Similarity 31.2%; Pred. No. 2.4e-21;

Matches 100; Conservative 43; Mismatches 110; Indels 68; Gaps 5;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPQVDLYRL 59

Db 1 MDPKQITLLCLVLCIGQRIQAQSGDFMPFISAKSSVPFLDGSVKVQCQAIKREYLTQL 60

QY 60 EKLSSSRYQD-----QAVLFIPAMKRSIAGRYCSYQNGSLWSLPSQLLELVAT 108

Db 61 MIKNSYREIGRLKFWNETDPEFVIDHMDANKAGRYCQYRIGHYFRYFRYSDTLELVVT 120

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-635 <YAN>
A;Cross-references: GB:AF041036; NID:g2791693; PIDN:AAB96928.1; PID:g2791694
C;Comment: This protein function as inhibitory cell-surface molecule against cell activation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status pr

Query Match 20.5%; Score 365.5; DB 2; Length 635;
Best Local Similarity 37.5%; Pred. No. 5.2e-19;
Matches 78; Conservative 38; Mismatches 75; Indels 17; Gaps 3;
Qy 22 SGGLPKESLQALPSLSVLEKPVTLRCQPGVDLRLRLEKLSRSSRYQDQAVL----- 73
Db 220 SGNLQKPTIIKAEPGSVITASKRAMTICQGNLDAEYFLHNEGSKQTQSTQTTLQQPKNKR 279
Qy 74 -FIPAKRSLAGRYCYSYQNGSLWSLPSDQLELVATGVFA--KPSLSAQPGPAVSSGGDV 130
Db 280 FFIPSVTQHQAGQRCYCYSAGWSQSDTLELVVTGIYEHYKPLSLVLPSPVVTAGNM 339
Qy 131 TLQOQTRYGDFQALYKEG-----PAPYKNPWRWYRASPPIITVTAHSGTYCYCYFS 184
Db 340 TLHCASDFHYDKFLTKEDKFKGNSLQTEHISSSRQYRALFIIGTPTTHTGTFRCYGYF 399
Qy 185 SRDPLYMSAPSDPLELVVTGTSVTPSRL 212
Db 400 KNPQLMSVPSDLQOILLISGLSKPSLL 427

RESULT 7
G02630
Fcalpharab - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
R;van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lammers
C;Accession: G02630
A;Reference number: H01508
A;Accession: G02630
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-239 <VAN>
A;Cross-references: EMBL:U56236; NID:g1326228; PID:g1326229
Query Match 20.1%; Score 358.5; DB 2; Length 239;
Best Local Similarity 38.7%; Pred. No. 5.2e-19;
Matches 84; Conservative 35; Mismatches 85; Indels 13; Gaps 3;
Qy 1 MSPPTALFCLGLCLG-RVPAQSGELPKPSLQALPSSLVPLEKPVTLRCQPGPGVDLRL 59
Db 1 MDPQQTLLCLVLGLGRIQAGEGDFPFISAKSPVPLDGSVKIQCAIREAYLTQL 60
Qy 60 EKLSSSYQD-----QAVLFTPAMKRSLAGRYCYSYQNGSLWSLPSDQLELVAT 108
Db 61 MIKNSYREIGRLKLNWETDPFVIDHMDANKRAGYQCYRIGHYFRYSDTLELVVT 120
Qy 109 GVFAKPSLSAQPGPAVSSGGDVTLQOQTRY-GFQDFALYKEGDPAPYKNPWRWYRASPPI 167
Db 121 GLYKPFSLADRGVLVMPGENISLTCSSAHIPDFRFSLAKEGELSLPQHQSGEHPANFSL 180
Qy 168 ITVTAHSGTYCYCYFSRSRDPYLSAPSDPLELVVTG 204
Db 181 GPVDLVNSGYRCYCYGWNRSYLSWSPFNSALELVVTG 217

RESULT 8
JC5895
killer cell inhibitory receptor p91B precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C;Accession: JC5895
R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohyan
I. Biochem. 123. 358-368, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A;Reference number: JC5894; MUID:98218758; PMID:9538215
A;Accession: JC5895
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-680 <YAM>
A;Cross-references: GB:AF041035; NID:g2791691; PIDN:AA96927.1; PID:g2791692
C;Comment: This protein function as inhibitory cell-surface molecule against cell activa
C;Genetics:
A;Map position: 7
Query Match 20.0%; Score 356.5; DB 2; Length 680;
Best Local Similarity 22.9%; Pred. No. 2.6e-18;
Matches 106; Conservative 50; Mismatches 111; Indels 195; Gaps 7;
QY 22 SGLPEKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRSRYQDQAVL----- 73
Db 220 SGNLQKPTIKAEFGSVITSRAMTIWCQGNLDAEVFLHNEKSKQTKSTQTLOQGNKGR 279
QY 74 -FIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFA--KPSLSAQPGPAVSSGGDV 130
Db 280 FFIPSVTQQHAGQYRCYCSAGWSQSDTLELVVTGIVEYNEPRLSLLPSPVVRPGNM 339
QY 131 TLCOQRYGPDQALYKEGD-----PAPYKNRWRVRSFPITVTAHSGTYRCYSFS 184
Db 340 TLHCASGHHYDKILTKEDKFNALDTEHISRSRYQALFIIGPTPTHTGTRCYGY 399
QY 185 SRPEYLWSAPSDLELVVTGTSVTPS----- 210
Db 400 KNPQLWSVPSNLQIILISGLSKPSLLTHQHLDPGMTLTLCQFSMDMVDRLHKVG 459
QY 211 -----R 211
Db 460 GADIMQHSOQTDIGFSVANFTLGYSSTGGQYRCYGAENLSWSASSEPLDILITGQ 519
QY 212 LPTEPPSSV-----AE 222
Db 520 LPITPSLSVOPNHTVHSGETVSLLCWSMDSDVTFILSKESAAQPLKSKSHDQSQAE 579
QY 223 FS-----EATAELTVSPTNKVFVTFETSRSTTTPKES 254
Db 580 FMSAVTSHLSGTYRCYGAQDSFYLSSASAPVELTVS-----GTIESSSWPKRP 631
QY 255 DSPAGPARQYTKGNLVRICLGVAILIILAGFLAEDWHSRRK 296
Db 632 NPPIPTENQDHTMENLRMGMAVVVFTVLSILATEAWRSRQ 673
RESULT 9
G01925
KIR (Cl-11) NK receptor precursor protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G01925; I61726
R;Wagtmann, N.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08782
A;Accession: G01925
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-444 <WAG>
A;Cross-references: EMBL:U30274; NID:g1004360; PIDN:AA852522.1; PID:g1004361
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A;Reference number: A56247; MUID:95232526; PMID:7716543
A;Accession: I61726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-444 <RES>
A;Cross-references: GB:I41369; NID:g780307; PIDN:AAA69870.1; PID:g780308
C;Genetics:
A;Gene: NKAT-3
A;Map position: 19
Query Match 18.8%; Score 335; DB 2; Length 444;
Best Local Similarity 30.4%; Pred. No. 5.6e-17;
Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;
QY 1 MSPSPALFCGLGICGRVP-----AQSGPL-----PKPSLQALPSSLVPLEKPV 45
Db 82 MSPVTTAHAGNYTCRSGSHSPSGAPSNPVVIMVTGNHRKPSLLAHGPLVKSGSERVI 141
QY 46 LRCQGGPPGVDLYRLEKLSRSRYQDQAV-----LFIPAMKRSIAGRYC----- 88
Db 142 LQCMSIMEHFHFLHKEGSKDPSRLVGQIHDGVSKANFSIGMMALAGTYCYGSVTH 201
QY 89 -SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCOQRYGPDQALYK 147
Db 202 TPYQ-----LSAPSDLDIVVTGPEKPSLSAQPGKVOAGSVTLSCSSRSSYDMYHLR 257
QY 148 EGDPAKYKNP-----ERWTRASHPIITVTAHSGTYRCYSFSRDDPYLWSAPSDPLELV 202
Db 258 EGAHERRLPAVKVARTFQADFPL--GPATHGTYRCFGFHRHSPYEWSDPSDPLLVSV 315
QY 203 TGTSVTPSRLPTPEPSSVAEFSEATAELTVSFNKFVTTTETSRSTTSPKESDPAGPAR 262
Db 316 TG-----NPSSS-----WPSPTPEPSKSGNPR 337
QY 263 QYTKGNLVRICLGVAILIILAGFLAEDWHSRRKRLHGRGAVORELPPLPQTRKSH 322
Db 338 HLHI---LIGTSVVIILFILLFLLHLCWCKK-----NAAV-----MDQEPAGNR 383
QY 323 GCGDGGGQD 331
Db 384 NSEDSDEQD 392
RESULT 10
B53434
cell surface glycoprotein gp49B form 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
C;Accession: B53434
R;Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A;Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration
A;Reference number: A53434; MUID:94179223; PMID:8132564
A;Accession: B53434
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-296 <CAS>
A;Cross-references: GB:U05265; NID:g475446; PIDN:AAA17798.1; PID:g475448; GB:U05266; NID
C;Genetics:
A;Gene: gp49B
A;Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
C;Keywords: alternative splicing; glycoprotein
Query Match 18.5%; Score 330; DB 2; Length 296;
Best Local Similarity 36.1%; Pred. No. 8e-17;
Matches 88; Conservative 33; Mismatches 101; Indels 22; Gaps 6;
QY 6 TALFCLGLCL-GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLS 64
Db 6 TVLLYLGLILEPTAVQAGHLPKPIIWAEPGSVIAAVTSVITWCQSWRAQYVHYLKEKS 65
QY 65 SRVQD-----QAVLFTIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPS 115
Db 66 VNPMDTQVPLETKAKFNIPSTMTTAYGIKYCYESAAGFSHSDAMELVMTGAVENPS 125
QY 116 LSAQPGPAVSSGGDVTLCOQRYGPDQALYKEG-----DPAPYKNRWRVRSFP 167

Db 126 LSVYFSSNVTSGVSISSPFCSSSVIFGRFILLQEGKHGLSWLDSQHOANQPSY--ATFVL 183
Qy 168 ITVTAHSGYRCYFSFSDPYLWSAPSDPLELVVTGTSVTPGRRLPTEPPSSVAEF-SEA 226
Db 184 DAVTPNHNGTCYCYRNEPQVWSKPSNSLDLMISETK-DQSSTPTDDASVKNQTSQEN 242
Qy 227 TAEI 230
Db 243 NAEI 246

RESULT 11

A56247

natural killer cell-associated protein - human

C;Species: Homo sapiens (man)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C;Accession: A56247

R;Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A;Reference number: A56247; MUID:95232526; PMID:7716543

A;Accession: A56247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-348 <RES>

A;Cross-references: GB:L41267; NID:G780303; PIDN:AAA69868.1; PID:G780304

C;Genetics:

A;Gene: GDB:NKAT1

A;Cross-references: GDB:698165

A;Map position: 19

Query Match 18.4%; Score 328; DB 2; Length 348;

Best Local Similarity 31.0%; Pred. No. 1.4e-16;

Matches 101; Conservative 34; Mismatches 107; Indels 84; Gaps 11;

Qy 1 MSPSPATLFCGLGCL--GRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGGPVLDYR 58

Db 1 MSLLVVSMACVGFLLQGANP-HEGVHRKPSLLAHGPGPLVKSEETVILQWSDVMFHF 59

Qy 59 LEKLSSRYQD-----QAVLFIPAMKRSIAGRYC-----SYQNGSLWSL 98

Db 60 LHR--EGMENDTLRLIGEHDGVSXANFSISRTMTQDLAGTYRCVGVSVTHSPYQ----VSA 113

Qy 99 PSQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCTRYGDFQFALYKEDGAPYKNP- 157

Db 114 PSDFLDIVITGLYEKPSLSAQPGTVLAGEVNLSCSSRSYDMYHLRSRGEAHERLPA 173

Qy 158 ----ERWYRASFPITITVAHSGTYRCYFSFSDPYLWSAPSDPLELVVTGTSVTPSR 213

Db 174 GPKVNGTFFQADFPL--GPATHGTYRCFGSFHDSFYEWKSSDPLLVSVTGNPSNWPSP 231

Qy 214 TEPPSSVAEFSEATAELTVSFNTKVTTSRITTSPPKSDSPAGPARQYTKGNLVRI 273

Db 232 TEPSK-----TGPNRH-----LHI 246

Qy 274 CLG---AVILLIILAGLAEDWHSR 296

Db 247 LIGSVVILLIFLLFLLHRCWSNKK 272

RESULT 12

G01924

KIR (C1-2) NK receptor precursor - human

N;Alternate names: killer cell inhibitory receptor

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C;Accession: G01924; G01945

R;Wagtmann, N

submitted to the EMBL Data Library, June 1995

A;Reference number: G08780

A;Accession: G01924

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-444 <WAG>

A;Cross-references: EMBL:U30273; NID:G1004358; PIDN:AA52521.1; PID:G1004359

R;D'Andrea, A.; Chang, C.; Franz-Bacon, K.; Mcclanahan, T.; Phillips, J.H.; Lanier, L.L.
submitted to the EMBL Data Library, July 1995

A;Reference number: G08908

A;Accession: G01945

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-444 <DXA>

A;Cross-references: EMBL:U31416; NID:G973405; PIDN:AAC23725.1; PID:G973406

C;Genetics:

A;Gene: NKX1

Query Match 18.3%; Score 327; DB 2; Length 444;

Best Local Similarity 30.1%; Pred. No. 2.2e-16;

Matches 111; Conservative 34; Mismatches 128; Indels 96; Gaps 12;

Qy 1 MSPSPATLFCGLGCLGRVP-----AQSGPL-----PKPSLOALPSSLVPLEKPV 45

Db 82 MSPVTAHAGNYTCRSHSPHSPGWSAPSNPVIMVTGNHRKPSLLAHGPGPLVKSERVI 141

Qy 46 LRCQGGPVLDYRLEKLSSRYQDQAV-----LFIAPMKRSIAGRYC-----88

Db 142 LQWSDIMPEHFFLHKEGISKDPSRLVGQIHGVSXANFSIGPMMLALACTYRCYGVSVTH 201

Qy 89 -SYQNGSLWSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCTRYGDFQFALYK 147

Db 202 TPTYQ----LSAPSDPLDIVVTGYEKPSPLSAQGPVQAGESVTLSCSSRSSYDMYHL 257

Qy 148 EGDPAFYKNP-----ERWYRASFPITITVAHSGTYRCYFSFSDPYLWSAPSDPLELV 202

Db 258 ERGAHERLPAVKVNTTFOADFPL--GPATHGTYRCFGSFHDSFYEWKSSDPLLVSV 315

Qy 203 TGTSVTPSRLPTEPPSSVAEFSEATAELTVSFNTKVTTSRITTSPPKSDSPAGPAR 262

Db 316 TG-----NPSSS-----WPSPTSPSSKSGNPR 337

Qy 263 QYTKGNLVRIELGAVILLIILAGLAEDWHSRKRRLHRGRAVORPLPLPPLPQTRKSH 322

Db 338 HLHI---LIGTSVVIILFILLFLLHRCWSNKK-----NAAV-----MDQEPAGNR 383

Qy 323 GGODGGRQD 331

Db 384 NSEDSDEQD 392

RESULT 13

I61725

natural killer associated transcript 2 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999

C;Accession: I61725

R;Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A;Reference number: A56247; MUID:95232526; PMID:7716543

A;Accession: I61725

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-341 <RES>

A;Cross-references: GB:L41268; NID:G780305; PIDN:AAA69869.1; PID:G780306

C;Genetics:

A;Gene: NKAT-2

Query Match 18.1%; Score 323.5; DB 2; Length 341;

Best Local Similarity 30.1%; Pred. No. 2.8e-16;

Matches 99; Conservative 36; Mismatches 105; Indels 89; Gaps 12;

Qy 1 MSPSPATLFCGLGCL--GRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGGPVLDYR 58

Db 1 MSLMVSMVCGVGFLLQGANP-HEGVHRKPSLLAHGPGPLVKSEETVILQWSDVRFQHF 59

Qy 59 LEKLSSRYQD-----QAVLFIPAMKRSIAGRYC-----SYQNGSLWSL 98

Db 60 LHR--EGKFKDTLHLGEHHDGVSKANFSGPMQDLAGTYRCYGVSWTSPYQ-----LSA 113
QY 99 PSDQLELVATGVFAKPSLSAQPGPAYSAGDVTLCQTRYGFDQFALYKEGD-----P 151
Db 114 PSDPLDIVITGLYEKESLSAQPGPTVLAGESTVILSCSSRSYDMYHLSREGEHAHERFSA 173
QY 152 APYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSR 211
Db 174 GPKVNGT--FQADFPL--GPATHGGTYRCFGSPRDSFYEWSSNDDPLLVSVTGNPSNWP 229
QY 212 LPEPPSSVAESEAETAEITVSTNKVFTTETSRITTSPEKSDSPAGPARQYTYKGNLV 271
Db 230 SPTSPSE-----TGPNRH-----L 244
QY 272 RCLGGA---VILIIILAGFLAEDWHSRRK 296
Db 245 HWLIGTSVVIIIFILLFFLLHWCCKK 273
RESULT 14
T09402
immunoglobulin-like protein IGSF1 - human
C:Species: Homo sapiens (nan)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09402
R:Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.
Genomics 48, 157-162, 1998
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.
A:Reference number: Z16665; MUID:98190514; PMID:9521868
A:Accession: T09402
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1327 <MAZ>
A:Cross-references: EMBL:AF034198; NID:G2645889; PIDN:AAC52057.1; PID:G2645890
C:Genetics:
A:Gene: igsf1
A:Map position: Xq25
Query Match 18.0%; Score 322; DB 2; Length 1327;
Best Local Similarity 32.1%; Pred. No. 1.9e-15;
Matches 105; Conservative 37; Mismatches 133; Indels 52; Gaps 9;
QY 26 PKPSLOALPSSLVPEKPYTLRCQP---PGVDLYLEKLSSRY-----QDQAVLFIPIAM 78
Db 960 PKPWLFAEPSSVYVPMQGNVTLWCGRGVHGVGYILHKEGATSMQLWGSTSNDCGAFPTNI 1019
QY 79 KRSLAGRYCSYQ---NGSLWSLPDQLELVATGVFAKPSLSAQPGPAYSAGDVTLCQ 135
Db 1020 SGTSMGRYSCYHPDWTSIKIOPSNTLELVTLGLLPKPSLLAQPGPWPVAPGENMTLCQ 1079
QY 136 TRYGFQFALYKEG--DPAPYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSA 193
Db 1080 GELPDSTFVLLKEGAQEPLEQQRPS--GYRADFWMPAVRGEDSGIYSCVYLDSTPFAASN 1138
QY 194 PSDPLELVVTGTSVTPS-----RLPEPPSSVAEF-----SEATAELT- 231
Db 1139 HSDSLEIHWTDKPKPSLSAWPMTFKLGDITLCQRGPLPGVEFVLEHDGEAPQOQFSE 1198
QY 232 -----VSFTNKVFTTETSRITTSPEKSDSPAGPARQYTYKGNLVRI 275
Db 1199 DGDFFVNNVKGKIGNYSCSYRLQAYPDINSEPSDPLELVGAAGPVAQBCTVGNIVRSS 1258
QY 276 GAVILLIILAGFLAEDWHSRRKRLRHG 302
Db 1259 IVVVVVALGVVLAIEW-KKWPRLRTRG 1284

RESULT 15
A53434
cell surface glycoprotein gp49B form 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C:Accession: A53434
R:Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A:Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration
A:Reference number: A53434; MUID:94179223; PMID:8132564
A:Accession: A53434
A>Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-335 <CAS>
A:Cross-references: GB:U05265; NID:G475446; PIDN:AAAL7797.1; PID:G475447; GB:U05264; NID:
C:Genetics:
A:Gene: gp49B
A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 271/1; 288/3; 311/1
C:Keywords: alternative splicing; Glycoprotein

Query Match 17.8%; Score 317.5; DB 2; Length 335;
Best Local Similarity 34.0%; Pred. No. 7.6e-16;
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 6 TALFCLGLCL-GRVPAQSGPLPKPSLOALPSSLVPELEKPYTLRCQPGPGVDLYRLEKLS 64
Db 6 TVLLYLGLILEPRTAVQAGHLPKPIIWAEPGSIAYTSVITWCQGSWEAQYHYLYKEKS 65
QY 65 SRYQD-----QAVLFIPIAMKRLAGRYRCYONGSLWSLPDQLELVATGVFAKDS 115
Db 66 VNPWDTQVPLETRNKAKFNIPSMTYSAGIYKYYESAAGFSEHSDAMELVMTGAYENFS 125
QY 116 LSAQPGPAYSAGDVTLCQTRYGFDQFALYKEG-----DPAPYKPERWYRAFPI 167
Db 126 LSVTPSSNVTGVSISFSCSSSIVFGFRFIIQEGKHLGSLWTLDSQHOANQPSY--ATFVL 183
QY 168 ITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLTEPPSSVAEFSEAT 227
Db 184 DAVTPNNHGTFRCYGYRNEPQVWSPKPSNLSLDMISETK-DQSSTPTE--DGLETYQKIL 240
QY 228 AELTVSF 234
Db 241 IGVLVSF 247

Search completed: June 8, 2004, 18:13:24
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:12:38 ; Search time 18 Seconds
(without alignments)
980.655 Million cell updates/sec

Title: US-09-610-118-3

Perfect score: 1786

Sequence: 1 MSPSPFTALFCLGLCLGRVPA.....KSHGGQDGRQDVHRSRLCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	27.9	448	1 LIB4 HUMAN	Q8hj6 homo sapien
2	448	25.1	631	1 LIB3 HUMAN	Q75022 homo sapien
3	442.5	24.8	499	1 LIB4 HUMAN	P59901 homo sapien
4	441	24.7	483	1 LIB2 HUMAN	Q8n149 homo sapien
5	439.5	24.6	489	1 LIB1 HUMAN	Q75019 homo sapien
6	434	24.3	598	1 LIB2 HUMAN	Q8u423 h leukocyte
7	429	24.0	590	1 LIB5 HUMAN	Q75023 homo sapien
8	424.5	23.8	643	1 LIB5 PANTR	Q8ni27 pan troglod
9	421.5	23.6	650	1 LIB1 HUMAN	Q8nh16 h leukocyte
10	408.5	22.9	439	1 LIB3 HUMAN	Q8h6c8 homo sapien
11	392	21.9	287	1 FCAR HUMAN	P24071 homo sapien
12	342.5	19.2	387	1 K3S1 HUMAN	Q14943 homo sapien
13	340	19.0	377	1 K2L4 HUMAN	Q99706 homo sapien
14	335	18.8	444	1 K3L1 HUMAN	P43629 h killer ce
15	330.5	18.5	304	1 K2S2 HUMAN	P43631 homo sapien
16	329	18.4	348	1 K2L2 HUMAN	P43627 homo sapien
17	328	18.4	348	1 K2L1 HUMAN	P43626 h killer ce
18	325.5	18.2	304	1 K2S1 HUMAN	Q14954 homo sapien
19	323.5	18.1	341	1 K2L3 HUMAN	Q14952 homo sapien
20	320.5	17.9	304	1 K2S4 HUMAN	P43628 h killer ce
21	319	17.9	455	1 K3L2 HUMAN	P43630 homo sapien
22	317.5	17.8	335	1 G49B MOUSE	Q64281 mus musculus
23	307	17.2	304	1 K2S5 HUMAN	Q14953 homo sapien
24	299	16.7	304	1 K2S3 HUMAN	Q14952 homo sapien
25	289.5	16.2	303	1 G49A MOUSE	Q61450 mus musculus
26	269.5	15.1	432	1 K3L1 MOUSE	P83555 mus musculus
27	245.5	13.7	422	1 K3L1 RAT	P83556 rattus norv
28	143.5	8.0	495	1 ALBG HUMAN	P04217 homo sapien
29	136	7.6	291	1 DM43 DIDMR	P82957 didelphis m
30	126.5	7.1	3707	1 PGBM MOUSE	Q05793 mus musculus
31	123.5	6.9	267	1 FC3 RAT	P27645 rattus norv
32	118	6.6	4391	1 PGBM HUMAN	P98160 homo sapien
33	116	6.5	2774	1 MAPA RAT	P34926 rattus norv

RESULT 1
LIB4 HUMAN
ID LIB4_HUMAN STANDARD; PRT; 448 AA.
AC Q8NHJ6; O15468; Q75021; Q8N1C7; Q8NHL5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor
DE (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Immunoglobulin-
DE like transcript 3) (ILT-3) (Monocyte inhibitory receptor HMI8) (CD85k
DE antigen).
GN LILRB4 OR LIR5 OR ILT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Monocytes;
RX MEDLINE=97422556; PubMed=9278324;
RA Arm J.P., Nwankwo C., Austen K.F.;
RT "Molecular identification of a novel family of human Ig superfamily
RT members that possess immunoreceptor tyrosine-based inhibition motifs
RT and homology to the mouse gp49b1 inhibitory receptor.";
RL J. Immunol. 159:2342-2349 (1997).
[2]
SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=98208234; PubMed=9548455;
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
RT "A family of human lymphoid and myeloid Ig-like receptors, some of
RT which bind to MHC class I molecules.";
RL J. Immunol. 159:5192-5196 (1997).
[3]
SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT GLU-362.
RX MEDLINE=20395285; PubMed=10941837;
RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;
RT "Genomic organization of the human leukocyte immunoglobulin-like
RT receptors within the leukocyte receptor complex on chromosome
RT 19q13.4.";
RL Immunogenetics 51:659-669 (2000).
[4]
SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT ASP-223.
RX Canavez F.C.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Schaefer T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

34 115.5 6.5 1709 1 SN HUMAN Q9bzz2 homo sapien
35 113.5 6.4 1284 1 NRCA CHICK P35331 gallus gall
36 109 6.1 1240 1 NFAS HUMAN O94856 homo sapien
37 108 6.0 257 1 FCEA HUMAN P12319 homo sapien
38 108 6.0 341 1 FCQ2_CAVPO Q60513 cavia porce
39 107 6.0 261 1 FCQ3_MOUSE P08508 mus musculus
40 106.5 6.0 3375 1 UNS2_CABEL Q08561 caenorhabdi
41 106 5.9 285 1 FCQ2_RAT Q63203 rattus norv
42 106 5.9 739 1 VCA1_MOUSE P29533 mus musculus
43 106 5.9 1240 1 NFAS_RAT P97685 rattus norv
44 106 5.9 2161 1 SHK1_HUMAN Q9v566 homo sapien
45 105.5 5.9 330 1 FCQ2_MOUSE P08101 mus musculus

ALIGNMENTS

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B., Scherker A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[6] FUNCTION, INTERACTION WITH PTPN6, PHOSPHORYLATION, TISSUE SPECIFICITY, RP AND SUBCELLULAR LOCATION.

RP MEDLINE=97296504; PubMed=9151699; RX Cella M., Doehring C., Samadidis J., Dessing M., Brookhaus M., Lanzavecchia A., Colonna M.;

RA "A novel inhibitory receptor (ILT3) expressed on monocytes, RT macrophages, and dendritic cells involved in antigen processing." J. Exp. Med. 185:1743-1751 (1997).

[7] FUNCTION.

RP MEDLINE=21864601; PubMed=11875462; RX Chang C.C., Giubotariu R., Manavalan J.S., Yuan J., Colovai A.I., Piazza F., Lederman S., Colonna M., Cortesini R., Dalla-Favera R., Suciu-Poca N.;

RA "Tolerization of dendritic cells by T(S) cells: the crucial role of RT inhibitory receptors ILT3 and ILT4." Nat. Immunol. 3:237-243 (2002).

CC -!- FUNCTION: Receptor for class I MHC antigens. Recognizes a broad spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Involved in the down-regulation of the immune response and the development of tolerance, e.g. towards transplants. Interferes with TNFRSF5-signaling and NF-kappa-B upregulation. Inhibits receptor-mediated phosphorylation of cellular proteins and mobilization of intracellular calcium ions.

CC -!- SUBUNIT: Binds PTPN6 when phosphorylated.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Ligand binding leads to internalization and translocation to an antigen-processing compartment.

CC -!- ALTERNATIVE PRODUCTS: Name=1; IsoId=Q8NHJ6-1; Sequence=Displayed; Name=2; IsoId=Q8NHJ6-2; Sequence=VSP_008460; Note=Alternative use of an acceptor site. No experimental confirmation available;

CC -!- TISSUE SPECIFICITY: Detected in monocytes, macrophages, dendritic cells, lung, natural killer cells and B-cells.

CC -!- INDUCTION: Upon contact with CD8(+)CD28(-) alloantigen-specific T suppressor (Ts) cells.

CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.

CC -!- PTM: Phosphorylated.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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DR EMBL; U91925; AAB68665.1; -.

DR EMBL; AF025532; AAB87666.1; -.

DR EMBL; AF189768; AAG02024.1; -.

DR EMBL; AF283988; AAL36992.1; -.

DR EMBL; BC026309; AAH26309.1; -.

DR HSPB; P43626; INKR.

DR Genew; HGNC:6608; LILRB4.

DR MIM; 604821; -.

DR InterPro; IPR07110; Ig-like.

DR Pfam; PF00047; Ig; 2.

DR PROSITE; PS00835; IG LIKE; 2.

KW Immune response; Receptor; Repeat; Signal; Transmembrane;

KW Immunoglobulin domain; Phosphorylation; Antigen; Alternative splicing;

KW Polymorphism; Multigene family.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 448 LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR SUBFAMILY B MEMBER 4.

FT DOMAIN 22 259 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 260 280 POTENTIAL.

FT DOMAIN 281 448 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 27 118 IG-LIKE C2-TYPE 1.

FT DOMAIN 124 218 IG-LIKE C2-TYPE 2.

FT DISULFID 49 98 BY SIMILARITY.

FT DISULFID 144 195 BY SIMILARITY.

FT SITE 358 363 ITIM MOTIF 1.

FT SITE 410 415 ITIM MOTIF 2.

FT SITE 440 445 ITIM MOTIF 3.

FT VARSPLIC 348 348 Missing (in isoform 2).

FT VARIANT 223 223 /FTID=VSP_008460.

FT VARIANT 362 362 G -> D (in dbSNP:731170).

FT VARIANT 5 5 K -> B (in dbSNP:2764337).

FT CONFLICT 5 5 F -> L (IN REF. 4).

FT CONFLICT 20 20 H -> D (IN REF. 5).

FT CONFLICT 414 414 Q -> R (IN REF. 2 and 5).

SQ SEQUENCE 448 AA; 49297 MW; 76D1E24A82EA1399 CRC64;

Query Match. 27.9%; Score 498; DB 1; Length 448;

Best Local Similarity 36.0%; Pred. No. 1.6e-29;

Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

QY 1 MSPPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKEVTLRCQPPGVDLYRL 59

DB 1 MIFPTALLCLGLSLGPRTHMQAGLPKPTLWAEPSVSWGNSVTTCQGTLEAREYRL 60

QY 60 EKLSRRYQD-----QAVLPFAWKRSLAGRYCSYQNGSLWSLPSDQLLELVATGV 110

DB 61 DKESPAWDRQNPLEPKNKAIFPSMTEDYAGRYCYRSPVGVNSQPSDPLELVMTGA 120

QY 111 FAKPSLSAQPAPVSSGSDVTLOCTRYGFDQFALYKEGDPAPY-----KNPERWYRASF 165

DB 121 YSKPTLSALPSPLVTSGKSVTLCCQSSPMDTFLIKERAHPILHLRSHGACQHOAEF 180

QY 166 PITTVAAGHGTVCYCSFSSRDPLYWSAPSDPLELVVTGTSVTPSRILPTPPSSVAFPSF 225

DB 181 PMSPVTSVHGTYRCFSHGHSHYLLSHPSDPLELVSGSLGPRPSPPT-----229

QY 226 ATAEIVTSFNTKVTFTTSITTSITPSKESDSPAGPARQYTKG-----NLVRLCLGAVI 279

DB 230 -----RSVSTAAGPDQPLMPTGTVFHSGLRRHWEVLIGLVVSL 270

QY 280 LTIILAGP-LAEDWHSRKR-LRHRGRAVQRPPLPLPQTRKSHGGQDGRQ-----330

DB 271 LLSLLFLQLQHWQGHKHTLAQRQADFPQPPGAPEP-----KQGLQRSSFAA 322

QY 331 DVHSRGILCS 339

DB 323 DVQGENFCA 331

RESULT 2

LIB3 HUMAN

LIB3 HUMAN STANDARD; PRT; 631 AA.

ID LIB3 HUMAN

AC O75022; O15471; Q86U49;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 3 precursor
DE Leukocyte immunoglobulin-like receptor 3 (LIR-3) (Immunoglobulin-
DE like transcript 5) (ILT-5) (Monocyte inhibitory receptor HL9) (CD85a
DE antigen). LIR3 OR ILT5.
GN LIRB3 OR LIR3 OR ILT5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS ARG-59; GLN-90; ASN-122;
RP GLN-205; HIS-405; PHE-409; GLN-539 AND VAL-574.
RC TISSUE=Monocytes;
RX MEDLINE=97422556; PubMed=9278324;
RA Arm J.P., Nwankwo C., Austen K.F.;
RT "Molecular identification of a novel family of human Ig superfamily
RT members that possess immunoreceptor tyrosine-based inhibition motifs
RT and homology to the mouse gp49B1 inhibitory receptor.";
RL J. Immunol. 159:2342-2349 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), VARIANT ARG-400, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=98208234; PubMed=9548455;
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
RT "A family of human lymphoid and myeloid Ig-like receptors, some of
RT which bind to MHC class I molecules.";
RL J. Immunol. 159:5192-5196 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS GLN-90; GLN-205; HIS-405;
RP ARG-400; GLN-539 AND VAL-574.
RA Cuillier B., Bahram S.;
RT "Genomics and diversity of the immunoglobulin-like transcript 5
RT locus";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as receptor for class I MHC antigens.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O75022-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O75022-2; Sequence=VSP_008459;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Detected in monocytes and B-cells.
CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U91928; AAB68668.1; -;
CC EMBL; AF025533; AAB87667.1; -;
CC EMBL; AF256195; AAP30716.1; -;
CC HSSP; P43626; INKR.
CC Genew; HGNC:6607; LILRB3.
CC MIM; 604820; -;
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR008262; Lipase_AS.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00409; Ig; 1.

DR PROSITE; PS50835; IG-LIKE; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immune response;
KW Immunoglobulin domain; Phosphorylation; Glycoprotein; Antigen;
KW Multigene family; Alternative splicing; Polymorphism.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 631 LEUKOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR
FT SUBFAMILY B MEMBER 3.
FT DOMAIN 24 443 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 444 464 POTENTIAL.
FT DOMAIN 465 631 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 100 IG-LIKE C2-TYPE 1.
FT DOMAIN 111 229 IG-LIKE C2-TYPE 2.
FT DOMAIN 225 314 IG-LIKE C2-TYPE 3.
FT DOMAIN 338 419 IG-LIKE C2-TYPE 4.
FT SITE 512 517 ITIM MOTIF 1.
FT SITE 593 598 ITIM MOTIF 2.
FT SITE 623 628 ITIM MOTIF 3.
FT DISULFID 49 98 BY SIMILARITY.
FT DISULFID 144 196 BY SIMILARITY.
FT DISULFID 245 296 POTENTIAL.
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 437 437 G -> GPEPQPLNPPGSGPQNG (in isoform 2).
FT VARIANT 21 21 V -> M (in dbSNP:3745418).
FT VARIANT 59 59 Q -> R (in dbSNP:678876).
FT VARIANT 69 69 L -> W (in dbSNP:620207).
FT VARIANT 90 90 Q -> E (in dbSNP:1052963).
FT VARIANT 122 122 S -> N (in dbSNP:3826750).
FT VARIANT 205 205 R -> Q (in dbSNP:1063805).
FT VARIANT 400 400 Y -> R.
FT VARIANT 400 400 Y -> H (in dbSNP:1052992).
FT VARIANT 400 400 Y -> F (in dbSNP:8105096).
FT VARIANT 405 405 Y -> H (in dbSNP:1132604).
FT VARIANT 409 409 H -> F (in dbSNP:3193485).
FT VARIANT 539 539 H -> Q (in dbSNP:1053002).
FT VARIANT 574 574 A -> V (in dbSNP:1053008).
FT CONFLICT 53 53 L -> Q (IN REF. 3).
FT CONFLICT 61 61 D -> H (IN REF. 3).
FT CONFLICT 115 115 L -> M (IN REF. 3).
FT CONFLICT 120 120 A -> F (IN REF. 1).
FT CONFLICT 149 149 R -> G (IN REF. 1 AND 3).
FT CONFLICT 175 175 G -> R (IN REF. 3).
FT CONFLICT 201 201 M -> T (IN REF. 3).
FT CONFLICT 252 252 D -> N (IN REF. 3).
FT CONFLICT 263 263 D -> A (IN REF. 3).
FT CONFLICT 268 268 P -> S (IN REF. 3).
FT CONFLICT 290 290 N -> H (IN REF. 1).
FT CONFLICT 417 417 V -> M (IN REF. 1).
FT CONFLICT 525 525 G -> R (IN REF. 1 AND 3).
FT CONFLICT 561 561 P -> S (IN REF. 1 AND 3).
SQ SEQUENCE 631 AA; 69233 MW; CC84A1762FC022DD CRC64;

Query Match 25.1%; Score 448; DB 1; Length 631;
Best Local Similarity 26.4%; Pred. No. 1.2e-25;
Matches 129; Conservative 45; Mismatches 87; Indels 228; Gaps 10;

```

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRL 59
Db 1 MTPALTALCLGLSLGRTRVQAGFPKPTLWAPGSGVSWGSPVTLWCQSLFAQYQL 60
QY 60 EKLSSSYQD-----QAVLFIPAMKSLAGRYCSYQNGSLWSPDQLELVATGV 110
Db 61 DKEGSPFLDRNPNLEPKNKAQFIPSWTCHHAGRYCHYYSSAGWSPEPDPLELVMTGA 120
QY 111 FAKPSLSAQCPGPAVSSGGDVTLQC--QTRY----- 138
Db 121 YSKETLSALPSPVVASGNNVTLRCGSKRVHFFVLMKEGEHQLPRTLDSQQLHSGGQAL 180
QY 139 ----- 138
Db 181 FVGEVNPNSHRWRFTCYYYMYNTPRVWSPDPLEILPSGVSFKPSLLTLQGPVLAPQS 240
QY 139 -----GFDQALYKEG-----PAPYKNPE----- 158
Db 241 LTLQCGSDVGYDRFVLYKEGERDLPQPGQPQAGLSQANFTLGPVSPNSGQYRCYGAH 300
QY 159 -----RW----- 160
Db 301 NLSEWSPDPLNLMAGQIDYTVLSAQPGPTVASGENVTLCCQSWQFDFTLLTKEG 360
QY 161 -----YRASPIITVTAHSGTYRCYFSRDPYLSWSPDPLELVVTG 204
Db 361 AAHPPLRLRSMYGAKHYQAEFPMSPTSAHAGTYRCYSSNPYLLSHPEPLELVVSG 420
QY 205 TSVTPSLRTPPSS--VAEFSATAELTVSFINKVF-----TTETSRSTTSKES 254
Db 421 HSGSSLPPTGPPSTPGRLYLEVLIGVSAFVLLFLFLFLRLRRQRHSHKRTSDQKRT 480
QY 255 D--SPAGPA 261
Db 481 DFQRPAGAA 489

```

RESULT 3

```

L1A4 HUMAN
ID L1A4 HUMAN STANDARD; PRT; 499 AA.
AC P59901;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily A member 4 precursor
DE (Immunoglobulin-like transcript 7) (IL7-7) (CD85g antigen).
GN L1RA4 OR IL7.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Colonna M.;
RT "Immunoglobulin-like transcript 7.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 35-494 FROM N.A.
RA Canavez F.C.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=22457157; PubMed=12529506;
RA Tedla N., Bardeira-Melo C., Tassinari P., Sloane D.E., Samplaski M.,
RA Cosman D., Borges L., Weller P.F., Arm J.P.;
RT "Activation of human eosinophils through leukocyte
RT immunoglobulin-like receptor 7.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1174-1179 (2003).
CC -!- FUNCTION: May act as receptor for class I MHC antigens. Ligand
CC binding leads to the activation of eosinophils and to the release
CC of RNASE2, IL4 and leukotriene C4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Detected on eosinophils, neutrophils and

```

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CC monocytes.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; AF041261; AAD02203.1; -.
DR EMBL; AF283989; AAL36993.1; -.
DR MTM; 607517; -.
DR PROSITE; PS50835; IG LIKE; 4.
KW Receptor; Repeat; Signal; Immune response; Immunoglobulin domain;
KW Transmembrane; Antigen; Glycoprotein; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 499
FT DOMAIN 24 445
FT TRANSMEM 447 467
FT DOMAIN 468 499
FT DOMAIN 24 118
FT DOMAIN 123 213
FT DOMAIN 224 313
FT DOMAIN 324 413
FT DISULFID 49 98
FT DISULFID 143 195
FT DISULFID 244 295
FT DISULFID 344 395
FT CARBOHYD 138 138
FT CARBOHYD 239 239
FT CARBOHYD 279 279
FT CARBOHYD 300 300
FT CONFLICT 398 398
SQ SEQUENCE 499 AA; 55096 MW; 387DA38D45183676 CRC64;
Query Match 24.8%; Score 442.5; DB 1; Length 499;
Best Local Similarity 26.6%; Pred. No. 2.2e-25;
Matches 126; Conservative 57; Mismatches 111; Indels 179; Gaps 9;
QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDYRL 59
Db 1 MTPALTALCLGLSLGRTRVQAGFPKPTLWAPGSGVSWGSPVTLWCQSLFAQYQL 60
QY 60 EK-----LSSRYQDQAVLFIPAMKSLAGRYCSYQNGSLWSPDQLELVATGV 110
Db 61 DKEGNSMRHILKTLSENKVKLSIFSMWHEHAGRYCHYYQSPAGMSEPSDPLELVVT-A 119
QY 111 FAKPSLSAQCPGPAVSSGGDVTLQCQTRYGFDQALYKEGDP-----PYKNPERWYRAS 164
Db 120 YSRPTLSALPSPVTVSGVNTLRCASRLGLRGLTLEEGDRLSLWTLNSHQHNGKQAL 179
QY 165 FPIITVTAHSGTYRCYFSRDPYLSWSPDPLELVVTGTSVTPSL----- 212
Db 180 FPMGLTFSNRGTFCYGVENNTPYWSEPSDPLELVSGVSRKPSLLTLQGPVTPGEN 239
QY 213 ----- 212
Db 240 LTLQCGSDVGYIRYTLYKEGADGLPQPGQPQAGLSQANFTLSPVSRSYGGQYRCYGAH 299
QY 213 -----PTEP-----PS-SV----- 220
Db 300 NVSSEWSPDPLELIIAGQISDRPSLSVQPGTVTSGEKVTLLCCQSWDPMFTLLTKEG 359
QY 221 -----AEFSATAELTVSFINKVFTTETS----- 244
Db 360 AAHPPLRLRSMYGAKHYQAEFPMSPTSAHAGTYRCYSGTRSSNPYLLSHPEPLELVVSG 419
QY 245 --RSITTSKESDSPAGPARQYVTKNLVRLICLGAVALIILAGFLAEDWHSRR 295
Db 420 ATETLPAQKKSATAPHLQDYTVENLIRMGVAGVLLFLGLLFEAQHSQR 472

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RESULT 4
L1A2 HUMAN
ID L1A2 HUMAN STANDARD; PRT; 483 AA.
AC Q8N149; O75020;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily A member 2 precursor
DE (leukocyte immunoglobulin-like receptor 7) (LIR-7) (immunoglobulin-
DE like transcript 1) (ILT-1) (CD85h antigen).
GN L1A2 OR LIR7 OR ILT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=3820234; PubMed=9548455;
RA Borges L., Heu M.-L., Fanger N., Kubin M., Cosman D.;
RA "A family of human lymphoid and myeloid Ig-like receptors, some of
RA which bind to MHC class I molecules.";
RA J. Immunol. 159:5192-5196 (1997).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Lung, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: May act as receptor for class I MHC antigens.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC -!- Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8N149-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8N149-2; Sequence=VSP_008455;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expression levels are very low or not
CC detectable on monocytes, T-cells, B-cells, dendritic cells and
CC natural killer (NK) cells.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; AF025531; AAB87665.1; -.
CC EMBL; BC017412; AAB17412.1; -.

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DR EMBL; BC027916; AAB27916.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:6603; LILRA2.
DR MIN; 604812; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS0835; IG LIKE; 2.
KW Immune response; Receptor; Repeat; Signal; Transmembrane;
KW Immunoglobulin domain; Glycoprotein; Antigen; Alternative splicing;
KW Polymorphism; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 483
FT DOMAIN 24 449
FT TRANSMEM 450 470
FT DOMAIN 471 483
FT DOMAIN 27 113
FT DOMAIN 117 222
FT DOMAIN 224 313
FT DOMAIN 324 413
FT DISULFID 49 97
FT DISULFID 143 195
FT DISULFID 244 295
FT DISULFID 344 395
FT CARBOHYD 64 64
FT CARBOHYD 103 103
FT CARBOHYD 138 138
FT CARBOHYD 279 279
FT CARBOHYD 300 300
FT CARBOHYD 339 339
FT CARBOHYD 429 429
FT VARSPLIC 419 436
FT VARIANT 25 25
FT VARIANT 25 25
FT SEQUENCE 483 AA; 52991 MW; 6B57FFC81F8CCF6C CRC64;
Query Match 24.7%; Score 441; DB 1; Length 483;
Best local Similarity 37.3%; Pred. No. 2.7e-25;
Matches 126; Conservative 43; Mismatches 141; Indels 28; Gaps 11;
QY 1 MSPSPALFCLGLG-RVPAQSGSLPKPSLQALPSSLVLEKPVTLRCQGPQVD--L 56
Db 1 MTEILVLICLGLSLGRTHVQGHLPKPLMAEPGSLVITQSGSVTLRCQGSQAEEYHL 60
QY 57 YRLEKLSS--SRYQD---QAVLFIPAMKRSAGRYRCSYQNGSLWSIPSLQLEIVATGVF 111
Db 61 YRENKGASWVRRIQEPKNGQFFIPSIWEHAGRYHCQYYSHNSSEYSDPLELVITGAY 120
QY 112 AKPSLSAQPGPAYSQGGVTLQCTRYGDFQFALYKEGDPAPYKNPER-----WYR 162
Db 121 SKPTLSALPSPVVTLCGNTVLCQVSQVAFDGFILCKEGED---EHPQLNSHSHARGWSW 177
QY 163 ASPPIITVTAASGTVCYCSFSSRDPYLSAPSDPLELVITGTSVTPSLRPLTEPPSSVAE 222
Db 178 AIPSGVPSFSRWSRYCAYDSNSPYVWSLSDLELLVPGVSKKPS--LSVQPGPMVAP 236
QY 223 FSRATAELT--VSFTNKVFTTTSRITTSKESDSPAGPARQYVYTKGNLVRLCLGAVIL 280
Db 237 GESLTLQCVSDVDYDFVLYKEGERDFLQRPQWQPQ-AGLSQANFTLGP-VSPSHGQYR 294
QY 281 IILAGFLADWISRRKRL--RHRGRAVQRPPLPPLP 316
Db 295 CYSAHNLSSEWSAPSDPLDLITITQGYDPRSLSVQVVP 332
RESULT 5
L1A1 HUMAN
ID L1A1 HUMAN STANDARD; PRT; 489 AA.

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Franke C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN INTERACTION WITH PTPN6 AND FCGR1A, PHOSPHORYLATION, TISSUE
RP SPECIFICITY, AND FUNCTION.
RX MEDLINE=99057019; PubMed=9842885;
RA Fanger N.A., Cosman D., Peterson L., Braddy S.C., Maliszewski C.R.,
RA Borges L.;
RA "The MHC class I binding proteins LIR-1 and LIR-2 inhibit Fc
RT receptor-mediated signaling in monocytes."
RL Eur. J. Immunol. 28:3423-3434(1998).
RN [5]
RN FUNCTION.
RX MEDLINE=21864601; PubMed=11875462;
RA Chang C.C., Ciubotariu R., Manavalan J.S., Yuan J., Colovai A.I.,
RA Piazza F., Lederman S., Colonna M., Cortesini R., Dalla-Favera R.,
RA Suciu-Foca N.;
RA "Toleration of dendritic cells by T(S) cells: the crucial role of
RT inhibitory receptors IL13 and IL14."
RL Nat. Immunol. 3:237-243(2002).
RN [6]
RN INTERACTION TYPE I MHC ALLELES, AND FUNCTION.
RX MEDLINE=22758998; PubMed=12853576;
RA Shiroishi M., Tsumoto K., Amano K., Shirakihara Y., Colonna M.,
RA Braud V.M., Allan D.S.J., Makadze A., Rowland-Jones S., Maenaka K.;
RA Willcox B.E., Jones E.Y., van der Merwe P.A., Kumagai I., Maenaka K.;
RT "Human inhibitory receptors Ig-like transcript 2 (ILT2) and ILT4
RT compete with CD8 for MHC class I binding and bind preferentially to
RT HLA-G."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8856-8861(2003).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 22-219.
RX PubMed=12390682;
RA Willcox B.E., Thomas L.M., Chapman T.L., Heikema A.P., West A.P. Jr.,
RA Bjorkman P.J.;
RT "Crystal structure of LIR-2 (ILT4) at 1.8 A: differences from LIR-1
RT (ILT2) in regions implicated in the binding of the human
RL BMC Struct. Biol. 2:6-6(2002).
CC -!- FUNCTION: Receptor for class I MHC antigens. Recognizes a broad
CC spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Involved in the
CC down-regulation of the immune response and the development of
CC tolerance. Competes with CD8A for binding to class I MHC antigens.
CC Inhibits FCGR1A-mediated phosphorylation of cellular proteins and
CC mobilization of intracellular calcium ions.
CC -!- SUBUNIT: Binds PTPN6 when phosphorylated. Binds FCGR1A.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8N423-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8N423-2; Sequence=VSP_008458;
CC Note=Alternative use of an acceptor site. No experimental
CC confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed on monocytes and B-cells, and at

CC lower levels on dendritic cells. Detected at low levels in natural
CC killer (NK) cells.
CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- PTM: Phosphorylated on tyrosine residues. Dephosphorylated by
CC PTPN6.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; AF025528; AAB87662.1; -;
DR EMBL; AF283986; AAL36990.1; -;
DR EMBL; AF283987; AAL36991.1; -;
DR EMBL; BC036827; AAL36827.1; -;
DR HSSP; P43626; 1NKR.
DR Genew; HGNC:6606; LILRB2.
DR MIM; 604815; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Receptor; Repeat; Signal; Transmembrane; Immune response;
KW Immunoglobulin domain; Phosphorylation; Glycoprotein; Antigen;
KW Multigene family; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 598
FT LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR
FT SUBFAMILY B MEMBER 2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT IG-LIKE C2-TYPE 4.
FT ITIM MOTIF 1.
FT SITE 531 536
FT SITE 560 565
FT SITE 590 595
FT DISULFID 49 98
FT DISULFID 144 196
FT DISULFID 156 166
FT DISULFID 245 296
FT DISULFID 345 396
FT CARBOHYD 280 280
FT CARBOHYD 301 301
FT CARBOHYD 340 340
FT VARSPLIC 437 437
FT VARIANT 20 20
FT H -> R (in dbSNP:383369).
FT /FTID=VAR 016997.
FT D -> E (in dbSNP:373032).
FT /FTID=VAR 016998.
FT Y -> H (in dbSNP:7247538).
FT /FTID=VAR 016999.
FT W -> C (in dbSNP:7247451).
FT /FTID=VAR 017000.
FT H -> R (IN REF. 2; AAL36991).
FT R -> G (IN REF. 3).
FT CONFLICT 322 322
FT CONFLICT 583 583
FT SEQUENCE 598 AA; 65114 MW; B08463396E45904E CRC64;
SQ
Query Match 24.3%; Score 434; DB 1; Length 598;
Best Local Similarity 35.8%; Pred. No. 1.2e-24;


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FT VARSPLIC 435 435 P -> PA (in isoform 2).
FT CONFLICT 355 355 /FTID=VSP 008462.
FT SEQUENCE 590 AA; 64125 MW; 8E7AB249F12E44CD CRC64;
Query Match 24.0%; Score 429; DB 1; Length 590;
Best Local Similarity 34.7%; Pred. No. 2.7e-24;
Matches 121; Conservative 44; Mismatches 126; Indels 58; Gaps 9;
QY 1 MSPSPTALFCGLGCLG-RVPAQSGPLPKPSLQALPSSLVLPLEKPVTLRCQGPVGVLYRL 59
Db 1 MTLTSLVLCGLGVGPRTCVQAGTLKPLTMAEPASVIARGPVTLLWCQGLETEYRL 60
QY 60 EK--LSSRYQD-----QAVLIFIPAMKSLAGRYCSYQNGSLWSLPSDQLELVATGV 110
Db 61 DKEGLPWAKRQNLPLEGAKAKHIPSTVYDSAGRYCYETPAGWSEPSDPLELVATGF 120
QY 111 FAKPSLSAQGPVAVSSGGDVTLCQTRYGDFQFALYKEGDPAP-----YKNPERWYRASF 165
Db 121 YAEPTLLALPSPVAVSGGNVTLCQDTLDGLLTFVLVEEQKLPRTLYSQKLPKGPSQALF 180
QY 166 PIITVTAHSGTYRCYCSFSSRDPVLMGAPSDPLELVATGTSVTPSRLETPPPSSVAEFSE 225
Db 181 PVGPVTFSCRWFRFCYIYRNKPNQVWNSPDLLEILVPGVSRKESLLIPQ-GSVVARGGS 239
QY 226 ATAEITVSTFKNVTFTTSRITTSKESDSP-AGPARQYTKGNLVRI-----CLGAV 278
Db 240 LTLQCRSDVGVDFVLYKEGHDVLVQSGGQGPQAGLSQANFTLPGVSRSHGGQYRCYGAH 299
QY 279 IL-----IIILAG-----FLAEDWH 292
Db 300 NLSRWSAPSDFLDILLIAGLIPALSPVQPGPKVAGENVTLICQSMH 348
RESULT 8
LIB5_PANTR STANDARD; PRT; 643 AA.
AC Q8MJZ7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 5 precursor
DE (Leukocyte immunoglobulin-like receptor subfamily 8) (LIR-8).
OS GN LIRB5 OR LIR8.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21555186; PubMed=11698452;
RA Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,
RA Shum B.P., Parham P.;
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
RT reveals framework and rapidly evolving genes."
RL J. Immunol. 167:5786-5794 (2001).
CC -!- FUNCTION: May act as receptor for class I MHC antigens (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Contains 2 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1 (By similarity).
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
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CC EMBL; AF383164; AAL31873.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PR00047; ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS08335; IG_LIKE; FALSE NEG.
KW Receptor; Repeat; Signal; Transmembrane; Immune response;
KW Immunoglobulin domain; Phosphorylation; Glycoprotein; Antigen;
KW Multigene family.
FT SIGNAL 1 23 POTENTIAL
FT CHAIN 24 643 LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR
FT DOMAIN 24 458 SUBFAMILY B MEMBER 5.
FT TRANSMEM 459 479 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 480 643 POTENTIAL.
FT DOMAIN 27 116 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 111 228 IG-LIKE C2-TYPE 1.
FT DOMAIN 224 313 IG-LIKE C2-TYPE 2.
FT DOMAIN 337 418 IG-LIKE C2-TYPE 3.
FT SITE 605 610 IG-LIKE C2-TYPE 4.
FT SITE 635 640 ITIM MOTIF 1.
FT DISULFID 49 98 ITIM MOTIF 2.
FT DISULFID 144 195 BY SIMILARITY.
FT DISULFID 244 295 BY SIMILARITY.
FT DISULFID 344 395 POTENTIAL.
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 643 AA; 70504 MW; BEBC8F940B5F65AC CRC64;
Query Match 23.8%; Score 424.5; DB 1; Length 643;
Best Local Similarity 43.6%; Pred. No. 6.4e-24;
Matches 99; Conservative 31; Mismatches 82; Indels 15; Gaps 3;
QY 1 MSPSPTALFCGLGCLG-RVPAQSGPLPKPSLQALPSSLVLPLEKPVTLRCQGPVGVLYRL 59
Db 1 MTLTSLVLCGLGVGPRTCVQAGTLKPLTMAEPASVIARGPVTLLWCQGLETEYRL 60
QY 60 EKLSSRYQDQAVLFIPAMKRS-----AGRYCSYQNGSLWSLPSDQLELVATGV 110
Db 61 DKEGLPWAKRQNLPLEGAKAKHIPSTVYDSAGRYCYETPAGWSEPSDPLELVATGF 120
QY 111 FAKPSLSAQGPVAVSSGGDVTLCQTRYGDFQFALYKEGDPAP-----YKNPERWYRASF 165
Db 121 YAEPTLLALPSPVAVSGGNVTLCQDTLDGLLTFVLVEEQKLPRTLYSQKLPKGPSRALF 180
QY 166 PIITVTAHSGTYRCYCSFSSRDPVLMGAPSDPLELVATGTSVTPSRLL 212
Db 181 PVGPVTFSCRWFRFCYIYRNKPNQVWNSPDLLEILVPGVSRKPSLL 227
RESULT 9
LIB1_HUMAN STANDARD; PRT; 650 AA.
AC Q8NHL6; O75024; O75025; Q8NHJ9; Q8NHK0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 1 precursor
DE (Leukocyte immunoglobulin-like receptor 1) (LIR-1) (Immunoglobulin-
DE like transcript 2) (ILT-2) (Monocyte/macrophage immunoglobulin-like
DE receptor 7) (MIR-7) (CD85; antigen).
DE LILRB1 OR LIR1 OR ILT2 OR MIR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), VARIANTS PRO-68; THR-142 AND
RP ILE-155, INTERACTION WITH H301 AND PTPN6, PHOSPHORYLATION, TISSUE
```

RP SPECIFICITY, AND FUNCTION.
RX TISSUE=Lymphoblast;
RA MEDLINE=97429773; PubMed=9285411;
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,
RA Hsu M.-L.;
RT "A novel immunoglobulin superfamily receptor for cellular and viral
RT MHC class I molecules.";
RL Immunity 7:273-282(1997).
[2]
RN
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20395285; PubMed=10941837;
RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;
RT "Genomic organization of the human leukocyte immunoglobulin-like
RT receptors within the leukocyte receptor complex on chromosome
RT 19q13.4.";
RL Immunogenetics 51:659-669(2000).
[3]
RN
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Canavez F.C.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-68; THR-142 AND
RP ILE-155.
RX TISSUE=B-cell;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbalwan N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN
RP INTERACTION WITH PTPN6 AND FCGR1A, PHOSPHORYLATION, TISSUE
RP SPECIFICITY, AND FUNCTION.
RX MEDLINE=99057019; PubMed=9842885;
RA Ranger N.A., Cosman D., Peterson L., Braddy S.C., Maliszewski C.R.,
RA Borges L.;
RT "The MHC class I binding proteins LIR-1 and LIR-2 inhibit Fc
RT receptor-mediated signaling in monocytes.";
RL Eur. J. Immunol. 28:3423-3434(1998).
[6]
RN
RP MUTAGENESIS OF TYR-533; TYR-562; TYR-614 AND TYR-644, INTERACTION WITH
RP FCERIA, AND FUNCTION.
RX MEDLINE=21904516; PubMed=11907092;
RA Bellon T., Kitagawa F., Sayos J., Lopez-Botet M.;
RT "Mutational analysis of immunoreceptor tyrosine-based inhibition
RT motifs of the Ig-like transcript 2 (CD85j) leukocyte receptor.";
RL J. Immunol. 168:3351-3359(2002).
[7]
RN
RP X-RAY CRYSTALLOGRAPHY (2.1 ÅNGSTROMS) OF 25-221.
RX MEDLINE=20567323; PubMed=1114384;
RA Chapman T.L., Heikema A.P., West A.P. Jr., Bjorkman P.J.;
RT "Crystal structure and ligand binding properties of the D1d2 region
RT of the inhibitory receptor LIR-1 (ILT2).";
RL Immunity 13:727-736(2000).
CC
CC -!- FUNCTION: Receptor for class I MHC antigens. Recognizes a broad
CC spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Receptor for
CC H30/U118, a human cytomegalovirus class I MHC homolog. Ligand
CC binding results in inhibitory signals and down-regulation of the

CC immune response. Engagement of LILRB1 present on natural killer
CC cells or T-cells by class I MHC molecules protects the target
CC cells from lysis. Interaction with HLA-B or HLA-E leads to
CC inhibition of the signal triggered by FCERIA and inhibits
CC serotonin release. Inhibits FCGR1A-mediated phosphorylation of
CC cellular proteins and mobilization of intracellular calcium ions.
CC -!- SUBUNIT: Binds PTPN6 when phosphorylated. Binds FCERIA and FCGR1A.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q8NHL6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8NHL6-2; Sequence=VSP_008456;
CC Name=3;
CC IsoId=Q8NHL6-3; Sequence=VSP_008456, VSP_008457;
CC -!- TISSUE SPECIFICITY: Expressed predominantly on B-cells and
CC monocytes, and at lower levels on dendritic cells. Detected on a
CC low percentage of T-cells and natural killer (NK) cells.
CC -!- DOMAIN: Contains 4 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- PTP: Phosphorylated on tyrosine residues. Dephosphorylated by
CC PTPN6.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
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CC -----
CC EMBL; AF009220; AAB63521.1; -
CC EMBL; AF009221; AAB63522.1; -
CC EMBL; AF189277; AAG08984.1; -
CC EMBL; AF283984; AAL36988.1; -
CC EMBL; AF283985; AAL36989.1; -
CC EMBL; BC015731; AAH15731.1; -
CC PDB; 1GOX; 17-JAN-01.
CC Genew; HGNC:6605; LILRB1.
CC MIM; 604811; -
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; IGC2; 3.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Receptor; Repeat; Signal; Transmembrane; Immune response;
CC Immunoglobulin domain; Phosphorylation; Glycoprotein; Antigen;
CC Multigene family; Alternative splicing; Polymorphism; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 650
FT LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR
FT SUBFAMILY B MEMBER 1.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT IG-LIKE C2-TYPE 4.
FT ITIM MOTIF 1.
FT ITIM MOTIF 2.
FT ITIM MOTIF 3.
FT ITIM MOTIF 4.
FT DISULFID 49 98
FT DISULFID 145 157
FT DISULFID 157 167
FT DISULFID 246 297
FT DISULFID 346 397
FT MOD_RES 533 533
FT POTENTIAL.
FT POTENTIAL.
FT PHOSPHORYLATION.

```
FT MOD RES 614 614 PHOSPHORYLATION.
FT MOD RES 644 644 PHOSPHORYLATION.
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 437 437 S -> SA (in isoform 2 and isoform 3).
FT VARSPLIC 437 437 /FTid=VSP_008456.
FT VARSPLIC 550 550 R -> RQ (in isoform 3).
FT VARSPLIC 550 550 /FTid=VSP_008457.
FT VARIANT 68 68 L -> P (in dBSNP:1061679).
FT VARIANT 68 68 /FTid=VAR_016993.
FT VARIANT 142 142 I -> T (in dBSNP:1061680).
FT VARIANT 142 142 /FTid=VAR_016994.
FT VARIANT 155 155 S -> I (in dBSNP:1061681).
FT VARIANT 155 155 /FTid=VAR_016995.
FT VARIANT 620 620 L -> F (in dBSNP:634222).
FT VARIANT 620 620 /FTid=VAR_016996.
FT MUTAGEN 533 533 Y -> F: IMPAIRS RECEPTOR PHOSPHORYLATION
AND ABOLISHES INHIBITION OF SEROTONIN
RELEASE. NO EFFECT ON PTPN6 BINDING; WHEN
ASSOCIATED WITH F-562.
FT MUTAGEN 562 562 Y -> F: NO EFFECT ON PTPN6 BINDING; WHEN
ASSOCIATED WITH F-533.
FT MUTAGEN 614 614 Y -> F: NO EFFECT ON PTPN6 BINDING.
ABOLISHES PTPN6 BINDING; WHEN ASSOCIATED
WITH F-644.
FT MUTAGEN 644 644 Y -> F: REDUCES PTPN6 BINDING. ABOLISHES
PTPN6 BINDING; WHEN ASSOCIATED WITH
F-614.
FT CONFLICT 557 557 P -> L (IN REF. 3; AAL36989).
FT CONFLICT 625 625 E -> K (IN REF. 1; AAB63521 AND 4).
FT SEQUENCE 650 AA; 70819 MW; 549196EA4ED767C CRC64;

Query Match 23.6%; Score 421.5; DB 1; Length 650;
Best Local Similarity 39.2%; Pred. No. 1.1e-23;
Matches 120; Conservative 34; Mismatches 117; Indels 35; Gaps 13;

Qy 1 MSPSPTALFCILGCLG-RVPAQSGPLKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRL 59
Db 1 MTPILTIVLCIGLSIGLPRTHVQAGHPKPLTWAEPFSGVITQGSPTVTLRCQGGPQBYRL 60
Qy 60 --EKLSS--SRVQDAV----LFIPAKRSLAGRYCSYQNGSLM-SLPSDQLELVATG 109
Db 61 YREKKTALWITRIQELVKKQGFIPISITWTHAGRYCYGSDTAGRSSDPLLELVVVG 120
Qy 110 VFAPSLSAQCPGPAVSSGDDVTLOCTRYGDFQALYKRGD-----PAPYKNPERWY 161
Db 121 AYIETPLSAQSPVNVSGENVILQDSQVADGSLCKEGEDHPQLNSQPHARGSS-- 178
Qy 162 RASPIITVTAAHSGTVRCYSFSSRDPYLMASPDLELVVGTGTVPSRLPTPTPPSSVA 221
Db 179 RAIFSVGSPSRRWYRCYAYDNSPWEMLPSDLLELVGYSKKPS-LSVQPGPIVA 237
Qy 222 EFSATAEL--TVSFTNKVFTTTSRIT---TSPKESDSPA---GPARQYTKGNLV 271
Db 238 PEETILTQGSADAGYRFRVLYKDGDERFLQAGAPQAGLSQANFTLGFVRSRY--GGQY 295
Qy 272 RICLGA 277
Db 296 R-CYGA 300

RESULT 10
LIA3 HUMAN
ID LIA3 HUMAN STANDARD; PRT: 439 AA.
AC Q8N6C8; O15469; O15470; O75016; Q8N151; Q8N154; Q8NHJ1; Q8NHJ2;
AC Q8NHU3; Q8NHJ4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily A member 3 precursor
DE (leukocyte immunoglobulin-like receptor 4) (LIR-4) (Immunoglobulin-
DE like transcript 6) (ILT-6) (Monocyte inhibitory receptor HM43/HM31)
```

```
DE (CD85e antigen).
GN LILRA3 OR LIR4 OR ILT6.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Lung, and Monocytes;
RX MEDLINE=97422556; PubMed=9278324;
RA Arm J.P., Nwankwo C., Austen K.P.;
RT "Molecular identification of a novel family of human Ig superfamily
members that possess immunoreceptor tyrosine-based inhibition motifs
and homology to the mouse gp49B1 inhibitory receptor.";
RL J. Immunol. 159:2342-2349(1997).
RN [2]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Lung, and Monocytes;
RX MEDLINE=98208234; PubMed=9548455;
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
RT "A family of human lymphoid and myeloid Ig-like receptors, some of
which bind to MHC class I molecules.";
RL J. Immunol. 159:5192-5196(1997).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Peripheral blood leukocytes;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smalusz D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
SEQUENCE OF 1-420 FROM N.A., AND VARIANTS PRO-3; ARG-107 AND HIS-301.
RP Norman P.J., Carey B.S., Vaughan R.W.;
RT "Leukocyte receptor cluster: polymorphism and ethnic diversity of
leukocyte immunoglobulin-like receptor (LILR) A3.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as soluble receptor for class I MHC antigens.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC CC -!- TISSUE SPECIFICITY: Detected in B-cells, and at lower levels in
natural killer (NK) cells. Detected in peripheral blood monocytes
and lung.
CC CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC CC
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or send an email to license@isb-sib.ch).
CC CC
CC EMBL; U91926; AAB68666.1; -.
CC EMBL; U91927; AAB68667.1; -.
CC EMBL; AF025527; AAB87661.1; -.
CC EMBL; BC028208; AAB28208.1; -.
CC EMBL; AF482762; AAM18035.1; -.
CC EMBL; AF482763; AAM18036.1; -.
CC CC
CC DR EMBL; U91926; AAB68666.1; -.
CC DR EMBL; U91927; AAB68667.1; -.
CC DR EMBL; AF025527; AAB87661.1; -.
CC DR EMBL; BC028208; AAB28208.1; -.
CC DR EMBL; AF482762; AAM18035.1; -.
CC DR EMBL; AF482763; AAM18036.1; -.
CC CC
```

298 SGAY-----NLSEWAPSDDILLITQIRAPFLLSVRGPVVASGENVLLCQSOG 350

324 G 324
351 G 351

RESULT 11

FCAR HUMAN
ID FCAR HUMAN STANDARD; PRT; 287 AA.
AC P24071; Q13603; Q13604; Q15727; Q15728; Q92590;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Immunoglobulin alpha Fc receptor precursor (Iga Fc receptor) (CD89 antigen).
GN FCAR OR CD89.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX MEDLINE=91079769; PubMed=2258698;
RZ Maliszewski C.R., March C.J., Schoenborn M.A., Gimpel S., Shen L.;
RT "Expression cloning of a human Fc receptor for Iga";
RL J. Exp. Med. 172:1665-1672(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX TISSUE=Bone marrow;
RZ MEDLINE=95363085; PubMed=7636188;
RZ de Wit T.P.M., Morton H.C., Capel P.J.A., van de Winkel J.G.J.;
RT "Structure of the gene for the human myeloid Iga Fc receptor (CD89).";
RL J. Immunol. 155:1203-1209(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A.2 AND A.3).
RX TISSUE=Alveolar macrophage, and Monocytes;
RZ MEDLINE=96247667; PubMed=8666819;
RZ Paty C., Sibille Y., Lehen A., Monteiro R.C.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by alternative splicing that are differentially expressed between blood monocytes and alveolar macrophages";
RL J. Immunol. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS B AND B-DELTA-S2).
RX van Dijk T.B., Morton H.C., Caldenhoven E., Bracke M., Raaijmakers J.A.M., Lammers J.W.J., Koenderman L., Groot R.P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A.3).
RX MEDLINE=9643090; PubMed=8836118;
RZ Pleass R.J., Andrews P.D., Kerr M.A., Woof J.M.;
RT "Alternative splicing of the human Iga Fc receptor CD89 in neutrophils and eosinophils";
RL Biochem. J. 318:771-777(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM U02).
RX Toyabe S., Kuwano Y., Takeda K., Uchiyama M., Abo T.;
RT "Alternatively spliced forms of monocyte Iga Fc receptors in patients with Iga nephropathy";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX TISSUE=Blood;
RZ MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson P.D., Mollay S.,

ID AC Q14943; STANDARD; PRT; 387 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 3DS1 precursor (MHC class I
 DE NK cell receptor) (Natural killer associated transcript 10) (NKAT-10).
 GN KIR3DS1 OR NKAT10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96270004; PubMed=8662091;
 RA Doehring C., Samaridis J., Colonna M.;
 RA "Alternatively spliced forms of human killer inhibitory receptors.";
 RL Immunogenetics 44:227-230(1996).
 RN [2]
 RP VARIANT HIS-166.
 RX MEDLINE=98090086; PubMed=9430221;
 RA Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
 RA Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
 RA "Human diversity in killer cell inhibitory receptor genes.";
 RL Immunity 7:753-763(1997).
 CC -!- FUNCTION: Receptor on natural killer (NK) cells for HLA-C alleles.
 CC Does not inhibit the activity of NK cells.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in NK and T cell lines but not in B
 CC lymphoblastoid cell lines or in a colon carcinoma cell line.
 CC -!- POLYMORPHISM: The KIR genes are located in a segment of DNA on
 CC 19q13.4 in the leukocyte receptor complex that has undergone
 CC expansion and contraction over time, probably through unequal
 CC crossing-over. Thus, KIR haplotypes vary in the number and types
 CC of genes, although a few framework loci, such as the gene KIR3DL1,
 CC are present on all or nearly all haplotypes. KIR3DL1 and KIR3DS1
 CC segregate as alleles of the locus KIR3DL1/3DS1.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC -----
 DR EMBL; L76661; AAB36589.1; --
 DR HSSP; P43626; INKR.
 DR Genew; HGNC:6340; KIR3DS1.
 DR MIM; 604946; --
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
 DR GO; GO:0030106; F:MHC class I receptor activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR GO; GO:0030101; P:natural killer cell activation; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 3.
 DR PROSITE; PS50835; IG LIKE; FALSE NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 387
 FT KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 3DS1.
 FT DOMAIN 22 340
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 360
 FT POTENTIAL.
 FT DOMAIN 361 387
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 137 102
 FT IG-LIKE C2-TYPE 1.
 FT DOMAIN 137 202
 FT IG-LIKE C2-TYPE 2.
 FT DOMAIN 237 300
 FT IG-LIKE C2-TYPE 3.

FT DISULFID 49 95 BY SIMILARITY
 FT DISULFID 144 195 BY SIMILARITY
 FT DISULFID 244 293 BY SIMILARITY
 FT CARBOHYD 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 166 R -> H
 FT /FTID=VAR_010377.
 SQ SEQUENCE 387 AA; 42902 MW; 0E75CE730D15E100 CRC64;
 Query Match 19.2%; Score 342.5; DB 1; Length 387;
 Best Local Similarity 35.8%; Pred. No. 3.7e-18;
 Matches 101; Conservative 27; Mismatches 105; Indels 49; Gaps 9;
 QY 1 MDSPTPALFCGLGLCLGRVP-----AQSGL-----PKPSLQALPSLVPLEKPEVT 45
 DB 82 MSPVTTAHAGNYTCRGSHPSPTGWSAPSNPMVMTVGNHRTKPSLLAHPGLVKSGRVI 141
 QY 46 LRCQGGPGVDLYRLEK-----LSSRYQDQ-----AVLFIPAMKRSIAGRYRC----- 88
 DB 142 LQWSDIMPEHFFLHKWISKDFSLVQGHGVSANFISGSMRALAGTYRCYGSVTH 201
 QY 89 -SYONGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYK 147
 DB 202 TPYQ-----LSAPSDPLDIVVTGLYKPSLSAQPGPKVQAGESVTLSCSSSSSYDMVLSR 257
 QY 148 EGPDPAPYKNP-----PRWTFASPIITVTHAHSCTRCYSFSSRDPYLVWAPSDPLELV 202
 DB 258 EGAHERRUPFAVKVARTFOADPFL--GPATHGCTYRCFGSFRHSPYEWSDPSPDLLVSV 315
 QY 203 TGTSTVTPSRILTPPPSSVAEFSE-----ATAELTVSTNKVF 239
 DB 316 TGNPSSSWSPTEPSSKSGNRLHLILIGTSVVKIPFTILLF 357
 RESULT 13
 K2L4 HUMAN
 ID K2L4_HUMAN STANDARD; PRT; 377 AA.
 AC Q99706; O14621; O14622; O14623; O43534; P78400; P78401;
 AC Q99559; Q99560; Q99561; Q99562; Q9UQU7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2DL4 precursor (MHC class I
 DE NK cell receptor KIR103AS) (Killer cell inhibitory receptor 103AS)
 DE (KIR-103AS) (GSP).
 GN KIR2DL4 OR KIR103AS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97102173; PubMed=8946682;
 RA Selvakumar A., Steffens U., Dupont B.;
 RA "NK cell receptor gene of the KIR family with two IG domains but
 RA highest homology to KIR receptors with three IG domains.";
 RL Tissue Antigens 48:285-294(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5).
 RX MEDLINE=97378880; PubMed=9234477;
 RA Selvakumar A., Steffens U., Palanisamy N., Chaganti R.S.K., Dupont B.;
 RA "Genomic organization and allelic polymorphism of the human killer
 RA cell inhibitory receptor gene KIR103.";
 RL Tissue Antigens 49:564-573(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 6).
 RC TISSUE=Lymphoid;
 RA Biassoni R.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBSJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RX MEDLINE=98090086; PubMed=9430221;

Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.;
"Human diversity in killer cell inhibitory receptor genes.";
Immunity 7:753-763(1997).
[5]
SEQUENCE FROM N.A.
Chan H.W., Salter R.D.;
"Exon deletion contributes to structural diversity of 2DL4 killer
inhibitory receptors.";
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97213129; PubMed=9059894;
Selvakumar A.;
"Polymorphism and domain variability of human killer cell inhibitory
receptors.";
Immunol. Rev. 155:183-196(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1;
CC IsoId=Q99706-1; Sequence=Displayed;
CC Name=2; Synonyms=AS1;
CC IsoId=Q99706-2; Sequence=VSP_002609;
CC Name=3; Synonyms=AS;
CC IsoId=Q99706-3; Sequence=VSP_002610;
CC Name=4; Synonyms=ASD1;
CC IsoId=Q99706-4; Sequence=VSP_002609, VSP_002610;
CC Name=5; Synonyms=ASD2;
CC IsoId=Q99706-5; Sequence=VSP_002609, VSP_002610, VSP_002611;
CC Name=6;
CC IsoId=Q99706-6; Sequence=VSP_002608, VSP_002609, VSP_002610;
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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EMBL; U71199; AAB49756.1; -
EMBL; AF003123; AAB61926.1; -
EMBL; AF003116; AAB61926.1; JOINED.
EMBL; AF003117; AAB61926.1; JOINED.
EMBL; AF003118; AAB61926.1; JOINED.
EMBL; AF003119; AAB61926.1; JOINED.
EMBL; AF003121; AAB61926.1; JOINED.
EMBL; AF003122; AAB61926.1; JOINED.
EMBL; AF003120; AAB61926.1; JOINED.
EMBL; AF002979; AAB71387.1; -
EMBL; AF002980; AAB71388.1; -
EMBL; AF002981; AAB71389.1; -
EMBL; AF002982; AAB71390.1; -
EMBL; X97229; CAA65868.1; -
EMBL; X99479; CAA67842.1; -
EMBL; X99480; CAA67843.1; -
EMBL; X99481; CAA67844.1; -
EMBL; AF034771; AAB95164.1; -
EMBL; AF034772; AAB95165.1; -
EMBL; AF034773; AAB95166.1; -
EMBL; AF110035; AAD24763.1; -
EMBL; AF110032; AAD24763.1; JOINED.
EMBL; AF110033; AAD24763.1; JOINED.
EMBL; AF110034; AAD24763.1; JOINED.
EMBL; U73394; AAC51146.1; -
Genew; HGNC:6332; KIR2DL4.
MIM; 604945; -
GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 377
FT KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 2DL4.
FT DOMAIN 22 242
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT TRANSMEM 243 263
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 264 377
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 44 104
FT IG-LIKE C2-TYPE 2.
FT DOMAIN 139 202
FT BY SIMILARITY.
FT DISULFID 51 97
FT BY SIMILARITY.
FT DISULFID 146 195
FT CARBOHYD 141 141
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 27 121
FT Missing (in isoform 6).
FT FTId=VSP_002608.
FT Missing (in isoform 2, isoform 4, isoform
FT 5 and isoform 6).
FT FTId=VSP_002609.
FT Missing (in isoform 3, isoform 4, isoform
FT VARSPLIC 236 270
FT Missing (in isoform 6).
FT FTId=VSP_002610.
FT VARSPLIC 271 288
FT Missing (in isoform 5).
FT FTId=VSP_002611.
FT VARIANT 53 53
FT Y -> C (in dbSNP:618835).
FT FTId=VAR_010307.
FT L -> V.
FT VARIANT 87 87
FT FTId=VAR_010308.
FT T -> A.
FT VARIANT 138 138
FT FTId=VAR_010309.
FT A -> P (in dbSNP:1051456).
FT VARIANT 209 209
FT FTId=VAR_010310.
FT D -> N.
FT VARIANT 271 271
FT FTId=VAR_010311.
FT H -> N.
FT VARIANT 371 371
FT FTId=VAR_010312.
FT CONFLICT 229 229
FT T -> P (IN REF. 5).
FT SEQUENCE 377 AA; 41527 MW; 7ECAB0FC07F4143B CRC64;
Query Match 19.0%; Score 340; DB 1; Length 377;
Best Local Similarity 31.4%; Pred. No. 5.5e-18;
Matches 98; Conservative 42; Mismatches 112; Indels 60; Gaps 9;
QY 1 MSPSPTALFCLGLCLGR-VPAQSGPLPKPSI-QALPSSILVPLEKPVTLRCQGPVGVLYRL 59
DB 3 MSPTVILILACLGFLDOSVWAHVGGQDKPFCASNPVAVPGGHTLCHYRGENITFL 62
QY 60 EKLSS-----SRQDAVLFIAMKRLAGRYRC---SYNGSLMSLPSDQLVLVATG 109
DB 53 YKQGVVPPELYNRIFWNSFLISP-LTPAHAGTYRCRGFHPHSPTWGAAPNPLVIMVTG 121
QY 110 VFAPKPSLSAQPGVAVSSGGDVTLOQQTGYGDFQALYKEGDPAPYKNP-----ERWYAS 164
DB 122 LYEKPSLTARPGPTVRTGENVTLSQSSQSSPDYIHLREGGAHLRLPAVPSINGTFOAD 181
QY 165 FPIITVTAHSGTVCYCSFSSRDPVLMGAPSDPLVVTGTSVTPSRPLRCPSPSSVAEFS 224
DB 182 PFL--GPATGTYRCFGSGFSGSPYENSDADPLVSVTVGNPSSSWSPSTFP-----231
QY 225 EATAELTVSFINKVFTTSTTSITTSPPKESDSPAQPARYTKGNLVCICIGAVLILIA 284
DB 232 -----SF-----KTGIARHLHA---VIRYSVAILLTILP 258
QY 285 GFLAEDWESRRK 296
DB 259 FFLLRWCSSKKK 270

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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:12:38 ; Search time 55 Seconds
(without alignments)
1944.739 Million cell updates/sec

Title: US-09-610-118-3

Perfect score: 1786
Sequence: 1 MSPSPALFCLGLGRVPA.....KSHGGQGRQDVHSHGLCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	4 Q9UIF2	Q9uif2 homo sapien
2	1676	93.8	321	4 Q9HCN7	Q9hcn7 homo sapien
3	1355	75.9	620	4 Q9HCN6	Q9hcn6 homo sapien
4	478	26.8	481	6 Q8MJZ2	Q8mjz2 pan troglod
5	469	26.3	325	11 Q9Z0H5	Q9z0h5 rattus norv
6	464	26.0	631	6 Q8MJZ3	Q8mjz3 pan troglod
7	459	25.7	304	4 Q76036	Q76036 homo sapien
8	455	25.5	325	11 Q9Z004	Q9z004 mus musculu
9	455	25.5	325	11 Q8C567	Q8c567 mus musculu
10	455	25.5	645	6 Q8MJZ5	Q8mjz5 pan troglod
11	452	25.3	323	11 Q8C0U6	Q8c0u6 mus musculu
12	447.5	25.1	287	4 Q76016	Q76016 homo sapien
13	443.5	24.8	306	6 Q8MIZ8	Q8miz8 macaca mula
14	443	24.8	307	6 Q8MIZ9	Q8miz9 macaca mula
15	441.5	24.7	460	6 Q8MJZ4	Q8mjz4 pan troglod
16	440.5	24.7	306	6 Q95JB9	Q95jb9 macaca fasc

17	436	24.4	305	6 Q8MIZ7	Q8miz7 macaca mula
18	435.5	24.4	305	6 Q8MIZ6	Q8miz6 macaca mula
19	426.5	23.9	264	6 Q28109	Q28109 bos taurus
20	424.5	23.8	643	6 Q8MJZ7	Q8mjz7 pan troglod
21	424.5	23.8	662	6 Q8MJZ6	Q8mjz6 pan troglod
22	422	23.6	336	6 Q8SPQ5	Q8spq5 bos taurus
23	401.5	22.5	294	6 Q8MIZ5	Q8miz5 macaca mula
24	394	22.1	382	4 Q8NFB0	Q8nfb0 homo sapien
25	392	21.9	308	6 Q863H2	Q863h2 bos taurus
26	372.5	20.9	697	11 Q8K4V6	Q8k4v6 mus musculu
27	372.5	20.9	841	11 Q8R2Z1	Q8r2z1 mus musculu
28	365.5	20.5	635	11 Q55002	Q55002 mus musculu
29	364.5	20.4	369	6 Q8MKI2	Q8mkiz2 macaca mula
30	362.5	20.3	841	11 Q54999	Q54999 mus musculu
31	361.5	20.2	357	6 Q8MKI1	Q8mkiz1 macaca mula
32	358	20.0	663	11 Q70434	Q70434 mus musculu
33	356.5	20.0	680	11 Q55001	Q55001 mus musculu
34	351	19.7	275	4 Q9UEK0	Q9uek0 homo sapien
35	349.5	19.6	367	6 Q8MK08	Q8mk08 macaca mula
36	348.5	19.5	375	4 Q8NHK5	Q8nhk5 homo sapien
37	347.5	19.5	287	4 Q99565	Q99565 homo sapien
38	347	19.4	367	6 Q8MK07	Q8mk07 macaca mula
39	347	19.4	377	4 Q86U48	Q86u48 homo sapien
40	345.5	19.3	370	4 Q8NH18	Q8nh18 homo sapien
41	344.5	19.3	287	4 Q8N735	Q8n735 homo sapien
42	344	19.3	447	6 Q7YR16	Q7yry6 gorilla gor
43	343.5	19.2	375	4 Q8NHK3	Q8nhk3 homo sapien
44	343.5	19.2	375	4 Q8NHK4	Q8nhk4 homo sapien
45	343.5	19.2	382	4 Q43469	Q43469 homo sapien

ALIGNMENTS

RESULT 1

ID Q9UIF2 PRELIMINARY; PRT; 339 AA.
AC Q9UIF2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DR Platelet glycoprotein VI precursor (Platelet glycoprotein VI-1).
GN GPVI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura Y.;
RT "Platelet glycoprotein VI.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
EX PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, and
alternative splice forms of the platelet collagen receptor
glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB035073; BAA89353.1; -.
DR EMBL; AB043819; BAB12245.1; -.
DR FIR; JC7509; JC7509.
DR HSP; P43626; INKR.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0007167; P:enzyme linked receptor protein signaling pa. . .; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
KW Signal.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 339 POTENTIAL.
 SQ SEQUENCE 339 AA; 36923 MW; 423757695E030CC CRC64;
 Query Match 100.0%; Score 1786; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-148;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 Db 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120
 Db 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120
 QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 QY 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 Db 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 QY 241 TETSRITTSFKESDSPAGPARQYTKGNLVRLICLGAVILLIILAGFLAEDWHSRKRRLH 300
 Db 241 TETSRITTSFKESDSPAGPARQYTKGNLVRLICLGAVILLIILAGFLAEDWHSRKRRLH 300
 QY 301 RGRAVQRPPLPLPOTRKSHGQDGRQDVHSRGLCS 339
 Db 301 RGRAVQRPPLPLPOTRKSHGQDGRQDVHSRGLCS 339

RESULT 2

Q9HCN7 PRELIMINARY; PRT; 321 AA.
 ID Q9HCN7
 AC Q9HCN7
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Platelet glycoprotein VI-2.
 GN GPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=20483673; PubMed=11027634;
 RA Ezumi Y., Uchiyama T., Takayama H.;
 RT "Molecular cloning, genomic structure, chromosomal localization, and
 RT alternative splice forms of the platelet collagen receptor
 RT glycoprotein VI.";
 RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
 DR EMBL; AB043820; BAF1246.1; -.
 DR HSSP; P43626; INKR.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 SQ SEQUENCE 321 AA; 35158 MW; 93FBF89845958345 CRC64;

Query Match 93.8%; Score 1676; DB 4; Length 321;
 Best Local Similarity 94.7%; Pred. No. 1.3e-138;
 Matches 321; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 Db 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120
 Db 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120

QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 QY 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 Db 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 QY 241 TETSRITTSFKESDSPAGPARQYTKGNLVRLICLGAVILLIILAGFLAEDWHSRKRRLH 300
 Db 241 TETSRITTSFKESDSPAGPARQYTKGNLVRLICLGAVILLIILAGFLAEDWHSRKRRLH 300
 QY 301 RGRAVQRPPLPLPOTRKSHGQDGRQDVHSRGLCS 339
 Db 283 RGRAVQRPPLPLPOTRKSHGQDGRQDVHSRGLCS 321

RESULT 3

Q9HCN6 PRELIMINARY; PRT; 620 AA.
 ID Q9HCN6
 AC Q9HCN6
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Platelet glycoprotein VI-3.
 GN GPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=20483673; PubMed=11027634;
 RA Ezumi Y., Uchiyama T., Takayama H.;
 RT "Molecular cloning, genomic structure, chromosomal localization, and
 RT alternative splice forms of the platelet collagen receptor
 RT glycoprotein VI.";
 RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
 DR EMBL; AB043821; BAB1247.1; -.
 DR HSSP; P43626; INKR.
 DR Genew; HGNC:14388; GP6.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005518; F:collagen binding; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0030168; P:platelet activation; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 SQ SEQUENCE 620 AA; 67308 MW; FEBB64C55F679615 CRC64;

Query Match 75.9%; Score 1355; DB 4; Length 620;
 Best Local Similarity 100.0%; Pred. No. 4.2e-110;
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 Db 1 MSPSPALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120
 Db 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWLSLPSDQLVLVATGVFAKPSLSAQ 120
 QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 Db 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTAAHSGTYRC 180
 QY 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 Db 181 YSFSSRDPLWLSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
 QY 241 TETSRITTSFKESDSPAG 259

DB 443 YTVENLIRMGAGLVLVILGILLIFEAQHSQR 473

RESULT 5

Q9ZOH5 PRELIMINARY; PRT; 325 AA.

ID Q9ZOH5 AC Q9ZOH5; PRELIMINARY; PRT; 325 AA.

AC Q9ZOH5; PRELIMINARY; PRT; 325 AA.

DT 01-MAY-1999 (TEMBLrel. 10, Created)

DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)

DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)

DT NKACNR.

GN AR-1 OR KILR-1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=101116;

[1]

RN SEQUENCE FROM N.A.

RN TISSUE=Lymphoid;

RA Falco M., Cantoni C., Bottino C., Moretta L., Biassoni E.;

RT "Identification of the rat homologue of the human NKp46 triggering receptor.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN=PVG;

RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;

RT "Molecular characterization of KILR-1, a novel immunoglobulin-like gene in the rat, expressed by NK cells.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ012741; CAA10161.1; -.

DR EMBL; AF082533; AAC69890.1; -.

DR HSP; P43626; INKR.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003593; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

KW Receptor.

SEQUENCE 325 AA; 37178 MW; 502C10AA02F65FA4 CRC64;

Query Match 26.3%; Score 469; DB 11; Length 325;

Best Local Similarity 37.7%; Pred. No. 8.2e-33;

Matches 116; Conservative 38; Mismatches 116; Indels 38; Gaps 5

QY 1 MSPPTALFCGLGICLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGLYR- 58

DB 1 MLFTLRLLCGLCLSORINTEKTLPKPIWAKPSIMVTKGNSVNIWCQAQASAEQL 60

QY 59 -----LKLSSRYQDQAVLFIIPAMKSLAGRYCSYQNGSLWSLPSQLELVATGV 110

DB 61 VFEGSPFALBRPKSSRMNKKVFISQMTSHTAGIYTCFYQSGELWSESSNPLXLVVTGL 120

QY 111 FAPSLSAQPGPAVSSGDVTLQCQTRYGDQFALYKEGDPAKYKNPERWYRASFPILTV 170

DB 121 YDPTLLVWHPGPEVTLGENTVTFSCHLKTATSKFFLLKERESNHIQHKYGNITQAEFFMGVP 180

QY 171 TAAHSGYRCVFSRSRPPYLWSAPSDPLELWVTGTSVTPSLRTPPEPSSVA--BFSEATA 228

DB 181 TRAIRGYRC--FGSYNDYAWSFSEPVTLITGEVENTSLAPDTPVSSLDYWEFDIST- 237

QY 229 ELTVSFNTKVFTTTSRISITTSPPKESDPAGPARQYYTKGNLVRICLGAVILLIAGFLA 288

DB 238 -----KESGLQKDSAPWDHTAQNLRIGLACIIWALVWLLA 274

QY 289 EDWHSRRK 296

DB 275 EDWLSRRK 282

RESULT 6

Q8MUJ23 PRELIMINARY; PRT; 631 AA.

ID Q8MUJ23

DR SMART; SM00409; IG; 2.
 KW Receptor.
 SQ SEQUENCE 325 AA; 37265 MW; ED24E48ABF22F029 CRC64;
 Query Match 25.5%; Score 455; DB 11; Length 325;
 Best Local Similarity 38.0%; Pred. No. 1.4e-31;
 Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;
 QY 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLOALPSSLVLEKPVTLRCQGPVVDLYR- 58
 Db 1 MLPTLTALLCLGCLCSQINTEKETLTPKPIIWAQPSIMVTNGNSVNIWCQAQASAYQL 60
 QY 59 -----LEKLSSRYQDQAVLFIIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGV 110
 Db 61 YFEGSFALERPSPSRMKNVRFISQMTSHTAGIYTCFYQSGELWSKSNPLKLVVTGL 120
 QY 111 FAKPSLSAQPGPAVSSGGDVTLCQOTRYGDFDQALYKEGDPAPYKPERWYRASFPITV 170
 Db 121 YDTPNLWVYPRPEVTLGENTVTFQCLKTATSKFLLKERGSNHIONKYGNIOAEFFMGPV 180
 QY 171 TAAHSGTYRCYSRSSRDPYLWSAPSDPLELVVTGTSVTPSRLETPPSSVA--EFSATA 228
 Db 181 TRAHRTYRC--FGSYNDYAWSPPEVTLITGGVENSLSAPTDPTSSLDYWEFDLSTN 238
 QY 229 ELTVSFTNKVFTTSTRSITTSKESDSPAGPARQYTKGNLVIRICIGAVILIILAGFLA 288
 Db 239 E-----SGLQKDS-----AFWDHTTQNLIRIGLACIILITLVWLLT 274
 QY 289 EDHSRRK 296
 Db 275 EDWLSRRK 282
 RESULT 9
 Q8C567 PRELIMINARY; PRT; 325 AA.
 AC Q8C567;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Lymphocyte antigen 94.
 GN NCr1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK079401; BAC37635.1; -.
 DR MGD; MGI:1336212; Ncr1.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 2.
 SQ SEQUENCE 325 AA; 37237 MW; 42272A97653E3E34 CRC64;
 Query Match 25.5%; Score 455; DB 11; Length 325;
 Best Local Similarity 38.0%; Pred. No. 1.4e-31;
 Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;
 QY 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLOALPSSLVLEKPVTLRCQGPVVDLYR- 58
 Db 1 MLPTLTALLCLGCLCSQINTEKETLTPKPIIWAQPSIMVTNGNSVNIWCQAQASAYQL 60
 QY 59 -----LEKLSSRYQDQAVLFIIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGV 110

Db 61 YFEGSFALERPSPSRMKNVRFISQMTSHTAGIYTCFYQSGELWSKSNPLKLVVTGL 120
 QY 111 FAKPSLSAQPGPAVSSGGDVTLCQOTRYGDFDQALYKEGDPAPYKPERWYRASFPITV 170
 Db 121 YDTPNLWVYPRPEVTLGENTVTFQCLKTATSKFLLKERGSNHIONKYGNIOAEFFMGPV 180
 QY 171 TAAHSGTYRCYSRSSRDPYLWSAPSDPLELVVTGTSVTPSRLETPPSSVA--EFSATA 228
 Db 181 TRAHRTYRC--FGSYNDYAWSPPEVTLITGGVENSLSAPTDPTSSLDYWEFDLSTN 238
 QY 229 ELTVSFTNKVFTTSTRSITTSKESDSPAGPARQYTKGNLVIRICIGAVILIILAGFLA 288
 Db 239 E-----SGLQKDS-----AFWDHTTQNLIRIGLACIILITLVWLLT 274
 QY 289 EDHSRRK 296
 Db 275 EDWLSRRK 282
 RESULT 10
 Q8MJZ5 PRELIMINARY; PRT; 645 AA.
 AC Q8MJZ5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor b.
 GN LIRB.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21555186; PubMed=11698452;
 RA Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,
 RA Shum B.P., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 reveals framework and rapidly evolving genes."
 RL J. Immunol. 167:5786-5794 (2001).
 DR EMBL; AF383166; AAL31875.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR Immunoglobulin domain; Receptor.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 645 AA; 69898 MW; A032ED6BDE8FB144 CRC64;
 Query Match 25.5%; Score 455; DB 6; Length 645;
 Best Local Similarity 39.8%; Pred. No. 3.4e-31;
 Matches 121; Conservative 36; Mismatches 115; Indels 32; Gaps 10;
 QY 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLOALPSSLVLEKPVTLRCQGPVVD--L 56
 Db 1 MTPTLTVLICLGLSLGPRTHVQAGTLPKPIRAEPDSVITQGSPTVTLRCQGSLEAQNHL 60
 QY 57 YRLEKLSS--SRYQDQAV---LFIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGV 110
 Db 61 YREKKSASWIKRIQPLVKKGQFPISITWEHAGRYCQYYSQWSEPSDPELVVTGA 120
 QY 111 FAKPSLSAQPGPAVSSGGDVTLCQOTRYGDFDQALYKEGDPAPYKPERWYRASFPITV 161
 Db 121 YSKPTLSALPSPVTVSGNVTLQCGSLAFGGFTLCKEGED---EHPQCVNSQSHLGS 177
 QY 162 RASPTITVTAHSGTTRCYFSRDRDYLWSASPDPLELVVTGTSVTPSRLETPPSSVA 221
 Db 178 WAIFSVGFVSPSRWRYCYGYDMSPPVMSPLSGLELLVPGVSKKPS--LSVQPGPVVA 236
 QY 222 EFSATAEL--TVSFTNKVFTTSTRSITTSKESDSPAGPARQYTKGNLVIRI----- 273

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Db 237 PGBILTLQCGSDGVYDRFVLYKEGEDFLQIPGRQPQ-AGLSQANFTLGPVSRSHGQYR 295
QY 274 CLGA 277
Db 296 CCGA 299

RESULT 11
Q80UY6 PRELIMINARY; PRT; 323 AA.
AC Q80UY6;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Ncr1 protein (fragment).
GN NCR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N. TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N. TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042788; AAH42788.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
FT NON_TER
FT 1
SQ SEQUENCE 323 AA; 37021 MW; B427A0B46AB9E90A CRC64;

Query Match 25.3%; Score 452; DB 11; Length 323;
Best Local Similarity 37.9%; Pred. No. 2.5e-31;
Matches 116; Conservative 36; Mismatches 116; Indels 38; Gaps 6;

QY 3 PPSPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYR--- 58
Db 1 PTLTALLCLGCLCSQRINTEKETLPKPIIWAKPSIMVTNGNSNIWCQGAQASAEYQLYF 60
QY 59 -----LEKLSRRYQDQAVLPIPAKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFA 112
Db 61 EGSFFALERKPSRSWNKVRFFISQMTSTAGTYTCFQSGELWSKSNPLKLVVTVGLYD 120
QY 113 KPSLSAQPGFAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTVA 172
Db 121 TPNLWVYPRPEVTLGENVTFFCQLKTATSKFFLLKRGSGNHQNKYGNIOAEFFMGPVTR 180
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QY 173 AHSGTYRCYFSGRDPVYLGAPSDLELVVTGTSVTPSRLPTRPPSSVA--EFSEATAEL 230
Db 181 AHGTYRC--FGSYNDYAMSFPEPVTLLITGGVENSFLAPTPTSSLDYWEFDLSTNE- 237
QY 231 TVSFYTKNVFTTETSRTSPKESDSPAGPARQYTYTKGNLVIRICLGAVILLIILAGFLAED 290
Db 238 -----SGLQKDS-----AFWDHTQNLIRIGLACIILITLVWLLTED 274
QY 291 WHSRK 296
Db 275 WLSRK 280

RESULT 12
O76016 PRELIMINARY; PRT; 287 AA.
AC O76016;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE NK receptor, isoform b.
GN NKP46.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=98401029; PubMed=9730896;
RA Pessino A., Sivori S., Bottino C., Malaspina A., Morelli L.,
RA Moretta L., Biassoni R., Moretta A.;
RT "Molecular cloning of NKP46: a novel member of the immunoglobulin
RT superfamily involved in triggering of natural cytotoxicity.";
RT J. Exp. Med. 188:953-960(1998).
DR EMBL; AJ006121; CAA06872.1; -.
DR HSSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR Receptor.
SQ SEQUENCE 287 AA; 32600 MW; 52EB1B062B35C1C4 CRC64;

Query Match 25.1%; Score 447.5; DB 4; Length 287;
Best Local Similarity 34.7%; Pred. No. 5.3e-31;
Matches 111; Conservative 41; Mismatches 105; Indels 63; Gaps 6;

QY 1 MSPSPPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYR 59
Db 1 MSTPLALLCVGLCLSORISAQOQTLPKPIWAEHPHFVPEKQVTCQGNYGAVYQL 60
QY 60 -----EKLSSRYQDQAVLPIPAKRSIAGRYCSYQNGSLWSLPSDQLE 104
Db 61 HFEGLFAVDPRKPPRINKVFP-----YIPDMSRMAGQYSCIYRVELWSEPSNLLD 114
QY 105 LVATGVFAKPSISAQPGPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRAS 164
Db 115 LVVTENYDPTLSVHPGPEVISEKVTFYCRDLTATSMFLLLKEGSSHVQGYGKQVAE 174
QY 165 PFIITVTAHSGTYRCYFSGRDPVYLGAPSDLELVVTGTSVTPSRLPTRPPSSVAEFS 224
Db 175 FPLGPVTTAHRCTYRC--FGSYNNHAWSPFSEPVKLLVTGDIENTS LAPEDP----- 224
QY 225 EATAELTVSFTKNVFTTETSRTSPKESDSPAGPARQYTYTKGNLVIRICLGAVILLIIL 284
Db 225 -----TFPDH-----ALWDHTAQNLRLRGLAFLVLVALV 253
QY 285 GFIAEDWHSRRKRLRHGRGA 304
Db 254 WFLVEDWLSRKTRERASTA 273
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RESULT 13
Q8MIZ8      PRELIMINARY;      PRT;      306 AA.
AC Q8MIZ8; 2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Nkp46v1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;
RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification
of Nkp46SD and Nkp30S.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035219; AAK63121.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
SQ SEQUENCE 306 AA; 34650 MW; 0106E4D3DB465B21 CRC64;

Query Match 24.8%; Score 443.5; DB 6; Length 306;
Best Local Similarity 35.6%; Pred. No. 1.3e-30;
Matches 114; Conservative 40; Mismatches 119; Indels 47; Gaps 6;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRL 59
DB 1 MSSTIRALLCLGLCLQSRIAPKQTLPIRAESTYMWPKKQATLCCQSGYGAVEYQL 60
QY 60 -----EKLSRRYQDQAVLFIIPAMKRSLAGRYCSYONGSLWSLPSDQLE 104
DB 61 HFEGLFAVERPKPPEIRINGVKFH-----IPMNSRKAGRYSCIYRVGELWSERSDLLD 114
QY 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYKEGDPAPYKNPWRWRAS 164
DB 115 LVVTEYDTPTLVHPGPEVTSGEKVTFCYGLDRTATSMFLLLKGRSRDVQRSYGVKQAE 174
QY 165 PPIITVTAHSGTYRCYCSFSSRDPYLSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFS 224
DB 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKLVLTGDIENSTSLAPDTP----- 224
QY 225 EATAELTVSFNTKVFTTTTSRSLTSPKESDSPAGPARQYVTKGNLVRLICLGAVILILA 284
DB 225 -----TFNSWDTCLLTR-----ETGLQDLALWDHTAQNLRLMGLAFILVALV 269

Query Match 24.8%; Score 443.5; DB 6; Length 306;
Best Local Similarity 35.6%; Pred. No. 1.3e-30;
Matches 114; Conservative 40; Mismatches 119; Indels 47; Gaps 6;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRL 59
DB 1 MSSTIRALLCLGLCLQSRIAPKQTLPIRAESTYMWPKKQATLCCQSGYGAVEYQL 60
QY 60 -----EKLSRRYQDQAVLFIIPAMKRSLAGRYCSYONGSLWSLPSDQLE 104
DB 61 HFEGLFAVERPKPPEIRINGVKFH-----IPMNSRKAGRYSCIYRVGELWSERSDLLD 114
QY 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYKEGDPAPYKNPWRWRAS 164
DB 115 LVVTEYDTPTLVHPGPEVTSGEKVTFCYGLDRTATSMFLLLKGRSRDVQRSYGVKQAE 174
QY 165 PPIITVTAHSGTYRCYCSFSSRDPYLSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFS 224
DB 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKLVLTGDIENSTSLAPDTP----- 224
QY 225 EATAELTVSFNTKVFTTTTSRSLTSPKESDSPAGPARQYVTKGNLVRLICLGAVILILA 284
DB 225 -----TFNSWDTCLLTR-----ETGLQDLALWDHTAQNLRLMGLAFILVALV 269

Query Match 24.8%; Score 443.5; DB 6; Length 306;
Best Local Similarity 35.6%; Pred. No. 1.3e-30;
Matches 114; Conservative 40; Mismatches 119; Indels 47; Gaps 6;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRL 59
DB 1 MSSTIRALLCLGLCLQSRIAPKQTLPIRAESTYMWPKKQATLCCQSGYGAVEYQL 60
QY 60 -----EKLSRRYQDQAVLFIIPAMKRSLAGRYCSYONGSLWSLPSDQLE 104
DB 61 HFEGLFAVERPKPPEIRINGVKFH-----IPMNSRKAGRYSCIYRVGELWSERSDLLD 114
QY 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYKEGDPAPYKNPWRWRAS 164
DB 115 LVVTEYDTPTLVHPGPEVTSGEKVTFCYGLDRTATSMFLLLKGRSRDVQRSYGVKQAE 174
QY 165 PPIITVTAHSGTYRCYCSFSSRDPYLSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFS 224
DB 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKLVLTGDIENSTSLAPDTP----- 224
QY 225 EATAELTVSFNTKVFTTTTSRSLTSPKESDSPAGPARQYVTKGNLVRLICLGAVILILA 284
DB 225 -----TFNSWDTCLLTR-----ETGLQDLALWDHTAQNLRLMGLAFILVALV 269
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RESULT 14
Q8MIZ9      PRELIMINARY;      PRT;      307 AA.
AC Q8MIZ9; 2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Nkp46.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;
RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification
of Nkp46SD and Nkp30S.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035218; AAK63120.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
SQ SEQUENCE 307 AA; 34752 MW; DA1B8A36D2F9A751 CRC64;

Query Match 24.8%; Score 443; DB 6; Length 307;
Best Local Similarity 35.9%; Pred. No. 1.4e-30;
Matches 115; Conservative 40; Mismatches 119; Indels 46; Gaps 7;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRL 59
DB 1 MSSTIRALLCLGLCLQSRIAPKQTLPIRAESTYMWPKKQATLCCQSGYGAVEYQL 60
QY 60 -----EKLSRRYQDQAVLFIIPAMKRSLAGRYCSYONGSLWSLPSDQLE 104
DB 61 HFEGLFAVERPKPPEIRINGVKFH-----IPMNSRKAGRYSCIYRVGELWSERSDLLD 114
QY 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYKEGDPAPYKNPWRWRAS 164
DB 115 LVVTEYDTPTLVHPGPEVTSGEKVTFCYGLDRTATSMFLLLKGRSRDVQRSYGVKQAE 174
QY 165 PPIITVTAHSGTYRCYCSFSSRDPYLSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFS 224
DB 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKLVLTGDIENSTSLAPDTP----- 227
QY 225 EATAELTVSFNTKVFTTTTSRSLTSPKESDSPAGPARQYVTKGNLVRLICLGAVILILA 284
DB 228 -----TDSWDTCLLTRETG-----LQKDL---ALWDHTAQNLRLMGLAFILVALV 270

Query Match 24.7%; Score 441.5; DB 6; Length 460;
Best Local Similarity 40.4%; Pred. No. 3.3e-30;
Matches 122; Conservative 37; Mismatches 116; Indels 27; Gaps 11;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRL 59
DB 1 MTFILTVLILGLSLGRTHVQAGTLPKPILWAEFGSVITQSGSVTLRCQGGQTQYRL 60
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2004, 18:12:38 ; Search time 60 Seconds
(without alignments)
1596.393 Million cell updates/sec

Title: US-09-610-118-3
Perfect score: 1786
Sequence: 1 MGSPFALFCLGLGRVPA.....KSHGGDGRQDVHSGRLCS 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	4 AAB61255	Aab61255 Human TAN
2	1786	100.0	339	6 ADA84105	Ada84105 Human GP6
3	1786	100.0	339	6 ABU11221	Abu11221 Human TAN
4	1782	99.8	339	4 AAB61273	Aab61273 Human TAN
5	1782	99.8	339	4 AAB61274	Aab61274 Human TAN
6	1782	99.8	339	4 AAB61275	Aab61275 Human TAN
7	1782	99.8	339	4 AAB61276	Aab61276 Human TAN
8	1782	99.8	339	6 ABU11239	Abu11239 Glycoprot
9	1782	99.8	339	6 ABU11240	Abu11240 Glycoprot
10	1782	99.8	339	6 ABU11241	Abu11241 Glycoprot
11	1782	99.8	339	6 ABU11242	Abu11242 Glycoprot
12	1770	99.1	339	4 AAB31668	Aab31668 Amino aci
13	1759	98.5	339	4 RAY72790	Ray72790 Human pla
14	1678	94.0	319	4 AAB61257	Aab61257 Mature hu
15	1678	94.0	319	4 AAB49403	Aab49403 Human gly
16	1678	94.0	319	6 ABU11223	Abu11223 Human TAN
17	1311	73.4	501	6 ABP72518	Abp72518 Immunoglo
18	1307.5	73.2	512	6 ABP72519	Abp72519 Glycoprot
19	1304	73.0	249	4 AAB61261	Aab61261 Human TAN
20	1304	73.0	249	4 ABU11227	Abu11227 Human TAN
21	1304	73.0	369	4 RAY72791	Ray72791 Human GPV
22	1122	62.8	313	4 AAB61265	Aab61265 Mouse TAN
23	1122	62.8	313	4 AAB61280	Aab61280 Mouse TAN
24	1122	62.8	313	6 ABU11246	Abu11246 Glycoprot
25	1122	62.8	313	6 ABU11231	Abu11231 Mouse TAN

26	1118	62.6	313	4 AAB61278	Aab61278 Mouse TAN
27	1118	62.6	313	4 AAB61277	Aab61277 Mouse TAN
28	1118	62.6	313	4 AAB61279	Aab61279 Mouse TAN
29	1118	62.6	313	6 ABU11245	Abu11245 Glycoprot
30	1118	62.6	313	6 ABU11243	Abu11243 Glycoprot
31	1118	62.6	313	6 ABU11244	Abu11244 Glycoprot
32	1080.5	60.5	292	4 AAB61267	Aab61267 Mature mo
33	1080.5	60.5	292	6 ABU11233	Abu11233 Mouse TAN
34	1078	60.4	203	5 AAO19266	Aao19266 Human pla
35	937	52.5	267	4 AAB61268	Aab61268 Mouse TAN
36	937	52.5	267	6 ABU11234	Abu11234 Mouse TAN
37	498	27.9	447	6 ABUC09631	Abuc09631 Human mon
38	498	27.9	447	6 ABU79089	Abu79089 Immunoglo
39	498	27.9	448	2 AAW82551	Aaw82551 Human LIR
40	498	27.9	448	3 AAW53463	Aaw53463 Human gp4
41	498	27.9	448	3 AAB04176	Aab04176 Leukocyte
42	492	27.5	472	2 AAW69234	Aaw69234 FcR-IV pr
43	491	27.5	447	6 ABR39440	Abr39440 Human GEN
44	477	26.7	289	2 AAW82548	Aaw82548 Human LIR
45	477	26.7	289	3 AAB04173	Aab04173 Leukocyte

ALIGNMENTS

RESULT 1
AAB61255
ID AAB61255 standard; protein; 339 AA.

XX AAB61255;
XX AC
XX 04-APR-2001 (first entry)
XX DT

XX DE Human TANGO 268 protein.

XX DX Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX OS Homo sapiens.

XX XX
XX PN WO200100810-A1.
XX PD 04-JAN-2001.

XX PF 30-JUN-2000; 2000WO-US018152.
XX PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.

XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Busfield SJ, Vilelale J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
DR WPI: 2001-080877/09.
DR N-PSDB; AAF29470, AAF29471.

XX XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.
XX XX Claim 8; Fig 1A; 227pp; English.

XX CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 CC XX
 SQ Sequence 339 AA;

Query Match 100.0%; Score 1786; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 9.9e-142;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLE 60
 DB 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 DB 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 180
 DB 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 180
 QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFT 240
 DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFT 240
 QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAIVLIIILAGFLAEDWHSRRKRLRH 300
 DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAIVLIIILAGFLAEDWHSRRKRLRH 300
 QY 301 RGRVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
 DB 301 RGRVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 2

ADA84105
 ID ADA84105 standard; protein; 339 AA.
 XX ADA84105;
 AC ADA84105;
 XX 20-NOV-2003 (first entry)
 DT Human GP6 protein.
 XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
 KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
 KW vaccine.
 XX Homo sapiens.
 OS
 XX WO2002103028-A2.
 PN 27-DEC-2002.
 PD 30-MAY-2002; 2002WO-IB004189.
 XX 30-MAY-2001; 2001US-0293999P.
 PR 22-OCT-2001; 2001US-0330457P.
 PR 19-FEB-2002; 2002US-0357144P.
 XX (BIOW-) BIOMEDICAL CENT.
 PA Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LI;
 PI
 XX

DR WPI: 2003-175241/17.
 DR N-PSDB; ADA84104.
 XX
 PT Determining if a nucleic acid is a marker for a phenotype/cell type of
 PT interest, by global comparison of expressed sequence tags known to be
 PT expressed in the phenotype/cell type with all ESTs expressed in normal
 PT tissue.
 XX
 PS Claim 29; Page 493-495; 516pp; English.
 XX
 CC The invention relates to a novel method for determining if a nucleic acid
 CC is a marker for a predetermined phenotype/cell type of interest from a
 CC biological species. The method comprises performing a global comparison
 CC of a group of expressed sequence tags (ESTs) known to be expressed in the
 CC phenotype/cell type of interest with all ESTs expressed in normal tissue
 CC in order to identify ESTs that are preferentially expressed in the
 CC phenotype/cell of interest. A method of the invention is useful for
 CC determining whether a nucleic acid is a marker for a predetermined
 CC phenotype or cell type of interest from a biological species, preferably
 CC Arabidopsis or human. The cell type of interest is an abnormal cell such
 CC as a tumour cell, and the predetermined phenotype is a stress-induced
 CC phenotype such as hyperosmotic stress or high salt conditions. A method
 CC of the invention is also useful for determining the progression of colon
 CC cancer in a human, for detecting a tumour cell, and for regulating or
 CC preventing the growth of a tumour cell. An antibody of the invention is
 CC useful for detecting the absence or presence of peptides encoded by
 CC tumour-associated markers. A polypeptide of the invention is useful as an
 CC immunogen for vaccinating an animal. The present sequence represents a
 CC tumour-associated antigen of the invention.
 XX
 SQ Sequence 339 AA;

Query Match 100.0%; Score 1786; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 9.9e-142;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLE 60
 DB 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 DB 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 180
 DB 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 180
 QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFT 240
 DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAFSEATAELTVSFTNKVFT 240
 QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAIVLIIILAGFLAEDWHSRRKRLRH 300
 DB 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAIVLIIILAGFLAEDWHSRRKRLRH 300
 QY 301 RGRVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
 DB 301 RGRVORPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 3

ABU11221
 ID ABU11221 standard; protein; 339 AA.
 XX ABU11221;
 AC ABU11221;
 XX 06-FEB-2003 (first entry)
 DT Human TANGO 268 protein.
 XX
 DE Human; mouse; variable heavy; VH; antigen; cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;

TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary stenosis; atherosclerosis; immunological disorder; cerebral vascular disease; embryonic disorder; liver disorder; venous thromboembolism disease.

OS Homo sapiens.

XX WO200280968-A1.

PN 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W; Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

DR P-PSDB; ABX17291, ABX17290.

XX Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Disclosure; Fig 1; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically binding to a TANGO 268 (also referred as glycoprotein VI (GpVI)) antigen. The antibodies of the invention act to decrease or block TANGO 268 binding to extracellular matrix components, or as a Collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, morphology, differentiation and/or function of megakaryocytes and platelets, including during development e.g. embryogenesis, modulating leukocyte-platelet and platelet-endothelium interactions in inflammation and/or thrombosis, and modulating platelet aggregation and degranulation. They are also useful for modulating disorders associated with abnormal or aberrant megakaryocyte and/or platelet proliferation, migration, morphology, differentiation and/or function, e.g. bleeding disorders such as thrombocytopaenia. Other diseases which may be modulated by these antibodies are thrombotic disorders, cerebral vascular diseases (e.g. stroke and ischaemia) venous thromboembolism diseases (e.g. diseases involving leg swelling, pain and ulceration, pulmonary embolism, etc); coronary diseases (e.g. cardiovascular diseases including angina pectoris, myocardial infarction, coronary stenosis, atherosclerosis, etc); immunological disorders, developmental disorders, embryonic disorders, liver disorders, cerebral vascular diseases, venous thromboembolism disease, coronary diseases, and metastatic cancers. The antibodies of the invention only causes a transient decrease in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art methods. The present sequence represents a protein sequence used to create the antibodies of the invention

SQ Sequence 339 AA;

Query Match 100.0%; Score 1786; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No 9.9e-142;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPATLFCGLGCRVPAQSGPLRPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
 |||||
 Db 1 MSPSPATLFCGLGCRVPAQSGPLRPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60

QY 61 KLSRRYQDAVLFTPAMKRSAGRYRCSYQNGSLWSLPSDQLLELVATGVFAKPSLSAQP 120
 |||||
 Db 61 KLSRRYQDAVLFTPAMKRSAGRYRCSYQNGSLWSLPSDQLLELVATGVFAKPSLSAQP 120
 |||||
 QY 121 GRAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKKNPERWYRASFFLIITVTAHSGTYRC 180
 |||||
 Db 121 GRAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKKNPERWYRASFFLIITVTAHSGTYRC 180
 |||||
 QY 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
 |||||
 Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
 |||||
 QY 241 TETSRSIITTSKESDSPAGPARQYTKGNLVRLICLGAVILILAGFLAEDWHSRKRLRH 300
 |||||
 Db 241 TETSRSIITTSKESDSPAGPARQYTKGNLVRLICLGAVILILAGFLAEDWHSRKRLRH 300
 |||||
 QY 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
 |||||
 Db 301 RGRAVORPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
 |||||

RESULT 4
 AAB61273
 ID AAB61273 standard; protein; 339 AA.
 XX AAB61273;
 XX 04-APR-2001 (first entry)
 DT Human TANGO 268-related protein #1.
 DE Human, TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.
 XX Homo sapiens.
 OS WO200100810-A1.
 PN 04-JAN-2001.
 PD 30-JUN-2000; 2000WO-US018152.
 XX 30-JUN-1999; 99US-00345468.
 PR 06-DEC-1999; 99US-00454824.
 PR 14-FEB-2000; 2000US-00503387.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W; Gill DS, Qian MD, Kingsbury G;
 PI WPI; 2001-080877/09.
 DR N-PSDB; AAF29484.
 DR New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.
 PT Disclosure; Page 213-214; 227pp; English.
 XX The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GpVI), also called TANGO 268. The GpVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.

CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver
 XX
 XX
 SQ Sequence 339 AA;

Query Match 99.8%; Score 1782; DB 4; Length 339;
 Best Local Similarity 99.7%; Pred. No. 2.2e-141;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSPSPALFCGLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGPGVDLYRLE 60
 Db 1 MSPSPALFCGLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGPGVDLYRLE 60
 QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 Db 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
 QY 121 GRAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPIITVTAHSGTYRC 180
 Db 121 GRAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPIITVTAHSGTYRC 180
 QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSAEATLTVSFTNKVFT 240
 Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSAEATLTVSFTNKVFT 240
 QY 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
 Db 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300
 QY 301 RGRVORPLPPLPPLPQTRKSHGGQGGQGVHSGRLCS 339
 Db 301 RGRVORPLPPLPPLPQTRKSHGGQGGQGVHSGRLCS 339

RESULT 5

AAB61274
 ID AAB61274 standard; protein; 339 AA.

XX AAB61274;

DT 04-APR-2001 (first entry)

DE Human TANGO 268-related protein #2.

XX Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.

OS Homo sapiens.

XX WO200100810-A1.

XX 04-JAN-2001.

PF 30-JUN-2000; 2000WO-US018152.

XX 30-JUN-1999; 99US-00345468.

PR 06-DEC-1999; 99US-00454824.

PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villielal J, Jandrot-Perrus M, Vainchencker W;

PI Gill DS, Qian MD, Kingsbury G;

XX

DR WPI; 2001-080877/09.
 XX N-PSDB; AAF29485.

XX New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating and
 PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
 PT disorders.

XX Disclosure; Page 214-215; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders (e.g.
 CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
 CC immunological diseases (e.g. platelet disorder) and embryonic liver
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia
 CC following angioplasty and metastatic cancers, especially of the colon and
 CC liver

XX Sequence 339 AA;

Query Match 99.8%; Score 1782; DB 4; Length 339;
 Best Local Similarity 99.7%; Pred. No. 2.2e-141;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCGLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGPGVDLYRLE 60

Db 1 MSPSPALFCGLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGPGVDLYRLE 60

QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120

Db 61 KLSRRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120

QY 121 GRAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPIITVTAHSGTYRC 180

Db 121 GRAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKPNRWYRASFPIITVTAHSGTYRC 180

QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSAEATLTVSFTNKVFT 240

Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSAEATLTVSFTNKVFT 240

QY 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300

Db 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH 300

QY 301 RGRVORPLPPLPPLPQTRKSHGGQGGQGVHSGRLCS 339

Db 301 RGRVORPLPPLPPLPQTRKSHGGQGGQGVHSGRLCS 339

RESULT 6

AAB61275

ID AAB61275 standard; protein; 339 AA.

XX AAB61275;

XX 04-APR-2001 (first entry)

XX Human TANGO 268-related protein #3.

XX Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.


```
XX OS Homo sapiens.
XX PN WO200100810-A1.
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018152.
XX PR 30-JUN-1999; 99US-00345468.
XX PR 06-DEC-1999; 99US-00454824.
XX PR 14-FEB-2000; 2000US-00503387.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Busfield SJ, Vilelial J, Jandrot-Perrus M, Vainchencker W;
XX PI Gill DS, Qian MD, Kingsbury G;
XX DR WPI; 2001-080877/09.
XX DR N-PSDB; AAF29486.
XX PT New genes encoding human platelet-expressed collagen receptor,
XX PT glycoprotein VI, and its modulators, useful for preventing, treating and
XX PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
XX PT disorders.
XX PS Disclosure; Page 216; 227pp; English.
XX CC The present sequence is given in a specification relating to an isolated
XX CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX CC and polypeptides and their modulators, e.g. antisense nucleic acids,
XX CC ribozymes and antibodies, are useful for preventing, treating and
XX CC diagnosing disorders associated with aberrant expression or activity of
XX CC GPVI. These disorders include bleeding disorders (e.g.
XX CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
XX CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
XX CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
XX CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
XX CC immunological diseases (e.g. platelet disorder) and embryonic liver
XX CC disorders. Preferably they are used to prevent acute cardiac ischaemia
XX CC following angioplasty and metastatic cancers, especially of the colon and
XX CC liver.
XX PS Sequence 339 AA;
XX CC Query Match 99.8%; Score 1782; DB 4; Length 339;
XX CC Best Local Similarity 99.7%; Pred. No. 2.2e-141;
XX CC Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDLYRLE 60
DB 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDLYRLE 60
QY 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGVFAKPSLSAQP 120
DB 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPVSSGGDVTLCOTRYGDFQALYKEGDPAPYKPNRWYASFPIITVTAHSGTYRC 180
DB 121 GPVSSGGDVTLCOTRYGDFQALYKEGDPAPYKPNRWYASFPIITVTAHSGTYRC 180
QY 181 YFSRRDPYLWASDPLELVVTGTSVTPSRKLPTEPPSSVAHFSEATAELTVSFTNKVFT 240
DB 181 YFSRRDPYLWASDPLELVVTGTSVTPSRKLPTEPPSSVAHFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTTSPKESDSDPAGPARQYTTGNLVIRICLGAVILLIILAGFLAEDWHSRKRLRH 300
DB 241 TETSRSTTSPKESDSDPAGPARQYTTGNLVIRICLGAVILLIILAGFLAEDWHSRKRLRH 300
QY 301 RGRAVQRLPPLPPLPOTRKRSHGGDGRQDVHSGRLCS 339
DB 301 RGRAVQRLPPLPPLPOTRKRSHGGDGRQDVHSGRLCS 339
```

RESULT 7

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AAB61276
ID AAB61276 standard; protein; 339 AA.
XX AC AAB61276;
XX DT 04-APR-2001 (first entry)
XX DE Human TANGO 268-related protein #4.
XX KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
XX KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX KW platelet membrane glycoprotein receptor; bleeding disorder;
XX KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX KW cancer.
XX OS Homo sapiens.
XX PN WO200100810-A1.
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018152.
XX PR 30-JUN-1999; 99US-00345468.
XX PR 06-DEC-1999; 99US-00454824.
XX PR 14-FEB-2000; 2000US-00503387.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Busfield SJ, Vilelial J, Jandrot-Perrus M, Vainchencker W;
XX PI Gill DS, Qian MD, Kingsbury G;
XX DR WPI; 2001-080877/09.
XX DR N-PSDB; AAF29487.
XX PT New genes encoding human platelet-expressed collagen receptor,
XX PT glycoprotein VI, and its modulators, useful for preventing, treating and
XX PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
XX PT disorders.
XX PS Disclosure; Page 217; 227pp; English.
XX CC The present sequence is given in a specification relating to an isolated
XX CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX CC and polypeptides and their modulators, e.g. antisense nucleic acids,
XX CC ribozymes and antibodies, are useful for preventing, treating and
XX CC diagnosing disorders associated with aberrant expression or activity of
XX CC GPVI. These disorders include bleeding disorders (e.g.
XX CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
XX CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
XX CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
XX CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
XX CC immunological diseases (e.g. platelet disorder) and embryonic liver
XX CC disorders. Preferably they are used to prevent acute cardiac ischaemia
XX CC following angioplasty and metastatic cancers, especially of the colon and
XX CC liver.
XX PS Sequence 339 AA;
XX CC Query Match 99.8%; Score 1782; DB 4; Length 339;
XX CC Best Local Similarity 99.7%; Pred. No. 2.2e-141;
XX CC Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDLYRLE 60
DB 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLDLYRLE 60
QY 61 KLSRRYQDQAVLFIPAMKSLAGRYCSYQNGSLWSLPDQLELVATGVFAKPSLSAQP 120
```

Db 61 KLSRSSYQDAVLFIIPAMKRSAGRYRCSYQNGSLWSPSDQLELVATGVFAKPSLSAQF 120
QY 121 GPAVSSGGDVTLQCTRYGFDQFALYKGDPAKYKPERWYRASFPIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLQCTRYGFDQFALYKGDPAKYKPERWYRASFPIITVTAHSGTYRC 180
QY 181 YFSSRDPLYWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YFSSRDPLYWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLADWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLADWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

RESULT 8

ABU11239
ID ABU11239 standard; protein; 339 AA.

XX AC ABU11239;

XX DT 06-FEB-2003 (first entry)

XX DE Glycoprotein VI associated protein sequence #1.

XX KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.

XX OS Homo sapiens.

XX FN WO200280968-A1.

XX PD 17-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011122.

XX PR 09-APR-2001; 2001US-00829495.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX PI Gill DS, Qian DM, Kingsbury G;

XX DR WPI; 2003-058477/05.

XX PT Novel substantially purified antibody immunospecifically binding to TANGO
PT 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX PS Disclosure; Page 222-223; 236pp; English.

XX CC This invention relates to a novel purified antibody comprising a variable
CC heavy (VH) complementarity determining region (CDR1, VH CDR2 or VH CDR3;
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC The antibodies of the invention act to decrease or block TANGO 268
CC binding to extracellular matrix components, or as a Collagen or platelet
CC release and aggregation blocker. The antibodies of the invention are
CC useful for modulating proliferation, migration, morphology,

CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degranulation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such
CC as thrombocytopenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC protein sequence used to create the antibodies of the invention
XX SQ Sequence 339 AA;

Query Match 39.8%; Score 1782; DB 6; Length 339;

Best Local Similarity 99.7%; Pred. No. 2.2e-141;

Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPATLFCGLGCLGRVPAQSGPLPKPSLQALPSLVLEKPVTLRCOGPGVDLYRLE 60

Db 1 MSPSPATLFCGLGCLGRVPAQSGPLPKPSLQALPSLVLEKPVTLRCOGPGVDLYRLE 60

QY 61 KLSRSSYQDAVLFIIPAMKRSAGRYRCSYQNGSLWSPSDQLELVATGVFAKPSLSAQF 120

Db 61 KLSRSSYQDAVLFIIPAMKRSAGRYRCSYQNGSLWSPSDQLELVATGVFAKPSLSAQF 120

QY 121 GPAVSSGGDVTLQCTRYGFDQFALYKGDPAKYKPERWYRASFPIITVTAHSGTYRC 180

Db 121 GPAVSSGGDVTLQCTRYGFDQFALYKGDPAKYKPERWYRASFPIITVTAHSGTYRC 180

QY 181 YFSSRDPLYWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKVFT 240

Db 181 YFSSRDPLYWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKVFT 240

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLADWHSRRKRLRH 300

Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLADWHSRRKRLRH 300

QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

Db 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

RESULT 9

ABU11240

ID ABU11240 standard; protein; 339 AA.

XX AC ABU11240;

XX DT 06-FEB-2003 (first entry)

XX DE Glycoprotein VI associated protein sequence #2.

XX KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.

RESULT 12
AAB31668
ID AAB31668 standard; protein; 339 AA.
AC AAB31668;
XX
XX 30-APR-2001 (first entry)
DE Amino acid sequence of a human protein having a hydrophobic domain.
XX
XX Human; hydrophobic protein; secretory protein; membrane protein; sepsis;
KW tumour inhibition; immune deficiency; autoimmune disorder; anaemia; burn;
KW infectious disease; cancer; ulcer; periodontal disease; coagulation;
KW Parkinson's disease; fertility; immune response; thrombosis.
XX
XX Homo sapiens.
XX
XX WO200104297-A2.
FN
XX
XX 18-JAN-2001.
XX
XX 16-JUN-2000; 2000WO-JP003942.
XX
XX 08-JUL-1999; 99JP-00194359.
PR
XX (SAGA) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T;
XX
XX WPI; 2001-103081/11.
DR
XX N-PSDB; AAF25158, AAF25168.
XX
XX Isolated human proteins and polynucleotides are used in research and have
PT activities including cell proliferation/differentiation activity, immune
PT stimulating activity and receptor/ligand activity.
XX
XX Claim 1; Page 88-90; 151pp; English.
XX
XX The present sequence represents a human protein with hydrophobic domains.
CC The protein possesses a hydrophobic domain and so is a secretory protein
CC or a membrane protein. The protein is used as an antigen to prepare
CC antibodies. The polynucleotide sequence is useful as a source of probes
CC for genetic diagnosis. It is also useful for producing the protein in
CC large quantities and for gene therapy. The eukaryotic cells are used for
CC detecting the receptors or ligands corresponding to the protein and for
CC detecting small novel pharmaceuticals. The antibodies are also used for
CC detection, quantification and purification of the proteins. Both the
CC protein and polynucleotide may be used in research or as nutritional
CC sources or supplements. The protein may have cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, hematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity and tumour inhibition activity. It may therefore be used to
CC treat immune deficiencies resulting from autoimmune disorders or
CC infectious diseases, cancer, sepsis, anaemias, burns and ulcers,
CC periodontal disease, Parkinson's disease, induce fertility, improve
CC immune response and enhance coagulation or inhibit thrombosis
XX
XX Sequence 339 AA;
SQ
Query Match 99.1%; Score 1770; DB 4; Length 339;
Best Local Similarity 99.1%; Pred. No. 2.2e-140;
Matches 336; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Qy 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120

Db 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Qy 121 GPVSSGGDVTLLQCQTRYGFDQFALYKEGDPAPYKPNRWYRASFFPIITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLLQCQTRYGFDQFALYKEGDPAPYKPNRWYRASFFPIITVTAHSGTYRC 180
Qy 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEPSEATAELTVSFTNEVFT 240
Qy 241 TETSRITTSKESDSDPAGPARQYTKGNLVRTICLGVAVIILLAGFLAEDWHRRKRLRH 300
Db 241 TETSRITTSKESDSDPAGPARQYTKGNLVRTICLGVAVIILLAGFLAEDWHRRKRLRH 300
Qy 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
RESULT 13
AA72790
ID AAY72790 standard; protein; 339 AA.
XX
XX AAY72790;
XX
XX 31-MAY-2001 (first entry)
XX Human platelet membrane glycoprotein VI (GPVI).
XX Human platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23 /label= Signal peptide
FT Protein 24..339 /note= "Mature platelet membrane glycoprotein VI (GPVI) protein"
FT Domain 24..269 /label= Extracellular_domain
FT Misc-difference 74 /note= "Encoded by TTC"
FT Misc-difference 100 /note= "Encoded by AAC"
FT Misc-difference 114 /note= "Encoded by CCC"
FT Misc-difference 166 /note= "Encoded by CCC"
XX
XX WO200116321-A1.
XX
XX 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US023975.
XX
XX 01-SEP-1999; 99US-0152197P.
XX 08-OCT-1999; 99US-0158251P.
XX
XX (SAKA) OTSUKA PHARM CO LTD.
XX
XX Tandon N, Sun B, Nakamura T, Yamamoto N;
XX WPI; 2001-226691/23.
DR N-PSDB; AAD02855.
XX
XX Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its variant,
PT useful for treating a vascular disease and reducing platelet activation.
XX
XX Disclosure; Fig 3; 74pp; English.
PS

XX The present sequence is a human platelet membrane glycoprotein VI (GPVI).
CC The medicament comprising GPVI is useful for treating vascular disease,
CC and for reducing platelet activation which involves contacting platelets
CC with the medicament. The extracellular portion of GPVI is used
CC therapeutically to attenuate platelet activation and aggregation and to
CC treat thrombosis and other vascular diseases. Antibodies generated
CC against GPVI are used as research and immunotherapeutic agents
XX
SQ Sequence 339 AA;
Query Match 98.5%; Score 1759; DB 4; Length 339;
Best Local Similarity 99.1%; Pred. No. 1.9e-139;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIIPAMKRLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQP 120
Db 61 KLSRRYQDQAVLFIIPAMKRLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQTRYGFDQALYKEGDPAPYKNPWRWYRASFPIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGFDQALYKEGDPAPYKNPWRWYRASFPIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVGTSTVTPSRLETPPSSVAEFSSEATAELTVSFNKNVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVGTSTVTPSRLETPPSSVAEFSSEATAELTVSFNKNVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPPLPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPPLPLPQTRKSHGGQDGRQDVHSRGLCS 339
RESULT 14
AAB61257
ID AAB61257 standard; protein; 319 AA.
XX
AC AAB61257;
XX
DT 04-APR-2001 (first entry)
XX
DE Mature human TANGO 268 protein.
XX
KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200100810-A1.
XX
PD 04-JAN-2001.
XX
FF 30-JUN-2000; 2000WO-05018152.
XX
PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Villelail J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;

XX WPI; 2001-080877/09.
DR New genes encoding human platelet-expressed collagen receptor.
XX
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.
XX
PS Disclosure; Fig 2; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders (e.g.
CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
CC immunological diseases (e.g. platelet disorder) and embryonic liver
CC disorders. Preferably they are used to prevent acute cardiac ischaemia
CC following angioplasty and metastatic cancers, especially of the colon and
CC liver
XX
SQ Sequence 319 AA;
Query Match 94.0%; Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRRYQDQAVLFIIPAMKR 80
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRRYQDQAVLFIIPAMKR 60
QY 81 SLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQP GPAVSSGGDVTLCQTRYGF 140
Db 61 SLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQP GPAVSSGGDVTLCQTRYGF 120
QY 141 DOFALYKEGDPAPYKNPWRWYRASFPIITVTAHSGTYRCYCFSSRDPLYMSAPSDPLEL 200
Db 121 DOFALYKEGDPAPYKNPWRWYRASFPIITVTAHSGTYRCYCFSSRDPLYMSAPSDPLEL 180
QY 201 VVTGTSVTPSRLETPPSSVAEFSSEATAELTVSFNKNVTTTTSRITTSPKESDSPAG 260
Db 181 VVTGTSVTPSRLETPPSSVAEFSSEATAELTVSFNKNVTTTTSRITTSPKESDSPAG 240
QY 261 ARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRRKRLRHGRAVORPPLPLPQTRK 320
Db 241 ARQYTTKGNLVRICLGAVILIIILAGFLAEDWHSRRKRLRHGRAVORPPLPLPQTRK 300
QY 321 SHGGQDGRQDVHSRGLCS 339
Db 301 SHGGQDGRQDVHSRGLCS 319
RESULT 15
AAB49403
ID AAB49403 standard; protein; 319 AA.
XX
AC AAB49403;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human glycoprotein VI mature protein.
XX
DE Human; thrombolytic; cardiant; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein; platelet activation;
KW platelet-collagen interaction; thrombotic disorder;
KW cardiovascular disorder.
XX
OS Homo sapiens.

XX WO200068377-A1.
XX 16-NOV-2000.
XX 25-APR-2000; 2000WO-EP003683.
XX 07-MAY-1999; 99EP-00109094.
XX (MERE) MERCK PATENT GMBH.
XX Clemetson KJ;
XX WPI; 2001-007394/01.
XX N-PSDB; AAC83980.
XX Recombinant human glycoprotein VI, useful for treating thrombotic,
XX cardiovascular diseases or platelet-collagen interactions.
XX Claim 5; Fig 1; 27pp; English.
XX The present sequence is human glycoprotein VI (GPVI) mature protein. GPVI
XX is a platelet membrane glycoprotein which forms a complex together with
XX the Fcgamma common subunit, which is critical for platelet activation in
XX response to collagen. GPVI is useful as a screening tool for detecting
XX specific inhibitors of platelet-collagen interactions, and as a marker
XX for platelet age and platelet exposure to thrombotic and cardiovascular
XX disorders. GPVI is also useful for the manufacture of medicaments in the
XX therapeutic field of thrombotic and cardiovascular events, and disorders
XX related to platelet-collagen interactions
XX Sequence 319 AA;
SQ
Query Match 94.0%; Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 QSGELPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLYRLEKLSRRYQDQAVLFIPAMKR 80
Db 1 QSGELPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLYRLEKLSRRYQDQAVLFIPAMKR 60
Qy 81 SLAGRYRCSYQNGSLWSLPSDLELVATGVFAKPSLQAQPGPAVSSGGDVTLCQOTRYGF 140
Db 61 SLAGRYRCSYQNGSLWSLPSDLELVATGVFAKPSLQAQPGPAVSSGGDVTLCQOTRYGF 120
Qy 141 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYCFSSRDPYLWSAFSDPLEL 200
Db 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYCFSSRDPYLWSAFSDPLEL 180
Qy 201 VVTGTSVTPSLPTEPPSSVAERSEAEALTVSTNKVFTTETSRITTSFKESDSPAGP 260
Db 181 VVTGTSVTPSLPTEPPSSVAERSEAEALTVSTNKVFTTETSRITTSFKESDSPAGP 240
Qy 261 ARQYTTKGNLVRI CLGAVILLI LAGFLAEDWHSRRKRLRHGRAVQRPPLPPLPQTRK 320
Db 241 ARQYTTKGNLVRI CLGAVILLI LAGFLAEDWHSRRKRLRHGRAVQRPPLPPLPQTRK 300
Qy 321 SHGQDGRQDVHSGRLCS 339
Db 301 SHGQDGRQDVHSGRLCS 319

Search completed: June 8, 2004, 18:14:30
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